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Phylogeny and taxonomy of the genera of Erysiphaceae, part 6: *Erysiphe* (the "*Microsphaera* lineage" part 2)

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ABSTRACT

This is the sixth contribution in a series devoted to the phylogeny and taxonomy of powdery mildews. This part includes our third treatment of the species of the genus *Erysiphe*. It continues the previous contribution on the phylogenetic-taxonomic assessment of the species belonging to the "*Microsphaera* lineage." Since this is a large lineage, we have split the treatment of the "*Microsphaera* lineage" into two parts. Phylogenetic trees based on rDNA are supplemented by sequences of additional markers (*CAM, GAPDH, GS, RPB2*, and *TUB*). The "*Erysiphe trifoliorum* complex" is a challenging group that belongs to the "*Microsphaera* lineage." Adequate clarification of this complex will be possible when additional worldwide multilocus sequence analyses are performed. The new species *Erysiphe acetosae, E. acmisponis, E. lathyrina, E. salmoniana*, and *E. santalicola* are described, and the new combinations *E. biuncinata* and *E. pavoniae* are introduced. Specimens of several species have been sequenced for the first time, particularly North American species, such as *Erysiphe caryae, E. ceanothi, E. juglandis-nigrae*, and *E. ravenelii. Erysiphe syringae* is lectotypified and 15 species names are epitypified in order to provide ex-epitype reference sequences. For other species, non-ex-type reference sequences are proposed for phylogenetic-taxonomic purposes. Ex-type sequences for *Erysiphe baptisiicola, E. sesbaniae, Microsphaera sydowiana, M. umbilici*, and *Oidium pavoniae* have been retrieved.

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INTRODUCTION

In the first five contributions to this series devoted to the phylogeny and taxonomy of powdery mildews (Ascomycota, Helotiales, Erysiphaceae), Bradshaw et al. (2022b, 2022c, 2023a, 2023b, 2023c) gave phylogenetic-taxonomic overviews of species within the genera *Golovinomyces, Neoerysiphe*, and *Cystotheca*, the "*Uncinula* lineage" of *Erysiphe*, and the first part of the "*Microsphaera* lineage." This sixth part is a continuation of the fifth part, in which the treatment of species belonging to the "*Microsphaera* lineage" (in the sense of Takamatsu et al. 2015a) is completed. This lineage encompasses two phylogenetically-taxonomically challenging species complexes, the oak powdery mildew complex and the "*Erysiphe trifoliorum* complex." The oak *Erysiphe* complex includes the *Erysiphe alphitoides* complex, which is an additional complicated subcomplex. The *E. alphitoides* complex has recently been revised by phylogenetic multilocus analyses that confirmed almost all previously proposed species based on host/morphological differences (Bradshaw et al. 2023c). The comprehensive taxonomic revision of *Erysiphe* species infecting oak species in North America required intensive multilocus examinations (Bradshaw et al. 2024a) and is thus not included in the current study. The "*Erysiphe trifoliorum* complex," included in this study, is an additional challenging assemblage with species insufficiently resolved in rDNA analyses (Bradshaw et al. 2022a; Darsaraei et al. 2024).

The current series summarizes available sequence data for all species of each treated powdery mildew genus and supplements these surveys with newly generated sequences. Whenever possible, we have tried to obtain ex-type sequences or, if not possible, to designate epitypes with ex-epitype sequences as reference sequences for phylogenetic-taxonomic purposes. In this series, we have put a special focus on North American specimens. Sequences generated for this project will contribute to a future monograph of North American powdery mildews. The resulting analyses are intended to serve as a framework for future

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phylogenetic-taxonomic studies of the "*Microsphaera* lineage" of the genus *Erysiphe*. The contributions in this series are meant to be phylogenetic-taxonomic overviews of powdery mildew genera and species.

MATERIALS AND METHODS

Sample collection.—Specimens were collected between 2018 and 2022 from throughout the United States. Newly collected specimens were deposited in the Farlow Herbarium (FH), Harvard University. Additional specimens were evaluated from the Farlow Herbarium and other American herbaria (TABLE 1).

Morphological examinations.—Morphological examinations were accomplished following Bradshaw et al. (2022b). Morphological examinations of the asexual morph of recently collected samples were accomplished by placing clear adhesive tape on powdery mildew colonies and setting the tape onto a slide containing a drop of water, or by doing hand sections and mounting them onto a slide with potassium hydroxide (KOH), Melzer's reagent (MLZ), or Congo red. Examinations of the sexual morph were accomplished by using a clean needle to mount chasmothecia onto a microscope slide containing water, KOH, MLZ, or Congo red. Photographs were taken of the slides using a compound microscope with an Olympus SC50 camera (Tokyo, Japan) and a Zeiss AX10 microscope (Oberkochen, Germany) or an Olympus BX40 microscope.

Sequencing.—DNA extractions were done using the Chelex method (Hirata and Takamatsu 1996; Walsh et al. 1991). Polymerase chain reaction (PCR) was carried out for the internal transcribed spacer (ITS) and partial nuc 28S rDNA D1–D2 regions (28S) region using the primer pair PM10/PM28R (Bradshaw and Tobin 2020). If PCR was unsuccessful, a nested approach was applied using the primers AITS (Bradshaw and Tobin 2020)/TW14 (Mori et al. 2000) followed by PM10/PM28R or the primers AITS/PM11 (Bradshaw and Tobin 2020) followed by PM10/PM2 (Cunnington et al. 2003). For the *CAM* (calmodulin), *GAPDH* (glyceraldehyde-3-phosphate dehydrogenase), *GS* (glutamine synthetase), and *RPB2* (second largest subunit of RNA polymerase II) regions, the primer pairs PMCAM1/PMCAM4R, PMGAPDH1/PMGAPDH3R, GSPM2/GSPM3R, and PMRpb2_4/PMRpb2_6 R were used (Bradshaw et al. 2022). If these were unsuccessful for the *GS* and *RPB2* regions, the following primers from Bradshaw et al. (2023b) were used: EGS1/EGS2R and ERPB2_3/ERPB2_7 R. If the above primer pair for the *GAPDH* region was unsuccessful, the following primers were generated and used: EGAPDH1 (5′-GCG TGT ACC TAC TTC TAA CG-3′)/EGAPDH2 (5′-GTT GAG CGA GAT TCC AGC C-3′). For the *TUB* (β-tubulin) region, the primers BTF5b/BTR7a (Ellingham et al. 2019) were used followed by ETUB2 and ETUB2R (Bradshaw et al. 2023a).

Phylogenetic analyses.—Four phylogenetic trees were constructed from the concatenated ITS+28S+*CAM*+*GAPDH*+*GS*+*RPB2*+*TUB* sequences (FIGS. 1–4). In addition, single-locus trees were constructed from all the newly generated sequences (SUPPLEMENTARY FIGS. 1–6). Sequences were aligned and edited using MUSCLE in MEGA11:Molecular Evolutionary Genetics Analysis 11 (Tamura et al. 2021). A GTR+G+I evolutionary model was used for phylogenetic analyses, as it is the most inclusive model of evolution and includes all other evolutionary models (Abadi et al. 2019). A fixed parameter-rich model (such as GTR+G+I) can be used in lieu of running a test to select the most suitable evolutionary model (Abadi et al. 2019). The phylogeny was inferred using Bayesian analysis of the combined loci using a Yule tree prior (Gernhard 2008) and a strict molecular clock, in the program BEAST 1.10.4 (Suchard et al. 2018). A single Markov chain Monte Carlo (MCMC) chain of 10^7 steps was run, with a burn-in of 10%. Posterior probabilities were calculated from the remaining 9000 sampled trees. A maximum clade credibility tree was produced using TreeAnnotator 1.10.4 (part of the BEAST package). Stationarity was confirmed by running the analysis multiple times, which revealed convergence between runs. The resulting tree was visualized using FigTree 1.3.1 (Rambaut 2009). A maximum likelihood analysis was accomplished using raxmlGUI (Silvestro and Michalak 2012) under the default settings with a GTR+G+I evolutionary model. Bootstrap analyses were conducted using 1000 replications (Felsenstein 1985).

RESULTS

Phylogenetic analyses.—Sequences obtained from the specimens were deposited in GenBank (TABLE 1). The phylogenetic analyses evaluated a total of 321 powdery mildew specimens collected from throughout the world. Of these 321 specimens, 131 were sequenced for the current study. A maximum clade credibility tree was constructed using Bayesian analyses from the combined ITS+28S+*CAM*+*GAPDH*+*GS*+*RPB2*+*TUB* (FIGS. 1–4; SUPPLEMENTARY FIG. 1) sequences. Posterior probabilities ≥90 are displayed followed by bootstrap values

Table 1. Lists of taxa, hosts, vouchers, collection localities, and GenBank accession numbers of the specimens examined in the current study.

Taxon	Host	Voucher*	Collection locality	ITS+28S	*CAM*	*GAPDH*	*GS*	*RPB2*	*TUB*	Notes
Erysiphe acetosae	*Rumex acetosa*	HAL 3542 F	Germany	PP681001	PP720915	PP720294	PP720547	PP720487	PP720070	Isotype
Erysiphe acmisponis	*Acmispon parviflorus*	FH01122099	USA: Washington	PP681081	PP720911	PP720310	PP720539	PP720417	PP719981	Holotype
Erysiphe acmisponis	*Acmispon parviflorus*	FH01122100	USA: California	PP681082	PP720912	PP720311	PP720570	PP720418	PP719982	
Erysiphe acmisponis	*Acmispon subpinnatus*	HMAS 54813	China	PP680985						
Erysiphe alphitoides	*Wisteria sinensis*	NCSLG24441	United Kingdom	PP680959			PP720736		PP720090	
Erysiphe astragali	*Astragalus glycyphyllus*	HAL 3356 F	Germany	MZ265151	PP720916	PP720312	PP720540	PP720491	PP720075	Epitype
Erysiphe astragali	*Astragalus glycyphyllus*	HAL 3358 F	Germany	MZ265150	PP720917	PP720313	PP720541	PP720493	PP720077	
Erysiphe azaleae	*Rhododendron occidentale*	FH00941230	USA: Washington	PP681030	PP720756	PP720129	PP720563	PP720399	PP719955	
Erysiphe azaleae	*Rhododendron* sp.	FH01131045	USA: Washington	PP680845	PP720755	PP720128	PP720679		PP720029	
Erysiphe baeumleri	*Vicia cracca*	HAL 3354 F	Germany	MZ265153	PP720928	PP720328	PP720659	PP720490	PP720073	
Erysiphe baeumleri	*Vicia cassubica*	HAL 3355 F	Germany	MZ265154	PP720919	PP720325	PP720572		PP720074	
Erysiphe baeumleri	*Vicia sylvatica*	HAL 3357 F	Germany	MZ265155	PP720929	PP720329	PP720564	PP720492	PP720076	
Erysiphe baeumleri	*Vicia sylvatica*	HAL 3360 F	Germany	MZ265152	PP720918	PP720324	PP720703	PP720494	PP720078	Epitype
Erysiphe baptisiicola	*Baptisia australis*	BPI 564440	USA: Connecticut	PP680994	PP720944	PP720276			PP719892	Holotype
Erysiphe begoniicola	*Begonia rex*	UW309	USA: Washington	PP680987						
Erysiphe berberidis	*Berberis thunbergii*	FH01131054	USA: Massachusetts	PP681005	PP720894		PP720530	PP720449	PP720030	
Erysiphe berberidis	*Mahonia aquifolium*	FH01131055	USA: Washington	PP681006	PP720895	PP720318	PP720701	PP720450	PP720031	
Erysiphe betae	*Beta vulgaris* subsp. *vulgaris*	FH01131056	USA:Washington	PP681003	PP720989	PP720296	PP720705	PP720451	PP720032	
Erysiphe betae	*Dysphania ambrosioides*	HAL 2240 F	India	PP681002						
Erysiphe biuncinata	*Hammamelis virginiana*	FH01122141	USA: Pennsylvania	PP681077	PP720967		PP720661	PP720420	PP719984	
Erysiphe biuncinata	*Hammamelis* sp.	FH01131011	USA: Massachusetts	PP681107	PP720966	PP720119	PP720670	PP720436	PP720015	
Erysiphe biuncinata	*Hammamelis* sp.	FH01131013	USA: Massachusetts	PP680963	PP720965		PP720663	PP720437	PP720016	
Erysiphe biuncinata	*Hammamelis virginiana*	FH01131019	USA: Delaware	PP681076	PP720968	PP720336	PP720567	PP720442	PP720021	
Erysiphe biuncinata	*Hammamelis virginiana*	FH01131024	USA: North Carolina	PP681078	PP720964	PP720337	PP720569	PP720444	PP720024	Epitype
Erysiphe caryae	*Carya ovata*	BPI 555642	USA: Wisconsin	PP681028	PP720903	PP720302	PP720556			
Erysiphe caryae	*Carya sulcata*	ILL00087800	USA: Indiana	PP681093	PP720904		PP720709			
Erysiphe caryae	*Carya alba*	ILL00087801	USA: Illinois	PP681029	PP720905	PP720303	PP720708	PP720499		Epitype
Erysiphe castaneae	*Castanea* sp.	FH01122123	USA: New York	PP680965						
Erysiphe castaneae	*Castanea dentata*	FH01122149	USA: Massachusetts	PP681075	PP720978	PP720299	PP720568	PP720422	PP719986	
Erysiphe castaneae	*Castanea dentata*	FH01122150	USA: Massachusetts	PP681106	PP720979	PP720300	PP720552	PP720423	PP719987	Epitype
Erysiphe castaneae	*Castanea dentata*	FH01122151	USA: Tennessee	PP680840	PP720976	PP720301	PP720673		PP719988	
Erysiphe castaneae	*Castanea dentata*	FLAS F 22882	USA: Florida	PP680964	PP720977					
Erysiphe castaneae	*Castanea visca*	NY00262037	USA: New York	PP680966	PP720980					
Erysiphe ceanothi	*Ceanothus americanus*	FH01122163	USA: Wisconsin	PP680846	PP720892	PP720126	PP720740		PP719989	Epitype
Erysiphe ceanothi	*Ceanothus americanus*	WIS F 0024260	USA: Wisconsin	PP680847	PP720893	PP720127	PP720711			
Erysiphe convolvuli	*Convolvulus* sp.	FH00941200	USA: Massachusetts	PP680997	PP720996	PP720308	PP720546	PP720395	PP719949	
Erysiphe convolvuli	*Convolvulus arvensis*	FH00941244	USA: Colorado	PP680998	PP720997	PP720309	PP720565	PP720400	PP719956	
Erysiphe diffusa	*Desmodium virudiflorum*	FH00965531	USA: Wisconsin	PP681009		PP720282	PP720737	PP720415	PP719974	Specimen originally determined as *Erysiphe diffusa* var. *elongata*
Erysiphe diffusa	*Desmanthus illinoensis*	FH00965542	USA: Missouri	PP681010						Holotype of *Erysiphe desmanthi*
Erysiphe diffusa	*Desmodium canadense*	FH01122167	USA: Wisconsin	PP680973	PP720935		PP720738		PP719990	
Erysiphe diffusa	*Desmodium rhombifolium*	FH01122168	USA: Wisconsin	PP680974	PP720936	PP720283	PP720696			
Erysiphe diffusa	*Desmodium canadense*	FH01122169	Canada	PP680972	PP720934	PP720284			PP719991	
Erysiphe diffusa	*Desmodium illinoense*	FH01122170	USA: Wisconsin	PP681011	PP720937	PP720286	PP720697	PP720424	PP719992	
Erysiphe diffusa	*Glycyrrhiza lepidota*	FH01122171	USA: Wyoming	PP680969	PP720953	PP720281	PP720751	PP720425	PP719993	
Erysiphe diffusa	*Robinia pseudoacacia*	FH01122174	USA: North Carolina	PP680971	PP720938	PP720285	PP720698		PP719995	
Erysiphe diffusa	*Desmodium canadense*	NYSf3480	USA: Wisconsin	PP680970						Lectotype
Erysiphe digitata	*Rhododendron* sp.	FH00941229	USA: Washington	PP681026	PP720906	PP720289	PP720555	PP720398	PP719954	
Erysiphe epigena	*Quercus chenii*	FH00965518	China	OM436185	PP720991	PP720287	PP720687		PP719971	
Erysiphe epigena	*Quercus chenii*	FH00965520	China	OM436187	PP720992	PP720288	PP720688			

(*Continued*)

Table 1. (Continued).

Taxon	Host	Voucher*	Collection locality	ITS+28S	*CAM*	*GAPDH*	*GS*	*RPB2*	*TUB*	Notes
Erysiphe euonymi	*Euonymus atropurpureus*	ARIZ M AN01813	USA: Wisconsin	PP681086	PP720920	PP720327	PP720702		PP719887	
Erysiphe euonymi	*Euonymus europaeus*	ARIZ M AN01814	USA: Wisconsin	PP680989	PP720921					
Erysiphe euonymi	*Euonymus atropurpureus*	BPI 558210	USA: New York	PP680990	PP720922	PP720326			PP719890	
Erysiphe euonymi	*Euonymus atropurpureus*	FH01131020	USA: Delaware	PP681019	PP720926		PP720678	PP720443	PP720022	
Erysiphe euphorbiicola	*Euphorbia commutata*	FH01122180	USA: Virginia	OR424923		PP720269				
Erysiphe friesii	*Rhamnus cathartica*	HAL 657 F	Germany	PP680983	PP720999					
Erysiphe friesii	*Rhamnus cathartica*	POLL 0060000219	Germany	PP681007			PP720544	PP720520	PP720106	Epitype
Erysiphe heraclei	*Osmorhiza claytonii*	FH01131061	USA:Minnesota	PP681080	PP720987	PP720297	PP720548	PP720454	PP720035	
Erysiphe heraclei	*Hedera hibernica*	FH01131062	USA:California	PP681004	PP720988	PP720298	PP720549	PP720455	PP720036	
Erysiphe howeana	*Oenothera biennis*	FH01122089	USA: Massachusetts	PP681016						
Erysiphe howeana	*Baptisia* sp.	FH01122098	USA: New York	PP680986	PP720946				PP719980	Likely host misidentification or contamination
Erysiphe howeana	*Oenothera biennis*	FH01131063	USA: Massachusetts	PP681017	PP720952		PP720525	PP720456	PP720037	Reference Sequences
Erysiphe howeana	*Oenothera biennis*	FH01131064	USA: Massachusetts	PP681015	PP720951		PP720526	PP720457	PP720038	
Erysiphe intermedia	*Lupinus perennis*	FH01122224	USA: Wisconsin	PP681013	PP720907	PP720314	PP720542		PP720000	
Erysiphe intermedia	*Lupinus perennis*	FH01122225	USA: Maryland	PP680988	PP720909	PP720315			PP720001	
Erysiphe intermedia	*Lupinus* sp.	FH01131065	USA: Colorado	PP681012	PP720910	PP720316	PP720543	PP720458	PP720039	
Erysiphe intermedia	*Lupinus polyphyllus*	FH01131070	USA: Idaho	PP681014	PP720908	PP720317	PP720566	PP720463	PP720044	
Erysiphe juglandis nigrae	*Juglans* sp.	FH01131017	USA: Massachusetts	PP681071	PP720957	PP720120	PP720707	PP720440	PP720019	
Erysiphe juglandis nigrae	*Juglans nigra*	FH01131066	USA: Massachusetts	PP681069	PP720959	PP720123	PP720553	PP720459	PP720040	
Erysiphe juglandis nigrae	*Juglans nigra*	FH01131067	USA: Massachusetts	PP681100	PP720958	PP720124		PP720460	PP720041	Epitype
Erysiphe lespedezae	*Bauhinia* sp.	HAL 1430 F	India	PP680979	PP720896	PP720304	PP720535		PP720069	Isotype of *Pseudoidium caesalpiniacearum*
Erysiphe liriodendri	*Liriodendron tulipifera*	FH01122090	USA: Massachusetts	PP680842						
Erysiphe liriodendri	*Liriodendron tulipifera*	FH01131068	USA: Massachusetts	PP681088	PP720974	PP720330	PP720560	PP720461	PP720042	Epitype
Erysiphe liriodendri	*Liriodendron tulipifera*	FH01131069	USA: Delaware	PP681027	PP720975	PP720331	PP720561	PP720462	PP720043	
Erysiphe ludens	*Vicia americana*	FH01122195	USA: Washington	PP680999	PP720901		PP720704	PP720427	PP719996	
Erysiphe ludens	*Vicia americana*	FH01122196	USA: Colorado	PP680984	PP720902	PP720307				Epitype
Erysiphe magnifica	*Magnolia x soulangeana*	FH00941960	USA: Washington	PP680961						
Erysiphe magnifica	*Magnolia wilsonii*	FH01131074	USA: Massachusetts	PP681104	PP720970	PP720333	PP720664	PP720464	PP720045	
Erysiphe magnifica	*Magnolia acuminata*	FH01131075	USA: Massachusetts	PP681105	PP720972	PP720332	PP720558	PP720465	PP720046	Reference sequences
Erysiphe magnifica	*Magnolia wilsonii*	FH01131076	USA: Massachusetts	PP680962	PP720973	PP720334	PP720559	PP720466	PP720047	
Erysiphe magnifica	*Magnolia lilliflorum*	FH01131077	USA: Washington		PP720971		PP720710	PP720467	PP720048	
Erysiphe nemopanthi	*Illex verticillata*	FH01122198	Canada	PP681032						
Erysiphe nemopanthi	*Illex verticillata*	FH01122199	USA: Wisconsin	PP680843	PP720913	PP720305	PP720683		PP719997	
Erysiphe nemopanthi	*Illex verticillata*	FH01131081	USA: Massachusetts	PP681099	PP720914	PP720306	PP720536	PP720468	PP720049	
Erysiphe nemopanthi	*Illex verticillata*	NYSf2056.1	USA: New York	PP680844				PP720519		Holotype
Erysiphe pavoniae	*Pavonia zeylanica*	HAL 1432 F	India	PP681000	PP720990	PP720292		PP720488	PP720071	Holotype
Erysiphe peckii	*Campsis radicans*	BPI 556623	USA: Virginia	PP680976						
Erysiphe peckii	*Campsis radicans*	FH01122202	USA: Virginia	PP680977	PP720940	PP720272	PP720695		PP719998	
Erysiphe peckii	*Campsis radicans*	K(M) 169082	USA: Colorado	PP680975	PP720941		PP720668	PP720500	PP720083	Holotype
Erysiphe pisi	*Lathyrus odoratus*	ARIZ M AN01234	USA: Montana	PP681084	PP720943	PP720273	PP720690	PP720349	PP719886	
Erysiphe pisi	*Astragalus canadensis*	FH01122097	USA: South Dakota	PP680996	PP720945		PP720691		PP719979	
Erysiphe pisi	*Lathyrus odoratus*	FH01131043	USA: Washington	PP681024	PP720947		PP720527	PP720447	PP720027	
Erysiphe pisi	*Lathyrus odoratus*	WSP2516 Genotype 1	USA: Washington	PP681023	PP720948	PP720277	PP720689	PP720522	PP720107	
Erysiphe pisi	*Lathyrus odoratus*	WSP2516 Genotype 2	USA: Washington	PP680995	PP720954	PP720275	PP720692		PP720109	
Erysiphe pisi	*Lathyrus odoratus*	WSP55356	USA: Washington	PP681025	PP720949	PP720274	PP720693			
Erysiphe platani	*Platanus occidentalis*	FH00941224	USA: Massachusetts	PP681090	PP720961		PP720571	PP720397	PP719953	
Erysiphe platani	*Platanus orientalis*	FH01131086	USA: Massachusetts	PP681089	PP720962	PP720118	PP720669	PP720469	PP720050	
Erysiphe platani	*Platanus occidentalis*	FH01131087	USA: Delaware	PP681091	PP720963		PP720554	PP720470	PP720051	Epitype

(*Continued*)

Table 1. (Continued).

Taxon	Host	Voucher*	Collection locality	ITS+28S	*CAM*	*GAPDH*	*GS*	*RPB2*	*TUB*	Notes
Erysiphe polygoni	*Muehlenbeckia platyclada*	FH01122104	USA: Wisconsin	PP681079	PP720986	PP720293	PP720545	PP720419	PP719983	
Erysiphe quercicola	*Quercus robur*	FH00965519	France	OM436186	OR427471	OR427557	OR427641	OR427710	OR427745	
Erysiphe quercicola	*Quercus agrifolia*	FH01131088	Mexico	PP681092	PP720995	PP720291	PP720538	PP720471	PP720052	
Erysiphe quercicola	*Mangifera indica*	FLAS F 20906	USA: Florida	PP680841	PP720994					
Erysiphe ravenelii	*Gleditsia triacanthos*	FH01122210	USA: South Carolina	PP680980	PP720942	PP720270	PP720739		PP719999	Epitype
Erysiphe ravenelii	*Gleditsia triacanthos*	FH01122211	USA: Oklahoma	PP680981	PP720931	PP720271	PP720700			
Erysiphe robiniae	*Caragana arborescens*	FH00965530	Germany	PP680991	PP720924	PP720321			PP719973	Isolectotype of *Microsphaera caraganae*
Erysiphe russellii	*Oxalis stricta*	FH01122213	USA: Wisconsin	PP680992	PP720932					
Erysiphe russellii	*Oxalis stricta*	FH01122214	USA: Wisconsin	PP680993	PP720933	PP720278				
Erysiphe salmoniana	*Apios tuberosa*	FH01122166	USA: Tennessee	PP681008	PP720900	PP720279	PP720528			Holotype
Erysiphe salmoniana	*Apios tuberosa*	GAM00008745	USA: Georgia	PP680968	PP720955					
Erysiphe salmoniana	*Apios tuberosa*	WIS F 0025795	USA: Wisconsin	PP680967	PP720899		PP720699			
Erysiphe santalicola	*Santalum album*	HAL 3497 F	India	PP681085						Holotype
Erysiphe sp.	*Lathyrus odoratus*	BPI 564839	USA: Connecticut	PP681021	PP720923	PP720322	PP720532		PP719893	
Erysiphe sp.	*Arenaria macrophylla*	FH01122079	USA: California	PP680978	PP720985	PP720295	PP720674		PP719978	
Erysiphe sp.	*Baptisia australis*	FH01131014	USA: Massachusetts	PP681087	PP720925	PP720323	PP720533	PP720438	PP720017	
Erysiphe sp.	*Carya ovata*	FH01131016	USA: Massachusetts	PP681070	PP720956	PP720122	PP720706	PP720439	PP720018	
Erysiphe sp.	*Chionanthus virginicus*	FH01131018	USA: Massachusetts	PP681072	PP720969	PP720116	PP720551	PP720441	PP720020	
Erysiphe sp.	*Syringa vulgaris*	FH01131035	USA: Colorado	PP681073	PP720960	PP720117	PP720550	PP720445	PP720025	
Erysiphe sp.	*Acanthus mollis*	FH01131044	USA: Washington	PP681022	PP720927	PP720320	PP720534	PP720448	PP720028	
Erysiphe sydowiana	*Ceanothus velutinus*	FH00965537	USA: Washington	PP681031	PP720891	PP720125	PP720562	PP720416	PP719975	Holotype
Erysiphe syringae	*Forestiera acuminata*	BPI 558969	USA: Illinois	PP680960	PP720981	PP720121	PP720686		PP719891	
Erysiphe syringae	*Syringa x hyacinthifolia*	FH00941218	USA: Massachusetts	PP681101	PP720982		PP720557	PP720396	PP719952	
Erysiphe syringae	*Syringa oblata ssp. dilatata*	FH01131095	USA: Massachusetts	PP681102	PP720984	PP720335	PP720671	PP720472	PP720053	
Erysiphe syringae	*Ligustrum* sp.	FH01131096	USA: Washington	PP681074	PP720983					
Erysiphe trifoliorum	*Trifolium pratense*	FH01131023	USA: North Carolina	PP681018	PP720930		PP720531		PP720023	
Erysiphe umbilici	*Clementsia semenovii*	FH00965543	Uzbekistan	PP680982		PP720319			PP719976	Isolectotype
Erysiphe vignae	*Strophostyles pauciflora*	FH01122172	USA: Oklahoma	PP681083	PP720950	PP720280	PP720529	PP720426	PP719994	
Pseudoidium poinsettiae	*Euphorbia pulcherrima*	GAM00018822	Venuzuela	OR425010	PP720890					
Pseudoidium poinsettiae	*Euphorbia pulcherrima*	HAL 1674 F	USA: New York	OR425011	PP720897	PP720114				Holotype
Pseudoidium poinsettiae	*Euphorbia pulcherrima*	MSC0212191	USA: Michigan	OR425009	PP720898	PP720115	PP720694	PP720507	PP720089	

*ARIZ = University of Arizona Herbarium; BPI = U.S. National Fungus Collections; FH = Farlow Herbarium, Harvard University; FLAS = University of Florida Herbarium, Florida Museum of Natural History; GAM = University of Georgia; HAL = Martin-Luther-Universität Herbarium; K = Kew's Fungarium; MSC = Michigan State University Herbarium; NY = The New York Botanical Garden; NYS = New York State Museum; POLL = Herbarium Pollichiae Bad Dürkheim; WIS = University of Wisconsin Herbarium; WSP = Washington State Plant Pathology Herbarium.

greater than 70% for the maximum likelihood (ML) analyses conducted. The representative maximum clade credibility trees are illustrated in FIGS. 1–4.

Each taxon with sequence data from part 2 of the *Erysiphe* "*Microsphaera* lineage" is represented in the phylogenetic trees (FIGS. 1–4) besides *Erysiphe* taxa that infect North American oaks.

TAXONOMY

A comprehensive survey of the history of the genus name *Erysiphe* is provided in Bradshaw et al. (2023b) in connection with a phylogenetic-taxonomic treatment of the "*Uncinula* lineage" (in the sense of Takamatsu et al. 2015b). All *Erysiphe* species outside of the phylogenetically basal "*Uncinula* lineage" were treated by Takamatsu et al. (2015a) as the "*Microsphaera* lineage." This assemblage of species is split in our own analyses into two parts to avoid presenting trees that are too large and difficult to align and interpret. The first part of the treatment of species of the "*Microsphaera* lineage" (Bradshaw et al. 2024a) contained, amongst others, species of the "*Erysiphe aquilegiae* complex" comprising a diverse assemblage of species with insufficient resolution in ITS +28S analyses. The present, second part of the treatment of species of the "*Microsphaera* lineage" encompasses two additional challenging species complexes with insufficient resolutions in ITS+28 analyses, viz., the complex of *Erysiphe* species on oaks, including the "*E. alphitoides* complex," and the "*E. trifoliorum* complex." The oak powdery mildew complex is phylogenetically and taxonomically diverse, with many, previously undetected, cryptic species in North America that required a separate publication based on a multilocus analyses (Bradshaw et al. 2024). The "*E. alphitoides* complex" is an additional subcomplex within the oak powdery mildew complex, comprising numerous little understood species names described from hosts of other plant genera and families. A multilocus examination of the *E. alphitoides* complex has been carried out and recently published (Bradshaw et al. 2023c). A further complicated complex, insufficiently resolved on species level in ITS+28S analyses, referred to as the "*E. trifoliorum* complex," is composed of diverse powdery mildew species on legumes and in addition some species on hosts of other plant families. Bradshaw

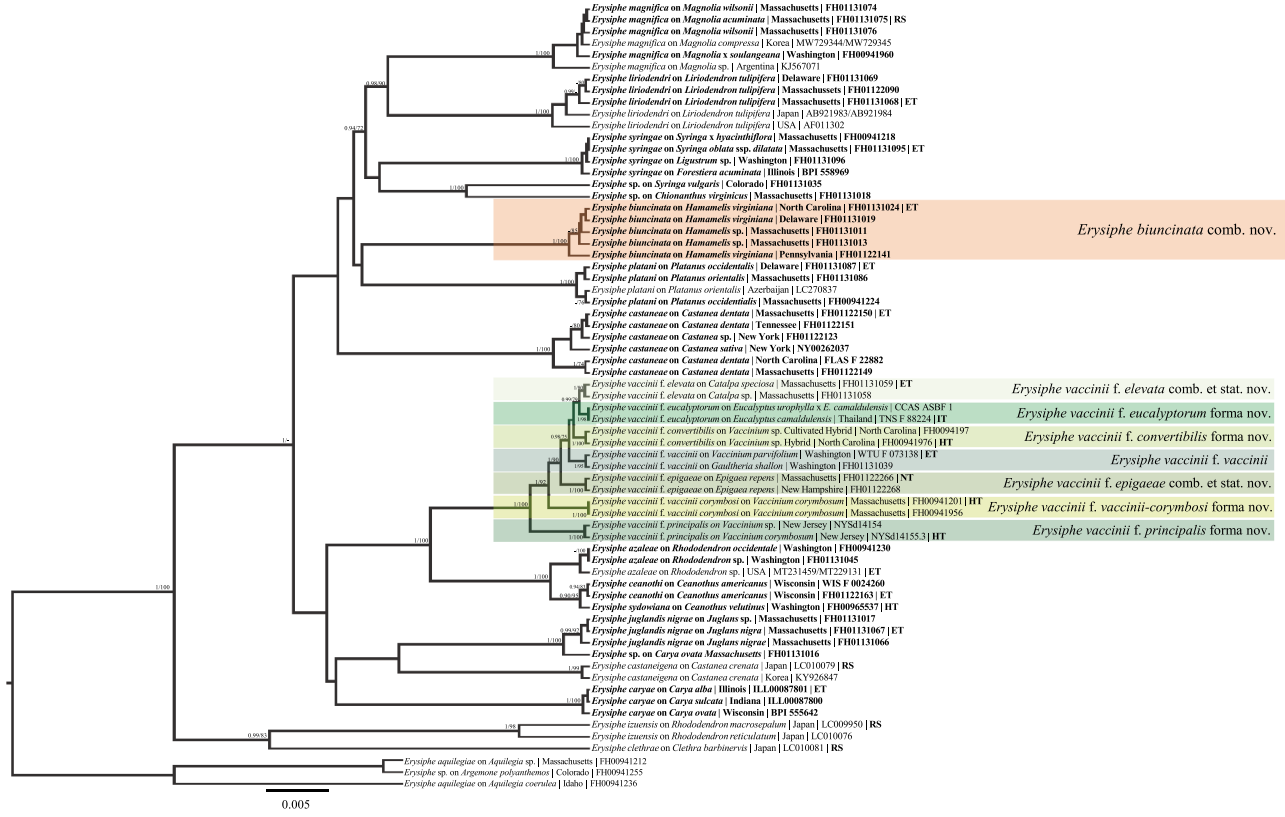

Figure 1. Bayesian maximum clade credibility tree of the concatenated ITS+28S+*CAM*+*GAPDH*+*GS*+*RPB2*+*TUB* regions of select *Erysiphe* taxa evaluated in the current study. Posterior probabilities ≥90 are displayed followed by bootstrap values greater than 70% for the maximum likelihood (ML) analyses conducted. ET = ex-epitype; HT = ex-holotype; IT = ex-isotype; RS = reference sequence. Quotations around a taxon signify that the name is no longer current. Taxa in bold were sequenced for the current study.

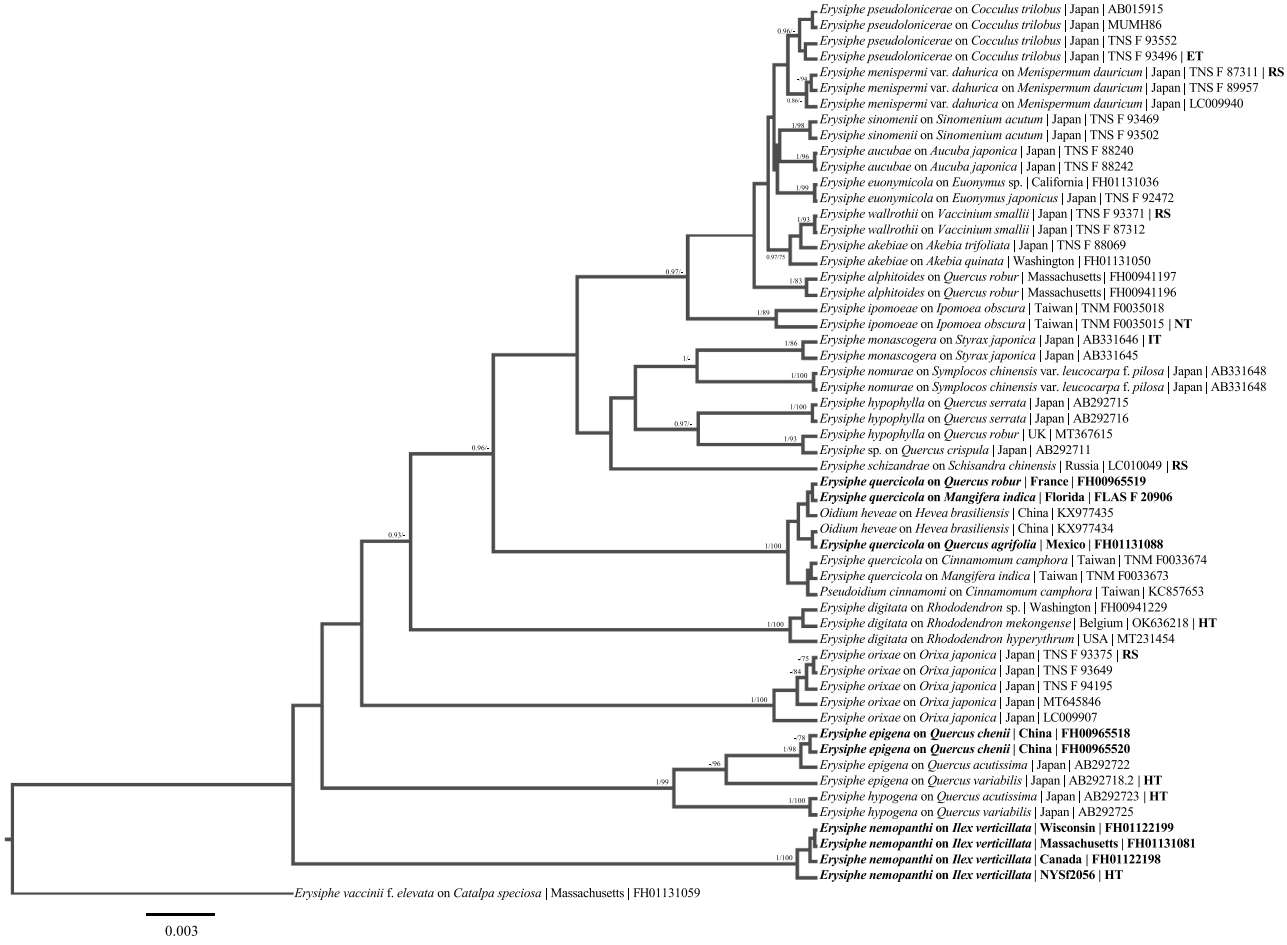

Figure 2. Bayesian maximum clade credibility tree of the concatenated ITS+28S+*CAM*+*GAPDH*+*GS*+*RPB2*+*TUB* regions of select *Erysiphe* taxa evaluated in the current study. Posterior probabilities ≥90 are displayed followed by bootstrap values greater than 70% for the maximum likelihood (ML) analyses conducted. ET = ex-epitype; HT = ex-holotype; IT = ex-isotype; PT = ex-paratype; RS = reference sequence. Quotations around a taxon signify that the name is no longer current. Taxa in bold were sequenced for the current study.

et al. (2022a) and Darsaraei et al. (2024) published in-depth discussions of this complex. In the present analyses, we sequenced multiple loci of many of the species nested within the complex.

Survey of phylogenetically demonstrated Erysiphe *species of the "*Microsphaera *lineage" (p.p., present analyses), including taxonomic novelties, new records, and epitypifications (excluding species of the* E. alphitoides *complex, the* E. vaccinii *complex, and the* E. trifoliorum *complex)*

Erysiphe acetosae M. Bradshaw, U. Braun & J.K. Mitch. sp. nov. FIG. 5

MycoBank MB853740

Etymology: Epithet derived from the species name of the type host, *Rumex acetosa*.

Diagnosis: Morphologically close to *Erysiphe polygoni*, but different in having mostly ellipsoid-ovoid to doliiform conidia; sequences forming a separate species clade. *Erysiphe rumicicola* differs from *E. acetosae* in forming longer chasmothecial appendages, 0.5–3.5 times as long as the chasmothecial diameter, with up to 10 septa, and sequences forming a clade in sister position to the *E. polygoni* clade.

Description: Mycelium on leaves, amphigenous, sometimes also caulicolous, forming white patches, later confluent, finally covering entire leaf surfaces, persistent; hyphae branched at right angles, hyaline, septate, thin-walled, smooth or almost so, 2–7 µm wide; hyphal appressoria solitary, slightly lobate to multilobate, 4–10 µm diam; conidiophores arising from the upper surface of hyphal mother cells, erect, 50–110 µm long, basal septum at the junction with the mother cell or slightly elevated (to 5 µm), foot cells 25–50 µm long and (6–)7–9(–10) µm wide,

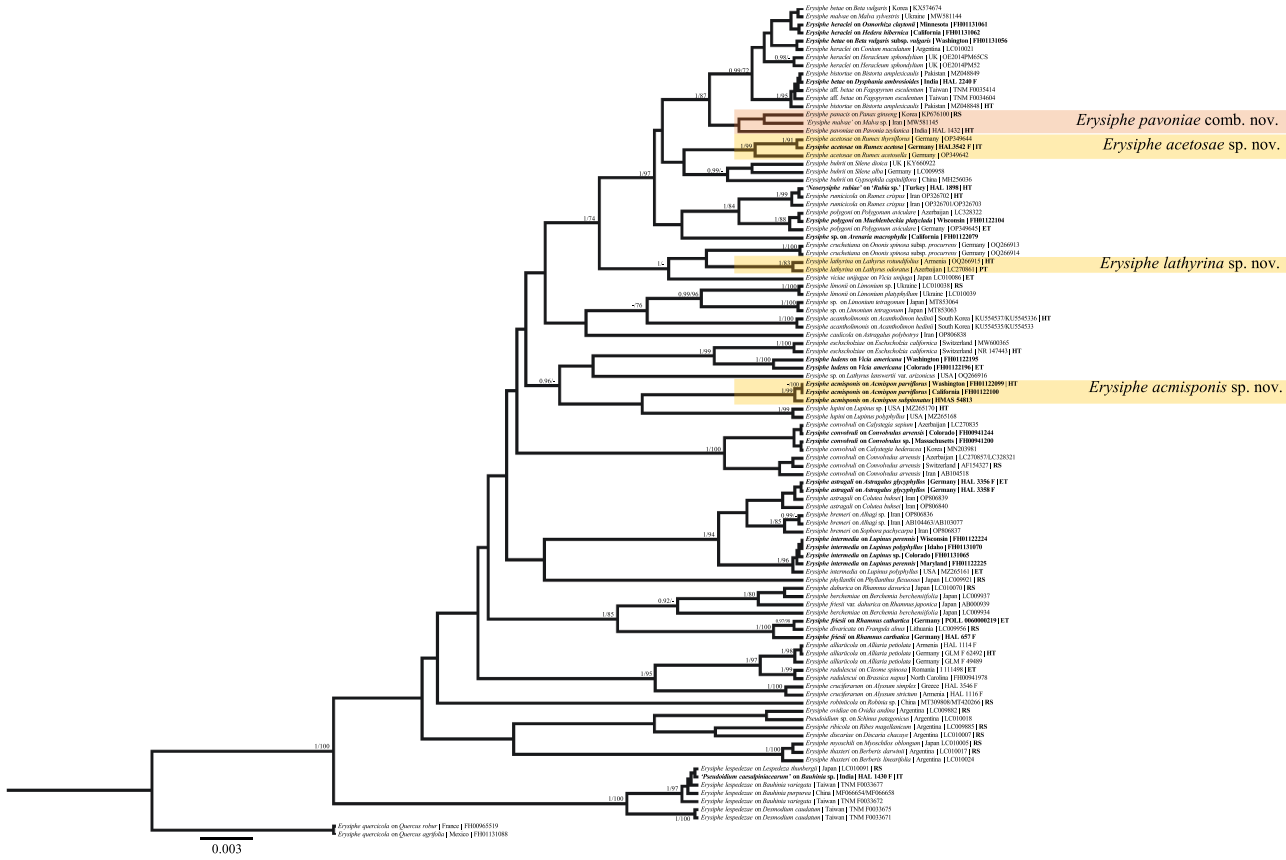

Figure 3. Bayesian maximum clade credibility tree of the ITS+28S+*CAM*+*GAPDH*+*GS*+*RPB2*+*TUB* regions of select *Erysiphe* evaluated in the current study. Posterior probabilities ≥90 are displayed followed by bootstrap values greater than 70% for the maximum likelihood (ML) analyses conducted. ET = ex-epitype; HT = ex-holotype; IT = ex-isotype; RS = reference sequence. Quotations around a taxon signify that the name is no longer current. Taxa in bold were sequenced for the current study.

straight, cylindrical to somewhat curved-sinuous, foot cells followed by 1–2 cells, 10–40 µm long, shorter than the foot cell, about as long as the foot cell or foot cell followed by a longer second cell and a shorter third cell; conidia formed singly, ellipsoid, ellipsoid-ovoid, doliiform, occasionally subcylindrical, 28–50 × 13–20 µm, length/width ratio 1.7–3.1, on average 2.3, apex of primary conidia rounded, both ends of secondary conidia truncate or almost so. Chasmothecia immersed in the dense mycelial felt, 80–140 µm diam, peridium cells irregularly polygonal, 8–25 µm diam, appendages numerous, equatorially arising from the lower half, differentiation between appendages and hyphae difficult, about as long as the chasmothecial diameter or shorter, usually unbranched, rarely irregularly branched, 3–8(–10) µm wide, at fist hyaline, later becoming yellowish to brown, 0–3-septate, walls thin, smooth to verruculose; with 3–6 asci per chasmothecium, broad ovoid-saccate, 40–75 × 28–50 µm, sessile or short-stalked, walls thin, 1–2 µm, terminal oculus inconspicuous, 12–20 µm diam, 2–4(–5)-spored; ascospores broad ellipsoid-ovoid, 18–40 × 12–22 µm, colorless.

Holotype: GERMANY. SACHSEN-ANHALT: Halle (Saale), Albert Schweizer Street, roadside, on *Rumex acetosa*, 10 Oct 2022, *U. Braun* (FH). *Isotype*: HAL 3542 F. Ex-holotype sequences: PP681001 (ITS+28S); PP720915 (*CAM*); PP720294 (*GAPDH*); PP720547 (*GS*); PP720487 (*RPB2*); PP720070 (*TUB*).

Additional collections examined: GERMANY. NORDRHEIN-WESTFALEN: Städteregion Aachen, Monschau, on *Rumex acetosella*, 23 Jul 2004, *U. Braun* (HAL 2119 F), sequence: OP349642.1 (ITS/28S); SACHSEN-ANHALT: Landkreis Wittenberg, Kemberg, on *R. thyrsiflorus* (≡ *R. acetosa* subsp. *thyrsiflorus*), 28 Aug 1978, *H. Jage* (HAL 1334 F), sequence: OP349644.1 (ITS+28S).

Host range and distribution (Amano 1986): On *Rumex* [subgen. *Acetosa*] (*acetosa, acetosella, thyrsiflorus*); Asia (China, Iran, Japan, Kazakhstan, Turkey, Turkmenistan, Uzbekistan), Canary Islands, Caucasus (Azerbaijan, Georgia), Europe (Bulgaria, Czech Republic, Denmark, Estonia, Finland, France, Germany, Hungary, Italy, Latvia, Lithuania,

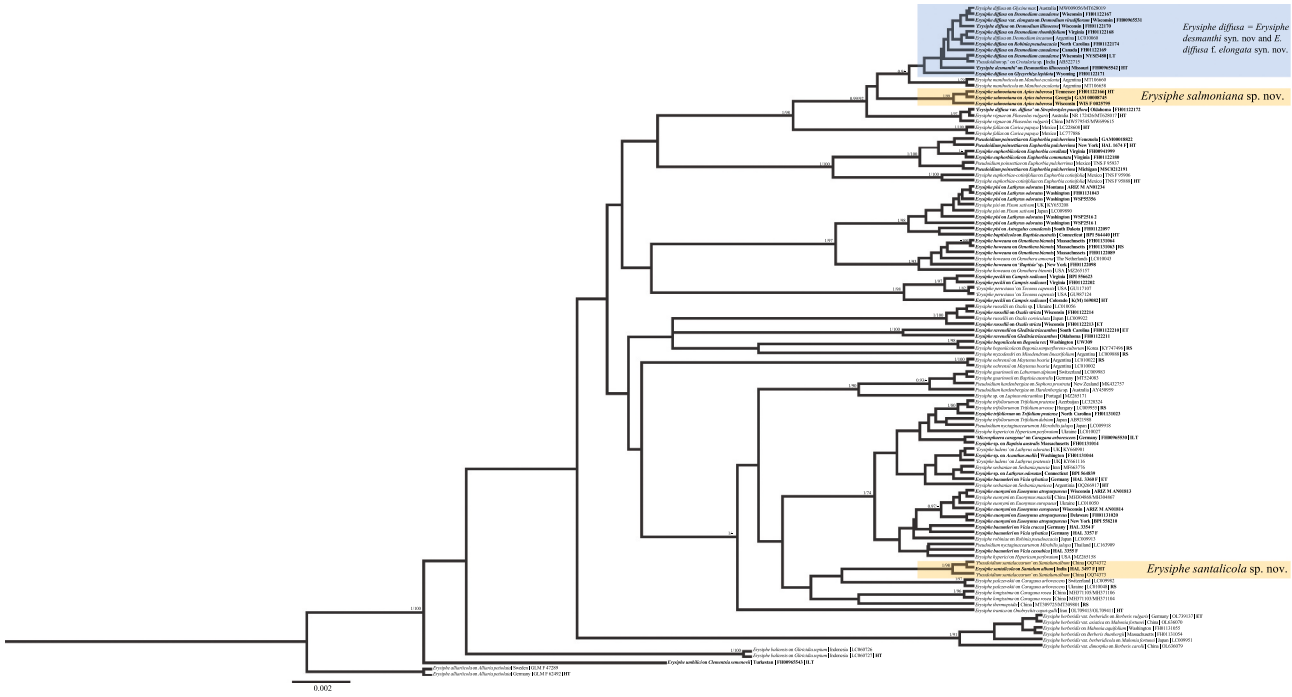

Figure 4. Bayesian maximum clade credibility tree of the ITS+28S+*CAM*+*GAPDH*+*GS*+*RPB2*+*TUB* regions of select *Erysiphe* evaluated in the current study. Posterior probabilities ≥90 are displayed followed by bootstrap values greater than 70% for the maximum likelihood (ML) analyses conducted. ET = ex-epitype; HT = ex-holotype; ILT = ex-isolectotype; RS = reference sequence; LT = ex-lectotype sequence. Quotations around a taxon signify that the name is no longer current. Taxa in bold were sequenced for the current study.

Netherlands, Norway, Poland, Romania, Russia, Spain, Switzerland, Sweden, UK, Ukraine, former Yugoslavia).

Notes: Darsaraei et al. (2023) published a comprehensive phylogenetic-taxonomic revision of *Erysiphe polygoni* s. lat. and introduced a new species, *E. rumicicola*, for collections on *Rumex* spp. formerly referred to *E. polygoni*. Sequences retrieved from *E. polygoni* on *Rumex acetosella* and *R. thyrsiflorus*, grouping outside of the *E. polygoni* and *E. rumicicola* clades, were treated and discussed under *Erysiphe* sp. At the end of 2022, a rich new specimen on *Rumex acetosa* with abundant chasmothecia was collected and sequenced, which confirmed the results published by Darsaraei et al. (2023). The sequences form a highly supported species clade, which warrants the recognition of *Erysiphe* collections on host species assigned to *Rumex* subgen. *Acetosa* as a distinct species. *Rumex acetosella, R. acetosa*, and allied species were previous assigned to separate genera (*Acetosella, Acetosa*) by some authors, but nowadays they are placed in *Rumex* subgen. *Acetosa*, based on current phylogenetic analyses (Schuster et al. 2015). The present phylogenetic analyses of *Erysiphe* on hosts belonging to *Rumex* subgen. *Acetosa* confirm results of previous cross-infection experiments. Hammarlund (1925) demonstrated that *Erysiphe* on *Rumex acetosella* was able to infect *R. acetosa* and vice versa, but other *Rumex* spp., including *R. aquaticus* and *R. crispus*, were resistant. The record of *E. acetosae* from the UK goes back to Charter and Woods (2019), who recorded *E. polygoni* (s. lat.) on *Rumex acetosella* from Wales.

Erysiphe acmisponis M. Bradshaw & Zhao Y. Zhang, sp. nov. FIG. 6

MycoBank MB853849

Etymology: Epithet derived from the name of the host genus, *Acmispon*, in genitive singular.

Diagnosis: Similar and previously assigned to *Erysiphe pisi* s. lat., but different by having short chasmothecial appendages, significantly shorter than the chasmothecial diameter. Furthermore, phylogenetically related to *E. lupini* and *E. ludens*, but not comparatively close to *E. pisi*, forming a separate highly supported species clade.

Description: Mycelium amphigenous, also caulicolous and on pods, often covering the entire stem, persistent. Chasmothecia scattered to gregarious, globose, present on leaves, stems, and pods, 93–138.5(–146.5) µm; peridium cells irregularly polygonal, 4.5–14 µm; appendages about 8–27, in the lower half, mycelium-like, short, simple or irregularly branched, coral-like, often very poorly developed, sometimes almost absent, significantly shorter than the chasmothecial diameter,

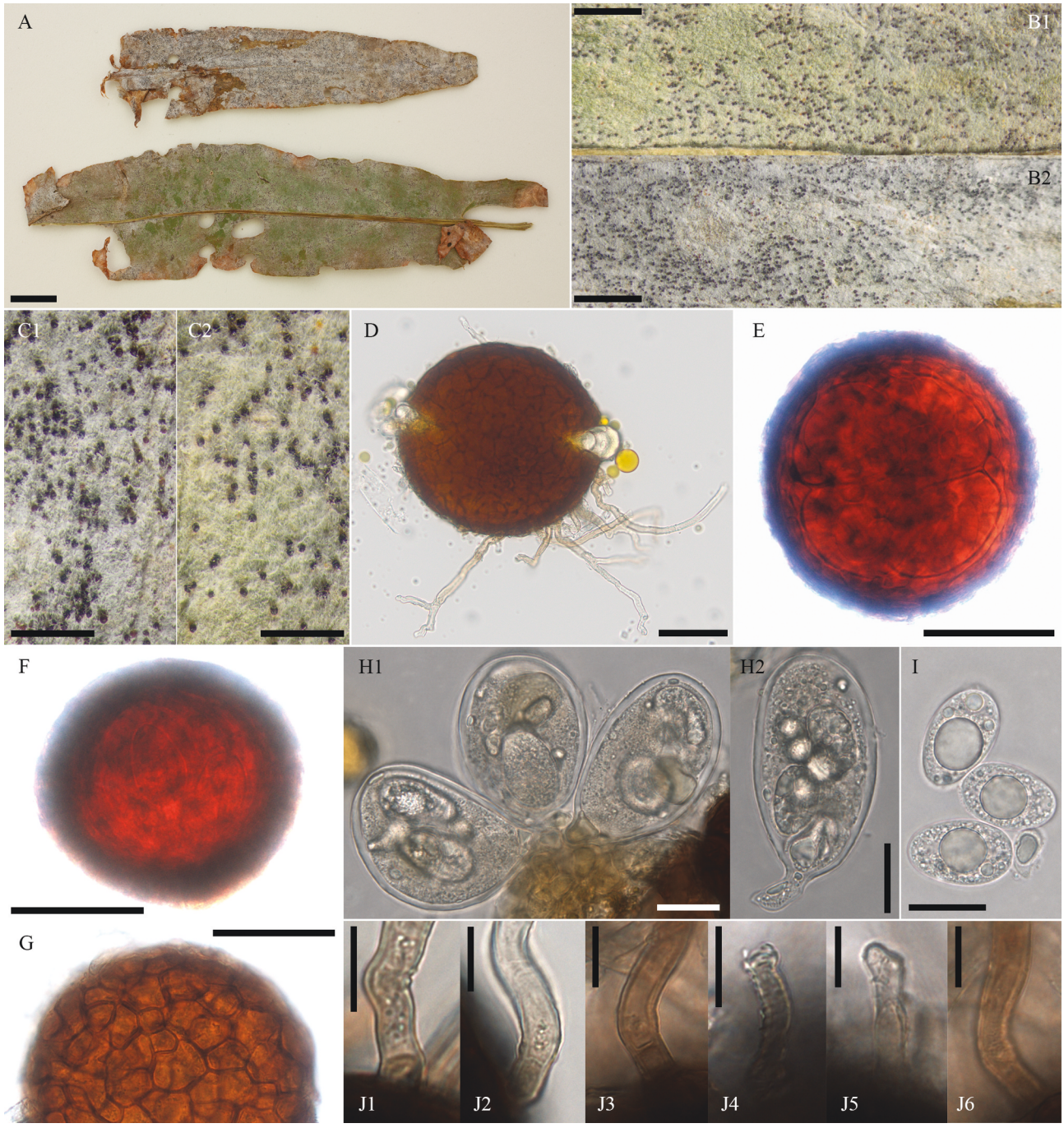

Figure 5. Morphological details of the sexual morph (chasmothecia) of *Erysiphe acetosae*, sp. nov., on *Rumex acetosa*. All images derived from the holotype preserved in FH. (A–C) Infected leaves and chasmothecia including lower (A, B1, C2) and upper (A, B2, C1) leaf surfaces. (D) Chasmothecium with appendages. (E–F) Arrangement of asci within intact chasmothecia in top (E) and side (F) views. (G) Excipular cell arrangement in the peridium in frontal view. (H) Asci released from a broken chasmothecium with ascospores. (I) Free ascospores. (J) Appendages (J1–J3 and J6) and anchoring hyphae (J4 and J5) showing variation. J1–J3. Septa near brown base of appendages. J4–J5. Detail of reticulation on anchoring hyphae. J6. Detail of reticulation on base of appendage. Water after KOH pretreatment: D–J. Bars: A = 1 cm; B = 2 mm; C = 1 mm; D–G = 50 µm; H–I = 20 µm; J = 10 µm.

brown, or at least in the lower part, yellowish to brownish, paler brown or hyaline toward the tip, 1–2-septate, thin-walled, smooth or almost so; asci 3–10, ellipsoid-obovoid, subglobose, irregularly ovoid, (59–)51–77(–81) × (31–)38–54 µm; ascospores 2–6, triangular-obovoid, cashew-shaped, ellipsoid-ovoid, 19–26.5 × 10.5–16.5 µm.

Holotype: USA. WASHINGTON: Marysville, on *Acmispon parviflorus* (≡ *Hosackia parviflora*), Jun 1928, *J.M. Grant* (FH01122099). Ex-holotype sequences:

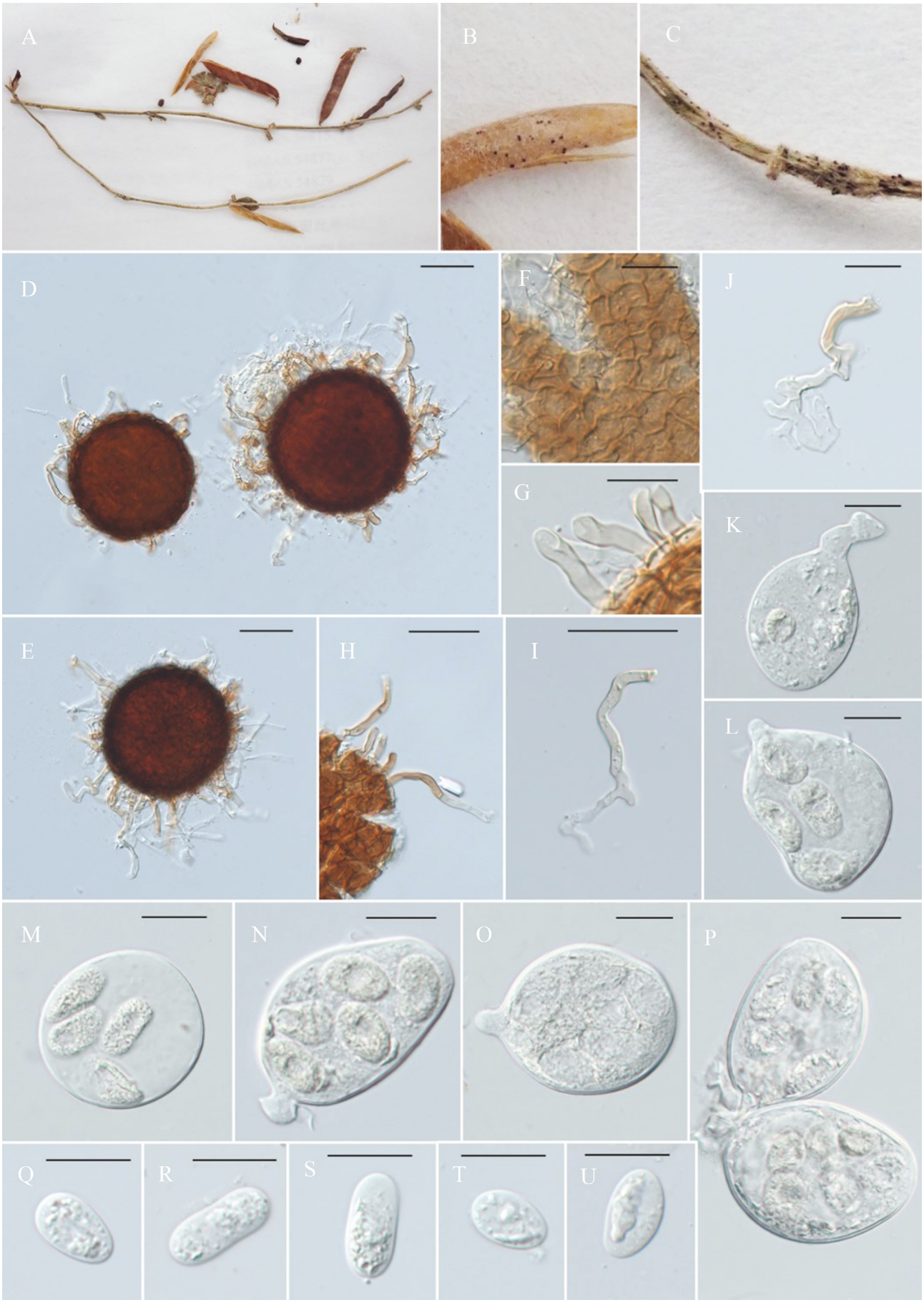

Figure 6. *Erysiphe acmisponis*, sp. nov., on *Acmispon parviflorus*. (A–C) Symptoms. (D–E) Chasmothecia. (F) Peridium cells. (G–J) Chasmothecial appendages. (K–P) Asci. (R–U) Ascospores. Bars: d–e, h–i = 50 µm; f–g, j–u = 20 µm.

PP681081 (ITS+28S); PP720911 (*CAM*); PP720310 (*GAPDH*); PP720539 (*GS*); PP720417 (*RPB2*); PP719981 (*TUB*).

Host range and distribution: On *Acmispon parviflorus* (≡ *Hosackia parviflora*, = *Lotus micranthus*), North America (USA: California, Washington).

Notes: Two sequences retrieved from *Erysiphe* on *Acmispon parviflorus* in the USA form a small, highly supported clade. This host is a North American species widely distributed in western North America, from Canada to California.

Erysiphe astragali DC., Fl franç 6:105. 1815, emend. Darsaraei et al. (2024).

Lectotype (designated by Braun 1987): FRANCE. "*Erysiphe astragali*, No. 235," on *Astragalus glycyphyllos*, herb. *de Candolle* (G 00122097). *Epitype* (designated by Bradshaw et al. 2022a): GERMANY. BRANDENBURG: Berlin-Schöneberg, Monomentenbrücke, on *Astragalus glycyphyllos*, 17 Jul 2007, *M. Ristow* (HAL 3356 F). Ex-epitype sequence: MZ265151 (ITS+28S).

≡ *Alphitomorpha astragali* (DC.) Wallr., Ann Wetterauischen Ges Gesammte Naturk N F 4:244. 1819.

≡ *Microsphaera astragali* (DC.) Trevis., Spighe e Pagli:39. 1853.

≡ *Trichocladia astragali* (DC.) Neger, Flora 88:351. 1901.

≡ *Alphitomorpha holosericea* Wallr., Verh Ges Naturf Freunde Berlin 1:41. 1819, nom. illeg. (Art. 52.1).

≡ *Erysiphe holosericea* (Wallr.) Link (as "*Erysibe*"), Sp pl 4 6(1):115. 1824.

≡ *Erysiphe communis* f. *holosericea* (Wallr.) Fr., Syst mycol 3:240. 1829, nom. sanct.

≡ *Alphitomorpha sericea* Wallr., Fl Crypt Germ 2:757. 1833, nom. illeg. (Art. 52.1).

= *Microsphaera coluteae* Kom., Bot Zap 4:270. 1895 [and in Jacz. et al., Fungi Ross Exs 79. 1895]. [*Holotype*: TURKMENISTAN. Zeravschan, pr. pag. Dark, on *Colutea arborescens*, 18 Aug 1893, *Komarov* (LE 193189).]

≡ *Trichocladia coluteae* (Kom.) Potebnia, Gribnye parazity vysshikh rasteny Kharkovskoy i smezhnykh guberny:239. 1915.

= *Trichocladia coluteae* f. *astragali* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:308. 1927.

= *Trichocladia coluteae* f. *oxytropis* [as *oxytropi*] Domashova. Mikoflora Khrebta Terskei Ala-Too Kirgizskoi:92. 1960.

= *Microsphaera crispula* U. Braun, Mycotaxon 15:132. 1982. *Holotype*: TURKMENISTAN. Zeravschan, on *Astragalus* sp., 1893, *Komarov* [Jacz. et al., Fungi Ross Exs 79] (LEP). *Isotypes*: Jacz. et al., Fungi Ross Exs 79 (e.g., BPI 557682, LE, LEP).]

≡ *Erysiphe crispula* (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:7. 2000.

Host range and distribution: On diverse host species of the genera *Astracantha, Astragalus, Caragana, Colutea*, and *Oxytropis*; Africa, Asia, Caucasus, Europe, North America (for details, see Braun and Cook 2012).

Notes: Darsaraei et al. (2024) published a comprehensive phylogenetic-taxonomic revision of *Erysiphe* spp. in Iran, including the newly detected *E. astragali* species complex, composed of *E. astragali, E. bremeri, E. coluteae, E. crispula, E. intermedia*, and *E. sophorae. Erysiphe coluteae* and *E. crispula* were reduced to synonymy with *E. astragali. Erysiphe intermedia* and *E. bremeri* (including *E. sophorae*) formed small, well-supported species clades, which support the recognition of two species.

Erysiphe azaleae (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:5. 2000.

≡ *Microsphaera azaleae* U. Braun, Mycotaxon 14:370. 1982, nom. cons. (Braun 2013).

Holotype: USA. PENNSYLVANIA: Delaware County, Wm. Trimble [Ellis, N Amer Fungi 770] (PH00041543). *Isotypes*: Ellis, N Amer Fungi 770 (e.g., BPI 558576), as "*Microsphaera platani*." *Epitype* (designated designated by Tymon et al. 2022): USA. OREGON: Nesika Beach, on *Rhododendron* sp., 11 Oct 1994, *J. Pscheidt* (OSC 97536). Ex-epitype sequences: MT231459 (ITS); MT229131 (28S).

= *Oidium ericinum* Erikss., Meddeland Kungl Landtbr-Akad Experimentalfält 1:47. 1885, nom. rej. [*Type*: SWEDEN. On *Erica gracilis* (not preserved).] *Neotype* (designated by Braun 2013): GERMANY. NIEDERSACHSEN: Braunschweig, on *Erica gracilis*, Nov 2002, *U. Brielmaier-Liebetanz* (HAL 2610 F). Ex-neotype sequence: OK662589 (ITS1/5.8S/ITS2).

= *Microsphaera penicillata* f. *rhododendri* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:354. 1927.

Host range and distribution (Braun and Cook 2012): On *Agauria* sp., *Calluna vulgaris, Erica* (*carnea, gracilis*, ×*darleyensis, vagans*), *Leucothoë axillaris, Rhododendron* (*aberconwayi, arborescens, campylocarpum, canadense, cinnabarinum, forrestii* [= *repens*], *fortunei, japonicum, luteum, macgregoriae, molle, mucronatulum, nudiflorum, obtusum, orbiculare, oreodoxa, occidentale, ponticum, prinophyllum, russatum, thomsonii, xanthocodon* [= *concatenans*], *zoelleri*, sp., various *Rhododendron* hybrids), *Vaccinium* sp.; North America (Canada, USA, widespread), Asia (Russia [Far East]), Europe (Austria, Belgium, Czech Republic, Finland, France, Germany, Italy, Netherlands, Poland, Russia, Slovakia, Sweden, Switzerland, UK, Ukraine).

Notes: The phylogeny and taxonomy of *Erysiphe azaleae* have been clarified by Tymon et al. (2022). Sequences obtained from this species form a well-supported species clade.

Erysiphe baptisiicola U. Braun, Mycotaxon 112:178. 2010.

Holotype: USA. CONNECTICUT: New Haven, Elm City Nursery, on *Baptisia australis*, Oct 1907, *G.P. Clinton* (BPI 564440). Ex-holotype sequences: PP680994 (ITS+28S); PP720944 (*CAM*); PP720276 (*GAPDH*); PP719892 (*TUB*).

Host range and distribution: On *Baptisia* (*australis, tinctoria*); North America (USA: Connecticut, Massachusetts, New York, Pennsylvania).

Notes: Braun and Cook (2012) postulated that *E. baptisiicola* belongs to the *Erysiphe pisi* complex; this has been confirmed by analyzing an ex-holotype sequence. On the other hand, Braun and Cook (2012) emphasized that *E. baptisiicola* differs from *E. pisi* in having chasmothecial appendages without or only with few rather inconspicuous septa and walls that are thick toward the base, and conidiophores with curved-sinuous foot cells and narrower conidia. The ex-holotype sequence of *E. baptisiicola* groups together with a sequence obtained from *Erysiphe* on *Astragalus canadensis* within the *E. pisi* clade (with low support), suggesting that this may represent a distinct species in multilocus analyses. Therefore, we prefer to maintain *E. baptisiicola*, at least tentatively. Final conclusions are pending a phylogenetic-taxonomic revision of the *E. pisi* complex.

Erysiphe begoniicola U. Braun & S. Takam., Schlechtendalia 4:5. 2000.

≡ *Microsphaera begoniae* Sivan., Trans Brit Mycol Soc 56(2):304. 1971, non *Erysiphe begoniae* R.Y. Zheng & G.Q. Chen, 1980.

Holotype: UK. Salisbury, Wiltshire, on *Begonia* sp. cult., ('cultivated Begonia' [no wild plant]) 11 Feb 1970, *A.V. Brooks* (IMI 146562). Reference sequence: KY747496.1 (ITS+28S) [Cho et al. 2017b].

= *Microsphaera tarnavschii* Eliade, Lucr Grăd Bot Bucureşti 1970–1971:395. 1972; type host: *Begonia* sp. cult.

= *Oidium begoniae* var. *macrosporum* A.A. Mendonça & Marta Sequ., Agron Lusit 24:109. 1962.

≡ *Pseudoidium macrosporum* (A.A. Mendonça & Marta Sequ.) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):437. 2012.

Host range and distribution (Braun and Cook 2012): On numerous cultivated host species of the genus *Begonia*; South Africa, Asia, Europe, North America, South America (Argentina), New Zealand (origin of this species unknown, and distribution insufficiently known; it is possible that some records of "*Oidium begoniae*" from Australia and South America also belong to *E. begoniicola*).

Notes: A sequence from South Korea and one from the USA are currently available and group together (the Korean sequence is proposed to serve as reference sequence). The type material of *E. begoniicola* is recent enough to be sequenced, so that an epitype would not be justified. The specimen from the USA (UW309) was never deposited in a herbarium.

Erysiphe berberidis DC., Fl franç 2:275. 1805 (var. *berberidis*).

Holotype: FRANCE. Paris, Mont-Rouge, garden of C. Cels, on *Berberis* sp. (G 00122113). *Epitype* (designated in Liu et al. 2022): GERMANY. SACHSEN: Landkreis Görlitz, Niesky, *Berberis vulgaris*, 8 Nov 2006, *H. Boyle & S. Hoeflich* (GLM-F78691). Ex-epitype sequence: OL739137 (ITS+28S).

≡ *Alphitomorpha penicillata* γ *berberidis* (DC.) Wallr., Verh Ges Naturf Freunde Berlin 1(1):40, 1819.

≡ *Erysibe penicillata* var. *berberidis* (DC.) Link, Sp pl 4 6(1):114. 1824.

≡ *Erysiphe penicillata* a. *berberidis* (DC.) Fr., Syst mycol 3:244. 1829.

≡ *Podosphaera berberidis* (DC.) Quel., Champ Jur Vosg 3:106. 1875.

≡ *Microsphaera berberidis* (DC.) Cooke, Microscopic fungi:219. 1865.

= *Microsphaera berberidis* f. *mahoniae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:319. 1927.

= *Microsphaera penicillata* f. *ilicis* Potebia, Gribnye parazity vysshikh rasteny Kharkovskoy i smezhnykh guberny:243. 1915.

≡ *Microsphaera ilicis* (Poteb.) Sandu-Ville, Mem Sect Şti Acad Româna Ser III 11(5):205. 1936.

Host range and distribution: On diverse *Berberis* spp., *Mahonia aquifolium*, and ×*Mahoberberis neubertii*; widespread in Asia, Europe, and North America (for details, see Braun and Cook 2012 and Liu et al. 2022).

Notes: Liu et al. (2022) provided a phylogenetic-taxonomic revision of the *E. berberidis* complex, based on ITS+28S sequence analyses. The results indicate a single species, *E. berberidis*, can be recognized. Other *Erysiphe* species and varieties of *E. berberidis* described on *Berberis* and *Mahonia* spp. have not been reflected in the phylogenetic trees, i.e., all analyzed sequences group together in a uniform large *E. berberidis* clade. Hence, a single species, *E. berberidis*,

is accepted. Morphological deviant collections in Asia have been recognized as morphological varieties [for details on morphology, host range, and distribution, see Liu et al. (2022)].

Erysiphe berberidis var. *asiatica* (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:6. 2000.

≡ *Microsphaera berberidis* var. *asiatica* U. Braun, Mycotaxon 18(1):114. 1983.

Holotype: JAPAN. Sapporo, on *Berberis amurensis* var. *japonica*, 3 Oct 1925, *Y. Homma* (TNS-F-214333).

Erysiphe berberidis var. *dimorpha* (Y.N. Yu & Z.Y. Zhao) L. Liu & U. Braun, Mycoscience 63:231. 2022.

≡ *Microsphaera berberidis* var. *dimorpha* Y.N. Yu & Z.Y. Zhao, Acta Microbiol Sin 21(2):145. 1981.

Holotype: CHINA. XINJIANG UYGUR: Guliu, on *Berberis heteropoda*, 23 Aug 1973, *C.Y. Zhao* 73206 (HMAS 33706).

≡ *Microsphaera dimorpha* (Y.N. Yu & Z.Y. Zhao) U. Braun, Mycotaxon 18(1):115. 1983.

≡ *Erysiphe dimorpha* (Y.N. Yu & Z.Y. Zhao) U. Braun & S. Takam., Schlechtendalia 4:7. 2000.

= *Microsphaera berberidicola* F.L. Tai, Bull Torrey Bot Club 73(2):115. 1946. [*Holotype*: CHINA. PROV. HENAN: On *Berberis dasystachya*, Oct 1939, *J.X. Wang* 507 (HMAS 11528).]

≡ *Erysiphe berberidicola* (F.L. Tai) U. Braun & S. Takam., Schlechtendalia 4:6. 2000.

= *Microsphaera multappendicis* Z.Y. Zhao & Y.N. Yu, Acta Microbiol Sin 21(2):146. 1981. [*Holotype*: CHINA. XINJIANG UYGUR: Ürümqui Shi, on *Berberis amurensis*, 15 Sep 1977, *Zhao* (HMAS 13608).]

≡ *Erysiphe multappendicis* (Z.Y. Zhao & Y.N. Yu) U. Braun & S. Takam., Schlechtendalia 4:11. 2000.

Erysiphe berchemiae (Sawada) U. Braun & S. Takam., Schlechtendalia 4:6. 2000.

≡ *Microsphaera berchemiae* Sawada, Bull Gov Forest Exp Sta Megoro 50:118. 1951.

Lectotype (designated by Braun 1987): JAPAN. PREF. IWATE: Morioka, on *Berchemia floribunda* [= *B. racemosa*], 14 Sep 1910, *T. Fukutani* (FH00965523). *Isolectotype*: IUM. Reference sequence: LC009934 (ITS +28S) [JAPAN. PREF. NIIGATA: Oyashirazu, Itoigawa, on *Berchemia floribunda*, 20 Oct 1996, *S. Takamatsu* (TNS-F-87299)].

Host range and distribution: On *Berchemia* (*floribunda, kulingensis, pauciflora, yunnanensis*), *Berchemiella berchemiifolia* [≡ *Berchemia berchemiifolia*]; Asia (China, Japan).

Notes: The single available sequence obtained from a collection on *E. berchemiae* on its type host, *B. floribunda*, falls in a complex with other *Erysiphe* species on hosts of the Rhamnaceae, including *E. divaricata, E. friesii* var. *friesii*, and *E. friesii* var. *dahurica*. A more comprehensive in-depth analysis of this complex is necessary.

Erysiphe betae (Vaňha) Weltzien, Phytopathol Z 47:127. 1963.

≡ *Microsphaera betae* Vaňha, Z Zuckerind Böhmen 27:180. 1903.

Lectotype (designated by Braun 1987): On *Beta vulgaris, Vaňha* (l.c.: pls. 1–2), original illustration.

= *Erysiphe communis* f. *betae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:235. 1927.

= *Oidium cylindricum* Sawada, Special Publ Coll Agric Natl Taiwan Univ 8:180. 1959, nom. inval. (Art. 39.1).

= *Oidium erysiphoides* f. *chenopodii* J.M. Yen, Cah Pacifique 11:92. 1967.

Host range and distribution (Braun and Cook 2012): On *Beta* (*atriplicifolia, corolliflora, diffusa, intermedia, lomatogona, macrorhiza, patellaris, patula, trigyna, vulgaris, vulgaris* subsp. *maritima* [≡ *maritima*]), *Dysphania* (*ambrosioides* [≡ *Chenopodium ambrosioides*, = *C. ambrosioides* var. *oblanceolatum*, = *C. anthelminticum*], *botrys*), *Spinacea oleracea*; North Africa, North America, South America, Asia (Asia Minor, Central Asia, China, incl. Taiwan, India, Iran, Israel, Japan, Pakistan, Russia [Siberia]), Caucasus, nearly all Europe (except the northernmost countries) [a map of the world distribution was published by Weltzien (1978)].

Notes: ITS+28S sequences retrieved from collections of *Erysiphe betae* group together with *E. heraclei* sequences and forms a single clade. Sequences from *Erysiphe* aff. *betae* on *Fagopyrum esculentum* in Taiwan belong to this complex but seem to represent a separate, undescribed species (Hsiao et al. 2022) (FIG. 3). The whole *E. heraclei* complex requires a comprehensive phylogenetic analysis, based on a multilocus approach, to get better resolution at the species level. Therefore, we currently refrain from designating an epitype, which should be a sample with several sequences that are included in a multilocus analysis.

Erysiphe bistortae Afshan, I. Zafar & Khalid, Mycotaxon 137(4):887. 2022.

Holotype: PAKISTAN. AZAD JAMMU AND KASHMIR: Las Dana, on *Bistorta amplexicaulis*, 26 Sep 2020, *N.S. Afshan & I. Zafar*, LDH-01 (LAH 36943). Ex holotype sequence: MZ048848 (ITS).

Host range and distribution: On *Bistorta amplexicaulis*; Asia (Pakistan).

Notes: This species, recently described from Pakistan (Zafar et al. 2022b), is referred to the *Erysiphe betae* complex, which is insufficiently resolved in ITS analyses. Multilocus analyses are recommendable to clarify the taxonomy of this species. The phylogenetic position of this species on a polygonaceous host is surprising. A closer affinity to *E. polygoni* could be expected.

Erysiphe biuncinata (Cooke & Peck) M. Bradshaw, U. Braun & Pfister, comb. nov.
MycoBank MB853741

Basionym: Podosphaera biuncinata Cooke & Peck, J Bot 10:11. 1872.

Lectotype (designated by Braun 1987): USA. NEW YORK: Poughkeepsie, on *Hamamelis virginiana*, undated, *Gerard* (K(M) 169068). *Syntype*: USA. NEW YORK: Sandlake, on *Hamamelis*, Sep 1871, *M. C. Cooke* (K(M) 169069). *Epitype* (designated here, MycoBank MBT10020085): USA. NORTH CAROLINA: Raleigh, on *Hamamelis virginiana*, 6 Sep 2021, *S. Moparthi* (FH01131024). Ex-epitype sequences: PP681078 (ITS+28S); PP720964 (*CAM*); PP720337 (*GAPDH*); PP720569 (*GS*); PP720444 (*RPB2*); PP720024 (*TUB*).

Host range and distribution: On *Hamamelis* (*japonica, mollis, vernalis, virginiana*); North America (Canada; USA: New England to Illinois, Missouri and southward).

Notes: Several sequences retrieved from specimens of *Podosphaera biuncinata* form a well-supported species clade within *Erysiphe*. This result was surprising, but this is not the first species of *Erysiphe* with a single ascus per chasmothecium as in *Podosphaera*. *Erysiphe monascogera* is another example. Besides the number of asci, the characteristics of the anamorphs are also relevant for the generic affiliation, but details of hyphal appressoria, conidiophores, and conidia of *E. biuncinata* are unreported.

Erysiphe bremeri U. Braun, Mycotaxon 15:133. 1982.

≡ *Erysiphe alhagi* Bremer, Ismen, Karel, Özkan & M. Özkan, Rev Fac Sci Univ Istanbul Ser B 12:140. 1947, non *E. alhagi* Sorokin, 1889.

Lectotype (designated by Braun and Cook 2012): TÜRKIYE (TURKEY). Ankara, on *Alhagi maurorum*, 10 Oct 1943, *H. Bremer* (M-0015828). *Isolectotypes*: Poelt & Scheuer, Reliqu Petrak 1616 (e.g., GZU, M-0015827, W).

= *Trichocladia alhagi* Golovin, Trudy Sredne-Aziatsk Gosud Univ N S Biol Nauk 14 5:7. 1950.

≡ *Microsphaera alhagi* (Golovin) U. Braun, Mycotaxon 14(1):369. 1982.

= *Trichocladia coluteae* f. *sophorae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:311. 1927. [*Lectotype* (designated by Braun and Cook 2012): KAZAKHSTAN ("Turkestan"). Turgay, Tschelkar, Bolshiye Barsuki, on *Pseudosophora alopecuroides*, 12 Oct 1910, *Androssow* [Tranz. & Serebr., Mycoth Ross 267] (M-0016089). *Isolectotypes*: Tranz. & Serebr., Mycoth Ross 267 (e.g., BPI 557557, LEP, LE, M-0019446).]

≡ *Erysiphe sophorae* (Jacz.) U. Braun, in Braun & Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):507. 2012.

Host range and distribution: On *Alhagi* (*canescens, maurorum* [= *camelorum, pseudalhagi*], *graecorum, kirghisorum, sparsifolia*), *Goebelia pachycarpa* [≡ *Sophora pachycarpa*], *Pseudosophora alopecuroides* [≡ *Sophora alopecuroides*], *Sophora* sp.; Asia (Afghanistan, China, Iraq, Iran, Israel, Kazakhstan, Tajikistan, Turkey, Turkmenistan, Uzbekistan), Caucasus (Armenia), Cyprus.

Notes: Darsaraei et al. (2024) examined the phylogeny and taxonomy of *Erysiphe* spp. on legumes in Iran. They confirmed *E. alhagi* as an independent species and that it includes *E. sophorae*, which was reduced to synonymy with *E. alhagi*. Sequences retrieved from *E. alhagi* and *E. sophorae* were identical and formed a small clade within the *E. astragali* complex.

Erysiphe buhrii U. Braun, Česka Mykol 32(2):80. 1978, nom. cons. (Braun 2013).

≡ *Erysiphe pisi* var. *buhrii* (U. Braun) Ialongo, Mycotaxon 44(1):255. 1992.

Holotype: GERMANY. SACHSEN-ANHALT: Halle (Saale), Dölauer Heide, on *Silene latifolia* subsp. *alba*, 1975, *U. Braun* (PR 781039). *Isotypes*: HAL 1380 F, HAL 1504 F. *Paratypes*: JE, LE, K, NY. Reference sequence: LC009958.1 (ITS+28S) [GERMANY. SACHSEN-ANHALT: Halle (Saale), Halle-Neustadt, center, on *Silene latifolia* subsp. *alba*, 2 Sep 1978, *U. Braun* (collected near the type locality) (TNS-F-87227)].

= *Oidium dianthi* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:461. 1927, nom. rej.

= *Oidium gypsophilae* Sandu, Stud Cercet Şti (Iaşi) Ser 2 Şti Agric 13:274. 1962.

For full synonymy, including diverse formae, see Braun and Cook (2012:367).

Host range and distribution (Braun and Cook 2012): On numerous host species of diverse genera of the Caryophyllaceae (*Acanthophyllum, Arenaria, Cerastium, Cucubalus, Dianthus, Eremogone, Gypsophila, Lychnis, Minuartia, Saponaria, Silene, Stellaria*); North Africa, North America (Mexico,

USA), South America (Argentina), Asia (Asia Minor, Central Asia, China, Iran, Iraq, Israel, Mongolia, Russia, Siberia, South Korea, Turkey), Caucasus (Armenia), almost all Europe.

Notes: Sequences retrieved from *E. buhrii* form a well-supported clade in ITS+28S analyses. A sequence obtained from *Erysiphe* "*buhrii*" on *Arenaria macrophylla*, collected in California, USA (FH01122079), groups separately and seems to represent an allied undescribed species. The type material of *E. buhrii* has not yet been sequenced. For the interim, we propose to use a sequence obtained from a specimen collected near the type locality as a reference sequence.

Erysiphe caryae (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:6. 2000.

≡ *Microsphaera caryae* U. Braun, Feddes Repert 92:509. 1981.

Holotype: USA. MISSOURI: Perryville, on *Carya tomentosa* [= *C. alba*], Oct 1886, *Demetrio* [Rabenh., Fungi Eur Exs 3953] (HAL, s.n.). *Isotypes*: Rabenh., Fungi Eur Exs 3953 (e.g., M-0015928, M-0015929, BPI 555639). *Epitype* (designated here, MycoBank MBT10020086): USA. ILLINOIS: Ogel County, on *Carya tomentosa* [= *C. alba*], 5 Sep 1888, *M.B. Waite* (ILL00087801). Ex-epitype sequences: PP681029 (ITS +28S); PP720905 (*CAM*); PP720303 (*GAPDH*); PP720708 (*GS*); PP720499 (*RPB2*).

= *Microsphaera penicillata* f. *caryae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:356. 1927.

≡ *Microsphaera juglandis* f. *caryae* (Jacz.) Golovin, Trudy Bot Inst Imeni VL Komarova Akad Nauk SSSR Ser 2 10:348. 1956.

Host range and distribution: On *Carya* (*illinoensis* [= *ovaliformis, pecan*], ?*ovata, sulcata, tomentosa* [= *alba*]); North America (USA, widespread).

Notes: Sequences obtained from *Erysiphe caryae* form a highly supported species clade.

Erysiphe castaneae U. Braun, Schlechtendalia 10:92. 2000.

≡ *Microsphaera americana* U. Braun, Mycotaxon 14:371. 1982, non *Erysiphe americana* U. Braun, 1993.

Holotype: CANADA. ONTARIO: Elgin County, Port Stanley, on *Castanea dentata*, 29 Aug 1912, *Dearness* (DAOM 136275). *Epitype* (designated here, MycoBank MBT10020087): USA. MASSACHUSETTS: Norfolk County, East Walpole, on *Castanea dentata*, 27 Aug 1933, *G.D. Darker* (FH01122150). Ex-epitype sequences: PP681106 (ITS+28S); PP720979 (*CAM*); PP720300 (*GAPDH*); PP720552 (*GS*); PP720423 (*RPB2*); PP719987 (*TUB*).

= *Microsphaera penicillata* f. *castaneae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:354. 1927.

Host range and distribution (Braun and Cook 2012): On *Castanea* (*alabamensis, crenata, dentata* [= *americana*], *ozarkensis, pumila, sativa* [= *vesca*], and hybrids with American species), *Castanopsis* (*chrysophylla*, sp.); North America (Canada; USA: eastern states, Massachusetts to Ohio and North Carolina).

Notes: Sequences, including an ex-epitype sequence, retrieved from *Erysiphe castaneae* form a well-supported species clade in the phylogenetic analyses.

Erysiphe castaneigena U. Braun & Cunnington, Schlechtendalia 14:85. 2006.

≡ *Microsphaera sinensis* Y.N. Yu, J NE Forest Inst 12 (4):32. 1982.

≡ *Erysiphe sinensis* (Y.N. Yu) U. Braun & Cunnington, Schlechtendalia 10:92. 2003, nom. illeg., non *E. sinensis* (F.L. Tai & C.T. Wei) U. Braun & S. Takam., 2000.

Holotype: CHINA. PROV. HUBEI: Zigui Xian, on *Castanea mollissima* [= *bungeana*], 24 Oct 1978, *Zheng & Lai* 84 (HMAS 40689). Reference sequence: LC010079.1 [JAPAN. PREF. TOYAMA: Kamiichi, on *Castanea crenata*, 24 Jun 1995, *Y. Sato* (TNS-F-88347)].

Host range and distribution: On *Castanea* (*crenata, henryi, mollissima*) and *Castanopsis delavayi*; Asia (China, Japan, Korea).

Notes: Cho et al. (2017a) collected numerous samples of this species in South Korea and provided results of sequence analyses. A specimen from Iran (IRAN 14248 F) was previously identified as *E. castaneigena* based on morphology (Abbasi et al. 2013). However, Darsaraei et al. (2023) sequenced this specimen and revealed it as *E. alphitoides*. The holotype of *E. castaneigena* is relatively young and suitable for sequencing attempts. For the interim, we propose to use LC010079.1 as reference sequence for phylogenetic purposes.

Erysiphe caulicola (Petr.) U. Braun, Mycotaxon 15:135. 1982.

≡ *Microsphaera caulicola* Petr., Sydowia 3:284. 1949.

Holotype: IRAN. PROV. SEMNAN: Shahrud-Bastam, "In declivibus australibus montium Shahvar ad supra Nekarman (Nigarman), Alm Racheh," on *Astragalus* sp., 20–26 Jul 1949, *K.H. & F. Rechinger* [Iter Iranicum II, 1949] (W, Acqu. 1949, no. 2077).

Host range and distribution (Braun and Cook 2012; Kabaktepe et al. 2020; Negrean and Denchev 2004): On *Astragalus* (*glycyphyllos, pseudoglaucus, vesicarius,*

virgatus, sp.); Asia (Iran, Kazakhstan, Turkey), Europe (Bulgaria, Hungary, Ukraine).

Notes: Negrean and Denchev (2004) recorded *E. caulicola* from Bulgaria on *Astragalus vesicarius*, and Kabaktepe et al. (2020) listed *E. caulicola* on *Astragalus* sp. from Turkey. Darsaraei et al. (2024) provided a single sequence of *E. caulicola* obtained from *Astragalus* sp. in Iran, which confirmed the independent species status of this powdery mildew.

Erysiphe ceanothi Schwein., Trans Amer Philos Soc 4:269. 1834.

≡ *Microsphaera ceanothi* (Schwein.) U. Braun, Mycotaxon 15:125. 1982.

Lectotype (designated by Braun 1987): USA. PENNSYLVANIA: Lehigh and Northampton, Bethlehem, on *Ceanothus americanus*, herb. *Schweinitz* (PH00062365). *Isolectotypes*: BPI 1052306, FH00972548. *Epitype* (designated here, Mycobank MBT10020088): USA. WISCONSIN: Dane County, Madison, on *Ceanothus americanus*, 10 Aug 1923, *J.R. Heddle* (FH01122163). Ex-epitype sequences: PP680846 (ITS+28S); PP720892 (*CAM*); PP720126 (*GAPDH*); PP720740 (*GS*); PP719989 (*TUB*).

= *Microsphaera penicillata* f. *ceanothi* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:360. 1927.

Host range and distribution: On *Ceanothus americanus*; North America (USA, throughout the entire area of distribution of the host).

Notes: Sequences obtained from *Erysiphe ceanothi* form a well-supported species clade, with *E. sydowiana* in sister position.

Erysiphe clethrae (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:7. 2000.

≡ *Microsphaera clethrae* U. Braun, Mycotaxon 15:121. 1982.

Holotype: JAPAN. Tokyo, Mt. Mitake, on *Clethra barbinervis*, 11 Nov 1978, *Y. Nomura*, YNMH 4749-3 (HAL 1451 F). *Isotype*: TNS. Reference sequence: LC010081.1 [JAPAN. PREF. TOYAMA: Mt. Kureha, on *Clethra barbinervis*, 29 Sep 1995, *Y. Sato* (TNS-F-88358)].

Host range and distribution: On *Clethra barbinervis*; Asia (Japan, endemic).

Notes: The type material of *Erysiphe clethrae* is relatively recently collected and suitable to be sequenced. For the interim, we propose LC010081.1 as reference sequence for phylogenetic-taxonomic purposes.

Erysiphe convolvuli DC., Fl franç 2:274. 1805.

Lectotype (designated by Braun 1987): FRANCE. "*Erysiphe convolvuli* fl. fr. 736," on *Convolvulus arvensis*, herb. *de Candolle* (G 00122098). Reference sequence: AF154327 (ITS) [Switzerland (Cunnington et al. 2003)].

= *Erysiphe convolvuli-sepii* Castagne, Cat pl Marseille:188. 1845; type host: *Calystegia sepium*.

= *Erysiphe convolvuli* var. *calystegiae* U. Braun, Nova Hedwigia 34:691. 1981. [*Holotype*: GERMANY. HESSEN: Rheingau-Taunus-Kreis, Eltville, Hattenheim, on *Calystegia sepium* [Fuckel, Fungi Rhen Suppl Fasc VIII No. 2237] (HAL, s.n.). *Isotypes*: Fuckel, Fungi Rhen Exs 2237 (e.g., FH, G).]

Host range and distribution: On diverse host species of *Calystegia* and *Convolvulus*; Africa, Asia, Caucasus, Europe, North and South America (for details, see Braun and Cook 2012). Furthermore, also occurring on *Ipomoea aquatica* and *I. tricolor* (Abasova et al. 2018; Takamatsu et al. 2015b).

Notes: Erysiphe convolvuli has been confirmed as an independent species in phylogenetic analyses (Takamatsu et al. 2015b; present analyses). However, sequences retrieved from collections on *Calystegia* spp., assigned to *Erysiphe convolvuli* var. *calystegiae*, are not different from sequences of *E. convolvuli* on *Convolvulus* spp. (such as LC270835, retrieved from *E. convolvuli* on *Calystegia sepium*; Abasova et al. 2018). Postulated differences in the number of ascospores per ascus (Braun and Cook 2012) are not consistent; hence, it is not suitable to maintain a special variety for collections on *Convolvulus* spp. *Ipomoea* spp. are infected by *E. convolvuli* (Abasova et al. 2018; Hsiao et al. 2022; Takamatsu et al. 2015b) as well as *E. ipomoeae* (Hsiao et al. 2022), which belongs to the *E. alphitoides* complex. Pan et al. (2020) recorded "*E. alphitoides*" on *Ipomoea obscura*, a report that refers to *E. ipomoeae. Erysiphe convolvuli* is part of a complex of species that requires mulilocus sequence analyses to be better resolved in the future. Therefore, we currently refrain from introducing a formal epitype and propose to use a reference sequence (AF154327) for the interim.

Erysiphe cruchetiana S. Blumer, Beitr Krypt-Fl Schweiz 7(1):193. 1933.

≡ *Erysiphe pisi* var. *cruchetiana* (S. Blumer) U. Braun, Nova Hedwigia 34:692. 1981.

Lectotype (designated by Braun 1987): GERMANY. On *Ononis arvensis*, "Ad O. arvensis folia, frequens. Autumno," [Fuckel, Fungi Rhen Exs Fasc VII no. 675, 1863, as *Erysiphe communis* f. *ononidis*] (HAL, s.n.). *Isolectotypes*: Fuckel, Fungi Rhen Exs 675 (e.g., FH, G). *Epitype* (designated by Darsaraei et al. 2024): GERMANY. BRANDENBURG: Landkreis Haveland,

Dallgow-Döberitz, ca. 0.7 km east northeast of nature reserve Dölbitzer Heide, on *Ononis repens*, 20 Sep 2010, *V. Kummer* (HAL 3488 F). Ex-epitype sequence: OQ266914.1 (ITS+28S).

= *Erysiphe communis* f. *ononidis* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:236. 1927.

Host range and distribution: On diverse host species of the genus *Ononis*; Africa (Morocco), Asia, Caucasus, Europe (for details, see Braun and Cook 2012).

Notes: Braun and Cook (2012) treated *E. cruchetiana* as variety of *E. pisi*. Schmidt and Braun (2020) examined the anamorph and conidial germination pattern of *Erysiphe* on *Ononis* spp. in detail, found differences to *E. pisi*, and recommended recognizing this species, *E. cruchetiana*, as originally described. Darsaraei et al. (2024) analyzed sequences retrieved from *E. cruchetiana* collected in Germany and Iran and confirmed the status as a separate species, confined to *Ononis* spp. as hosts.

Erysiphe cruciferarum Opiz ex L. Junell, Sv Bot Tidskr 61 (1):217. 1967, s. str. (emend. Bradshaw et al. 2024c).

≡ *Erysiphe cruciferarum* Opiz, Lotos 5:42. 1855, nom. nud.

≡ *Erysiphe pisi* var. *cruciferarum* (Opiz ex L. Junell) Ialongo, Mycotaxon 44(1):255. 1992.

Holotype: CZECH REPUBLIC. Praha, Lieben, on *Alyssum alyssoides*, 1841, *F.M. Opiz* (PRM194779). Ex-holotype sequences: KU672364 (ITS); KU672344 (28S).

= *Erysiphe communis* f. *alyssi* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:238. 1927.

Host range and distribution: On *Alyssum* (*alyssoides, dasycarpum, desertorum, hirsutum, macropodum, montanum, repens, simplex, strictum, strigosum, trichostachyum, turkestanicum*), *Aurinia* (*petraea* [≡ *Alyssum petraeum*], *saxatilis* [≡ *Alyssum saxatile*]), *Berteroa incana*; North Africa (Morocco), Asia (Iran, Kazakhstan, Turkmenistan, Uzbekistan), Caucasus (Armenia, Azerbaijan, Georgia), Europe (Austria, Bulgaria, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Italy, Lithuania, Netherlands, Poland, Portugal, Romania, Spain, Sweden, Switzerland).

Notes: Bradshaw et al. (2024c) published a comprehensive phylogenetic-taxonomic revision of *E. cruciferarum* s. lat. and pointed out that this species must be confined to *Alyssum* spp., *Aurinia* spp., and *Berteroa incana*, all belonging to the cruciferous tribe Alysseae. This result confirms the findings of Pastirčáková et al. (2016) that *E. cruciferarum* s. str. is confined to these hosts.

Erysiphe diffusa (Cooke & Peck) U. Braun & S. Takam., Schlechtendalia 4:7. 2000.

≡ *Microsphaera diffusa* Cooke & Peck, J Bot NS 1:13. 1872.

≡ *Trichocladia diffusa* (Cooke & Peck) Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:313. 1927.

Lectotype (designated by Braun 1987): USA. NEW YORK: Albany, on *Desmodium canadense*, Sep/Oct 1871, *C.H. Peck* (NYSf3480). *Isolectotypes*: K(M) 169041, NYSf1011. Ex-lectotype sequence: PP680970 (ITS+28S).

= *Oidium caricae* F. Noack, Bol Inst Agron Estado São Paulo 9(2):81. 1898. [*Holotype*: BRAZIL: SÃO PAULO: Campinas, on *Carica papaya*, Nov 1897, *F. Noack* (K(M) 102465). *Epitype* (designated by Liberato et al. 2004): BRAZIL. MINAS GERAIS: Viçosa, on *Carica papaya*, 29 May 2003, *J.R. Liberato* (VIC 26556).] Ex-epitype sequence: MF616622 (ITS).

≡ *Pseudoidium caricae* (F. Noack) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):369. 2012.

= *Trichocladia diffusa* f. *desmodii* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:313. 1927.

= *Trichocladia diffusa* f. *glycyrrhizae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:314. 1927.

= *Erysiphe communis* f. *desmanthi* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:253. 1927.

= *Microsphaera diffusa* f. *elongata* U. Braun, Mycotaxon 20:492. 1984. [*Holotype*: USA. WASHINGTON: Bremerton, on *Psoralea physodes*, 15 Aug 1912, *Bartholomew* (FH00965532).]

≡ *Erysiphe diffusa* var. *elongata* (U. Braun) U. Braun, Taxonomic Manual of the Erysiphales (Powdery Mildews):454. 2012.

= *Microsphaera trifolii* var. *desmanthi* U. Braun, Mycotaxon 19:375. 1984, syn. nov. [*Holotype*: USA. MISSOURI: St. Louis, on *Desmanthus illinoensis*, Oct 1886, herb. *Trelease* (collected by *L.H. Pammel*) (FH00965542).] Ex-holotype sequence: PP681010 (ITS+28S).

≡ *Erysiphe trifolii* var. *desmanthi* (U. Braun) U. Braun, Schlechtendalia 4:15. 2000.

≡ *Erysiphe desmanthi* (U. Braun) U. Braun, Mycotaxon 112:176. 2010.

Host range and distribution (phylogenetically proven hosts): Caricaceae—*Carica papaya* (Braun et al. 2017); Fabaceae—*Crotalaria* sp., *Cymopsis tetragonoloba, Desmanthus illinoenis, Desmodium* (*canadense, illionense, incanum, laevigatum* [= *rhombifolium*], *viridiflorum*), *Erythrina indica, Flemingia prostrata, Glycine* (*clandestina, max* subsp. *max, max* subsp. *soja* [≡ *soja*], sp.), *Glycyrrhiza lepidota, Macrotyloma uniflora, Mimosa caesalpiniifolia, Sohmaea diffusa* [≡ *Meibomia diffusa*], *Wisteria sinensis*; Rutaceae—*Bergera koenigii* (Moparthi et al. 2023); Asia (China, India, Japan,

South Korea, Taiwan, Vietnam), Australia, Europe (Spain), North America (Canada, USA), South America (Brazil, Argentina).

Host range and distribution (according to Braun and Cook 2012, based on morphology): On *Alysicarpus longifolius, Bauhinia* (*variegata*, sp.), *Cologania* sp., *Crotalaria* (*brevidens* [= *intermedia*], *juncea, maxillaris, retusa*), *Desmodium* (*canadense, canescens, cuspidatum* [= *bracteoseum*], *glutinosum, grandiflorum, griffithianum* [= *adscendens*], *heterocarpon* var. *strigosum* [= *polycarpum*], *illinoense, incanum* [= *frutescens*], *longifolium, nudiflorum, paniculatum* [= *dillenii*], *perplexum, rhombifolium, rigidum, scorpiurus, sessilifolium, tortuosum* [= *purpureum*], *viridiflorum*, sp.), *Dolichos biflorus, Glycine* (*max*, sp.), *Glycyrrhiza lepidota, Indigofera* sp., *Lespedeza* (*bicolor, capitata, hirta, repens, stipulacea, striata, stuevei, violacea, virginica*), *Lupinus* (*angustifolius, perennis*), *Oxytropis campestris, Robinia pseudoacacia, Ruprechtia physodes, Senna occidentalis, Styphnolobium japonicum* [≡ *Sophora japonica*]; North America (Canada, Mexico, USA, widespread), Central and South America, Galapagos Islands, Asia (China, Korea, Japan, Far East of Russia).

Notes: Erysiphe diffusa in the present circumscription undoubtedly represents a heterogenous complex. There is no support in our analysis (FIG. 4). Phylogenetic multilocus analyses are urgently needed. For the time being, we prefer to maintain *E. diffusa* in the current wider circumscription, at least tentatively. In this circumscription, *E. diffusa* is a widespread powdery mildew species on diverse hosts of the Fabaceae in Asia and North and South America. However, it has been shown by means of sequence analyses that sequences retrieved from hosts of other plant families, including *Carica papaya* (Caricaceae) (Braun et al. 2017) and *Bergera koenigii* (Rutaceae) (Moparthi et al. 2023), group together with sequences obtained from *E. diffusa* on legumes. Sequence analyses of type material of *Microsphaera desmanthi* group its sequences with *E. diffusa* sequences. Therefore, we tentatively consider *M. desmanthi* a synonym of *E. diffusa*. The description of this species (Braun 1984; as *Microsphaera trifolii* var. *desmanthi*) was possibly based on an immature collection with rarely branched apices of chasmothecial appendages. Kelly et al. (2021) recently introduced *Erysiphe vignae*, based on Australian anamorphs on *Phaseolus* and *Vigna* spp., as sister species to *E. diffusa*. This name undoubtedly refers to previous collections on *Phaseolus* spp. assigned to *E. diffusa*. It was to be expected that the chasmothecia resemble those of *E. diffusa*. This assumption turned out to be correct. The *E. vignae* specimen on *Strophostyles leiosperma* (≡ *Phaseolus leiospermus*) with chasmothecia (FH01122172), confirmed the overall similarity of the *E. vignae* teleomorph with chasmothecia of *E. diffusa*. However the two species are distinguishable on the base of the length of the chasmothecial appendages (see under *E. vignae*). A North American collection on *Strophostyles leiosperma* (≡ *Phaseolus leiospermus, Strophostyles pauciflora*), originally identified as *Microsphaera diffusa*, has been sequenced and falls within the *E. vignae* clade, which is not surprising since *Strophostyles*, along with *Phaseolus* and *Vigna*, are referred to the legume tribe Phaseoleae subtribe Phaseolinae. *Erysiphe diffusa* collections on *Apios americana* turned out to be an additional new species, described herein as *Erysiphe salmoniana*, sp. nov. The holotype of *M. desmanthi* is very old, and only sequence data for the ITS2 region were accomplished.

Erysiphe discariae (Havryl.) U. Braun & S. Takam., Schlechtendalia 4:7. 2000.

≡ *Microsphaera discariae* Havryl., Nova Hedwigia 61:448. 1995.

Holotype: ARGENTINA. PROV. NEUQUÉN: Dept. Huiliches, lago Tromen, on *Discaria chacaye*, Feb 1994, *M.I. Messuti* [*Havrylenko* 228] (LPS 45277). *Isotypes*: BCRU 386, BCRU 387. Reference sequence: LC010007.1 (only 28S) [ARGENTINA. PROV. RÍO NEGRO: Chall Huaco, on *Discaria chacaye*, 18 Apr 2001, *S. Takamatsu* (TNS-F-87766)].

Host range and distribution: On *Discaria chacaye*; South America (Argentina: Neuquén, Río Negro, Tierra del Fuego).

Notes: So far, only a single 28S sequence obtained from *E. discariae* is available, which groups with sequences of *E. ribicola, E. ovidiae* (LC009882.1, only 28S), and *Erysiphe* (Pseudoidium) sp. on *Schinus patagonicus* (LC010018.1, ITS+28S) [ARGENTINA. PROV. RÍO NEGRO: San Carlos de Bariloche, Nahuel Huapi Lake, Victoria Island, 29 Feb 2004, *S. Takamatsu* (TNS-F-87818)] in an insufficiently resolved complex (Takamatsu et al. 2015b). Additional sequences retrieved from *E. discariae* are urgently necessary.

Erysiphe divaricata (Wallr.) Schltdl., Fl berol 2:169. 1824.

≡ *Alphitomorpha divaricata* Wallr., Verh Ges Naturf Freunde Berlin 1(1):39. 1819.

≡ *Erysiphe* (as "*Erysibe*") *divaricata* (Wallr.) Link, Sp pl 4 6(1):112. 1824.

≡ *Microsphaera divaricata* (Wallr.) Sacc., Syll fung 1:11. 1882.

≡ *Microsphaera alni* var. *divaricata* (Wallr.) E.S. Salmon, Mem Torrey Bot Club 9:146. 1900.

[*Type*: On *Frangula alnus*, Germany, Wallroth, not preserved.] *Neotype* (designated by Braun and Cook

2012): GERMANY. SACHSEN: Königstein and Schandau, on *Frangula alnus*, Sep 1886, 1893, Oct 1892, *W. Krieger* [Krieger, Fungi Saxon Exs 1223] (HAL, s.n.). *Isoneotypes*: Krieger, Fungi Saxon Exs 1223 (e.g., BPI 557181, CUP, M-0016146, NY02941221). Reference sequence: LC009956 (ITS +28S) [LITHUANIA. Vilnius: On *Frangula alnus*, 25 Aug 1999, *B. Grigaliūnaitė* (TNS-F-87468)].

= *Erysiphe* (as "*Erysibe*") *divaricata* var. *frangulae* Link, Sp pl 4 6(1):113. 1824.

= *Erysiphe penicillata* d. *rhamni-frangulae* Fr., Syst mycol 3:244. 1829.

≡ *Microsphaera penicillata* var. *rhamni-frangulae* (Fr.) W.B. Cooke, Mycologia 44:573. 1952.

Host range and distribution: On *Frangula alnus*; Europe (from Portugal to the European part of Russia and the Baltic states, also in northern Europe, Finland, Sweden).

Notes: ITS+28S sequences obtained from *Erysiphe divaricata* groups together with *E. friesii* sequences. Sequences of the two species are insufficiently differentiated, although *E. divaricata* is morphologically readily distinguishable from *E. friesii* by having chasmothecia with much longer chasmothecial appendages, (1.5–)3–5 (–7) times as long as the chasmothecial diameter. Phylogenetic multilocus analyses are necessary to clarify the status of the two species. Therefore, we currently refrain from introducing an epitype.

Erysiphe epigena S. Takam. & U. Braun, Mycol Res 111:821. 2007.

Holotype: JAPAN. PREF. AICHI: Nagoya, Higashiyama Botanical Garden, on *Quercus variabilis*, 15 Nov 1996, *S. Takamatsu* (TNS-F-872266 [formerly MUMH 148]). *Isotype*: HAL 2001 F. Ex-holotype sequence: AB292718 (ITS+28S).

= *Microsphaera alphitoides* var. *chenii* U. Braun, Mycotaxon 15:139. 1982. [*Holotype*: CHINA. PROV. ANHUI: Pan Pien Chi, Ch'ing Yang Hsien, Chiu hua Shan, on *Quercus chenii*, 26 Oct 1932, *Cheo* 1412 (FH00965518).] Ex-holotype sequence: OM436185. Ex-paratype sequence: OM436187.

≡ *Erysiphe alphitoides* var. *chenii* (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:5. 2000.

Host range and distribution: On *Quercus* (*acutissima, chenii, variabilis*); Asia (China, Japan).

Notes: Based on sequence analyses of type material, Bradshaw et al. (2022e) reduced *Microsphaera alphitoides* var. *chenii* to synonymy with *E. epigena*.

Erysiphe euphorbiicola U. Braun & S. Takam., Schlechtendalia 4:8. 2000.

≡ *Microsphaera euphorbiae* Berk. & M.A. Curtis, Grevillea 4:160. 1876, non *Erysiphe euphorbiae* Peck, 1874.

≡ *Trichocladia euphorbiae* (Berk. & M.A. Curtis) Jacz., Karm Opred Grib Vip 2 Muchn-rosj grib: 297. 1927.

Lectotype (designated by Braun and Cook 2012): USA. "Carol. inf.," on *Euphorbia* sp., ex herb. *Berkeley, Ravenel* 1125 (K(M) 169052). *Isolectotype*: FH00972668.

= ?*Oidium poinsettiae* U. Braun, Minnis & Yáñez-Moral., Schlechtendalia 19:55. 2009. [*Holotype*: USA. New York, Riverhead, Long Island Horticultural Research Laboratory, on *Euphorbia pulcherrima*, Feb 1994, *M. Daughtrey* (HAL 1674 F).] Ex-holotype sequences: OR425011 (ITS+28S); PP720897 (*CAM*); PP720114 (*GAPDH*).

≡ ?*Pseudoidium poinsettiae* (U. Braun, Minnis & Yáñez-Moral.) U. Braun, Minnis & Yáñez-Moral., in Braun & Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):616. 2012.

Host range and distribution: On *Euphorbia* (*corollata, dentata, heterophylla, hypericifolia* [= *brasiliensis*], *hyssopifolia, maculata, marginata, nutans* [= *preslii*], ?*pulcherrima*, sp.); North America (Mexico; USA: widespread from Kansas and Iowa to Michigan and to Montana and Georgia), southward to Central America, West Indies, and South America (e.g., Costa Rica, Cuba, Dominican Republic, El Salvador, Guatemala, Puerto Rico, Venezuela), introduced in Europe (Denmark, Germany, Sweden, UK).

Notes: Phylogenetic analyses of sequences retrieved from specimens of *Erysiphe euphorbiicola* and *Pseudoidium poinsettiae* suggest that a single species might be involved, i.e., ITS sequences of the poinsettia powdery mildew are not different from the common American *Euphorbia Erysiphe*. However, the whole *E. euphorbiicola* complex requires multilocus analyses for final conclusions. Therefore, a potential synonymy of *Oidium poinsetiae* with *E. euphorbiicola* remains unclear and tentative (Bradshaw et al. 2024c). The postulated morphological differences of the anamorphs of *E. euphorbiicola* and *O. poinsettiae* (de Jesús Yáñez-Morales et al. 2009) do not hold true; the characteristics of the conidiophores undoubtedly have much variation. Interestingly, an examined collection on *Euphorbia heterophylla* from Honduras (BPI 558180) was assigned to *O. poinsettiae*, based on its morphology (Braun and Cook 2012). *Euphorbia heterophylla* is also a host of *E. euphorbiicola*.

Erysiphe friesii (Lév.) U. Braun & S. Takam., Schlechtendalia 4:8. 2000 (var. *friesii*).

≡ *Calocladia friesii* Lév., Ann Sci Nat Bot Sér 3 15:155. 1851.

≡ *Microsphaera friesii* (Lév.) Sacc., Syll fung 1:13. 1882.

Lectotype (designated by Braun 1987): On *Rhamnus cathartica*, Léveillé (1851:pl. 8, fig. 94), original drawing. *Epitype* (designated here, MycoBank MBT10020089): GERMANY. RHEINLAND-PFALZ: Bad Dürkheim, Kaierslautener Street, Pfalzmuseum of Natural History, garden of the museum, on *Rhamnus cathartica*, 24 Nov 2022, *J. Kruse* (POLL 0060000219). Ex-epitype sequences: PP681007 (ITS+28S); PP720544 (*GS*); PP720520 (*RPB2*); PP720106 (*TUB*).

= *Alphitomorpha penicillata* α *rhamni-catharticae* Schltdl., Verh Ges Naturf Freunde Berlin 1:49. 1819.

≡ *Erysiphe* (as "*Erysibe*") *penicillata* var. *rhamni-catharticae* (Schltdl.) Link, Sp pl 4 6(1):114. 1824.

= *Erysiphe penicillata* c. *rhamni-cathartici* Fr., Syst mycol 3:242. 1829.

= *Erysiphe penicillata* e. *rhamni* Rabenh., Deutschl Krypt-Fl 1:236. 1844.

= *Calocladia penicillata* f. *rhamni-carthatici* Thüm., Mycoth Univ 2054. 1881.

= *Microsphaera penicillata* f. *rhamni-cathartici* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:360. 1927.

Host range and distribution: On *Rhamnus* (*californica, cathartica, purshiana, saxatilis*); Asia (Central Asia and northwestern China), Caucasus (Armenia), Europe (widespread, from France eastward to Russia, and in northern Europe).

Notes: Braun and Cook (2012) accepted the separation of *E. friesii* into two varieties, viz., var. *friesii* and var. *dahurica*. However, the present phylogenetic analyses have shown that sequences obtained from Asian collections assigned to var. *dahurica* form a separate group, close to *E. friesii* together with sequences obtained from *E. berchemiae*. The *E. friesii* clade, made up of sequences of European origin, is also not clear. A sequence retrieved from *E. divaricata* on *Frangula alnus* falls in this clade. These results do not currently allow final taxonomic conclusions. The whole complex, including *E. berchemiae, E. divaricate*, and *E. friesii* s. lat., requires a phylogenetic multilocus approach. For the interim, we prefer to maintain *E. friesii* var. *dahurica* in the circumscription used in Braun and Cook (2012).

Erysiphe friesii var. *dahurica* (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:8. 2000.

≡ *Microsphaera friesii* var. *dahurica* U. Braun, Mycotaxon 16(2):420. 1983.

Holotype: JAPAN. PREF. IWATE: Morioka, on *Rhamnus davurica* var. *nipponica*, 23 Sep 1903, *Yamada* (TNS-F-217398). Reference sequence: LC010070.1 (ITS+28S) [CHINA. PROV. JILIN: Changchun, on *Rhamnus davurica*, 26 Aug 2007, *S. Takamatsu* (TNS-F-88080)].

Host range and distribution: On *Rhamnus* (*alnifolia, davurica, diamantiaca, japonica, nipponica, purpurea, ussuriensis*); Asia (China, Japan, Korea, Pakistan, Russia [Far East]).

Notes: See above under var. *friesii*. Var. *dahurica* has recently been recorded from Pakistan on *Rhamnus purpurea*, confirmed by sequence analyses (Afshan et al. 2023). A sequenced Japanese specimen, suitable as epitype, is currently not yet available.

Erysiphe guarinonii (Briosi & Cavara) U. Braun & S. Takam., Schlechtendalia 4:9. 2000.

≡ *Microsphaera guarinonii* Briosi & Cavara, Fung Paras Piante Colt Util Ess 172. 1892 [and Hedwigia 31:142. 1892].

≡ *Trichocladia guarinonii* (Briosi & Cavara) Škorič, Glasn Šumske Pokuse 1:100. 1926.

Lectotype (designated by Braun 1987): ITALY. Varallo, on *Laburnum anagyroides*, 1891 [Briosi & Cavara, Fung Paras Piante Colt Util Ess 172] (HAL, s. n.). *Isolectotypes*: Briosi & Cavara, Fung Paras Piante Colt Util Ess 172 (e.g., BPI 558444, CUP, M-0016330, PUL, S-F8772).

= *Trichocladia diffusa* f. *cytisi* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:314. 1927.

= ?*Erysiphe communis* f. *cytisi* Marchenko, Ukrayins'k Bot Zhurn 33(3):274. 1976.

= ?*Oidium hardenbergiae* Boesew., Rev Mycol 41:497. 1977.

≡ *Pseudoidium hardenbergiae* (Boesew.) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):606. 2012.

= *Erysiphe baptisiae* U. Braun & J. Kruse, Mycotaxon 112:176. 2010. [*Holotype*: GERMANY. NIEDERSACHSEN: Hannover, Herrenhausen/Leinhausen, Vinnhorster Weg, Schulbiologiezentrum, on *Baptisia australis* (cult.), 5 Oct 2009, *J. Kruse* (HAL 2337 F).] Ex-holotype sequence: MT524083 (ITS+28S).

Notes: Based on sequence analyses of the type material, Bradshaw et al. (2020b) reduced *E. baptisiae* to synonymy with *E. guarinonii. Oidium hardenbergii* is an additional potential synonym. A sequence retrieved from this species, collected in Australia on *Hardenbergia* sp. (AY450959.1), falls within the *E. guarinonii* clade. Furthermore, Bradshaw et al. (2022a) examined a sample of *Erysiphe* sp. on *Lupinus micranthus* from Portugal

(KR-M-0022477, sequence MZ265171) that is located at the base of the *E. guarinonii* clade. It is not yet clear whether it is referable to *E. guarinonii* or whether it represents an undescribed sister species. Additional sequences are necessary.

Erysiphe heraclei DC., Fl. franç. 6:107. 1815.

≡ *Alphitomorpha heraclei* (DC.) Wallr., Ann Wetterauischen Ges Gesammten Naturk N F 4:240. 1819.

≡ *Alphitomorpha communis* β *umbelliferarum* Wallr., Verh Ges Naturf Freunde Berlin 1(1):31. 1819.

≡ *Erysibe communis* var. *umbelliferarum* (Wallr.) Link, Sp pl 4 6(1):106. 1824.

≡ *Erysiphe communis* i. *umbelliferarum* (Wallr.) Fr., Syst mycol 3:241. 1829.

≡ *Ischnochaeta heraclei* (DC.) Sawada, Bull Gov Forest Exp Sta Meguro 50:113. 1951, nom. inval. (Art. 35.1).

≡ *Erysiphe pisi* var. *heraclei* (DC.) Ialongo, Mycotaxon 44:255. 1992.

Lectotype (designated by Braun 1987): "Schleich., Crypt. Exs. 89, *Sclerotium Heraclei* S. In fol. Heracl. Sphond.," on *Heracleum sphondylium*, herb. *de Candolle* (G 00122105). Reference sequence: KY660792.1 (ITS+28S; UK, on *Heracleum sphondylium*).

= *Erysiphe scandicis* DC., Fl franç 6:107. 1815; type host: *Scandix pecten-veneris*.

≡ *Erysiphe umbelliferarum* f. *scandicis* (DC.) Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:180 1927.

= *Erysiphe pycnopus* Mart., Fl Crypt Erlang:392. Nürnberg 1817; type host: not indicated ("on *Umbelliferae*").

= *Erysiphe umbelliferarum* de Bary, Abh Senkenberg Naturf Ges 7:410. 1870; type host: not indicated (on various Apiaceae).

= *Oidium erysiphoides* f. *umbelliferarum* Sacc., Syll Fung 4:41. 1886.

= *Oidium coriandri* Hosag., Vijay., Udaiyan & Manian, Indian J Forest 15(2):157. 1992.

[For full synonymy, including formae and invalid names, see Braun and Cook (2012:384).]

Host range and distribution: On numerous hosts of diverse genera of the Apiaceae, furthermore on Araliaceae (*Hedera* spp.), and Pittosporaceae (*Billardiera* and *Sollya* spp.); for details, see Braun and Cook (2012).

Notes: Erysiphe heraclei forms a well-supported species clade in ITS+28S analyses. Gorter and Eicker (1985) reported *Hedera helix* from South Africa as host of *E. heraclei* (see also Braun and Cook 2012). The occurrence of *E. heraclei* on *Hedera* has been confirmed in the present sequence analyses (material examined: on *Hedera hibernica*, USA, California, FH01131062). Sequences of *E. betae* are genetically indistinguishable from *E. heraclei* sequences in ITS+28S analyses, suggesting that *E. betae*, which is also morphologically barely distinguishable from *E. heraclei*, might be a synonym of the latter species. However, the confirmation requires multilocus analyses. Therefore, we prefer, for the interim, to maintain *E. betae* as a separate species. However, in preliminary multilocus analyses with few specimens, it seems that *E. betae* can be separated from *E. heraclei* (FIG. 3).

Erysiphe howeana U. Braun, Mycotaxon 14:373. 1982.

Holotype: CANADA. QUEBEC: Argenteuil County, Grenville, on *Oenothera* sp., 23 Aug 1935, *Victorin & Germain* (DAOM 148519). Reference sequences: PP681017 (ITS+28S); PP720952 (*CAM*); PP720525 (*GS*); PP720456 (*RPB2*); PP720037 (*TUB*). [USA. MASSACHUSETTS, Middlesex County, Cambridge, collected from the Experimental Garden behind the Farlow Herbarium at Harvard University, on *Oenothera biennis*, 23 Aug 2021, *M. Bradshaw* (FH01131063).]

= *Erysiphe communis* f. *oenotherae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:250. 1927.

Host range and distribution (Braun and Cook 2012): On *Fuchsia* sp., *Gaura* (*parviflora*, sp.), *Oenothera* (*affinis, albicaulis* s. lat., *biennis* s. lat., *canovirens, deflexa, elata* [= *hookeri*], *fruticosa, glazoviana* [= *erythrosepala*], *indecora, indecora* subsp. *bonariensis, laciniata* [= *sinuata*], *latifolia, longiflora, longifolia, mollissima, muricata, nuttallii, odorata, parviflora, procera, pycnocarpa, ravenii, rosea, rubicaulis, selowii, stricta, strigosa, villaricae*, sp.), *Zauschneria californica*; North America (Canada, USA, throughout the entire range of the hosts), introduced in Europe (widespread), South Africa, and South America (Argentina).

Notes: The holotype of this species is not too old to be sequenced. For the interim, we propose to use a reference sequence for phylogenetic-taxonomic purposes. One specimen from NY on "*Baptisia*" sp. falls in this clade; however, the host is likely misidentified or there was contamination.

Erysiphe hypophylla (Nevod.) U. Braun & Cunnington, Schlechtendalia 10:92, 2003.

≡ *Microsphaera hypophylla* Nevod., Griby SSSR 1:4. 1952.

Lectotype (designated by Braun and Cook 2012): RUSSIA. Moscow, on *Quercus robur*, 3 Oct 1950, *G. Nevodovsky* [Griby SSSR 1, 4] (LEP). Reference

sequence: AF298544 (ITS+28S) [JAPAN. PREF. TOCHIGI: On *Quercus robur*, 1981, *S. Takamatsu* (VPRI22120)].

= *Microsphaera silvatica* Vlasov, Trudy Inst Lesa 16:160. 1954.

= *Microsphaera alphitoides* var. *kazachstanica* Matveeva, Muchnistaya rosa duba i mery bor'by s nej v gorakh i predgor'jakh Zailijskogo Alatau Alma-Atinskoj oblasti, Thesis, Alma-Ata 1953 (pp. 3–19), not effectively published.

≡ *Microsphaera hypophylla* var. *kazachstanica* (Matveeva) ex Shvartsman, in Vasyagina et al., Fl Spor Rast Kazakhstana 3:292. 1961.

Host range and distribution (Braun and Cook 2012): On *Quercus* (*acutissima, bicolor, chenii, cuspidata, frainetto, mongolica* [= *liaotungensis*], *petraea, pubescens, robur*, ×*rosacea, serrata, variabilis*); Asia (Central Asia to China, Japan), almost all Europe, introduced into New Zealand.

Notes: The complex of species of *Erysiphe* (sect. *Microsphaera*) on oaks, mainly in Asia and Europe, has been phylogenetically and taxonomically examined by Takamatsu et al. (2007), followed by a recently published multilocus examination of oak powdery mildews of the genus *Erysiphe* in North America (Bradshaw et al. 2024b). *Erysiphe hypophylla* is a Eurasian powdery mildew species, introduced in New Zealand, but so far not yet known to be introduced in North America. The type material of *M. hypophylla* is not too old for attempts to retrieve sequences. Therefore, we refrain from introducing epitype material and propose, for the interim, a reference sequence, which refers to a collection on *Quercus robur*, used in the analyses published by Takamatsu et al. (2007). Bolay (2001, 2005) recorded, described, and illustrated *E. hypophylla* from Switzerland on *Paeonia californica* and *P. lutea* (Paeoniaceae). Takamatsu et al. (2006) sequenced these collections, and Takamatsu et al. (2007) assigned this *Paeonia* powdery mildew to *E. alphitoides*.

Erysiphe intermedia (U. Braun) U. Braun, in Braun et al., Mycotaxon 112:175. 2010.

≡ *Microsphaera trifolii* var. *intermedia* U. Braun, Zentralbl Mikrobiol 140(5):416. 1985.

≡ *Erysiphe trifolii* var. *intermedia* (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:15. 2000.

Holotype: USA. MASSACHUSETTS: Monson, on *Lupinus perennis*, Aug 1883, *A.B. Seymour* [Rabenh., Fungi Eur Exs 3243a] (HAL, s.n.). *Isotypes*: Rabenh., Fungi Eur Exs 3243a (e.g., B, BPI 563631, as "*Erysiphe martii*," and HBG). *Epitype* (designated by Bradshaw et al. 2022a): USA. WASHINGTON: Carnation, Oxbow Native Plant Nursery, on *Lupinus polyphyllus*, 10 Aug 2018, *M. Bradshaw* (HAL 3381 F). Ex-epitype sequence: MZ265161 (ITS+28S).

Host range and distribution: On *Lupinus* (*albus, angustifolius, latifolius, luteus, perennis, rivularis*); North America (Canada, USA, widespread).

Notes: Bradshaw et al. (2022a) published a phylogenetic-taxonomic revision of *E. intermedia*, in which they demonstrated that this species is confined to North America. European collections, previously assigned to this species (Braun and Cook 2012), pertain to *E. robiniae*, which belongs to the *E. trifoliorum* complex.

Erysiphe ipomoeae (J.M. Yen & Chin C. Wang) H.Y. Hsiao & Y.M. Shen, Diversity 14(3, no. 204):10. 2022.

≡ *Oidium erysiphoides* f. *ipomoeae* J.M. Yen & Chin C. Wang, Rev Mycol 37(3):138. ['1972'] 1973.

≡ *Oidium ipomoeae* (J.M. Yen & Chin C. Wang) U. Braun, Mycotaxon 25:268. 1986.

≡ *Pseudoidium ipomoeae* (J.M. Yen & Chin C. Wang) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):607. 2012.

[*Holotype*: TAIWAN. Fengshan, on *Ipomoea obscura*, 5 May 1972, *Yen & Wang* (not preserved).] *Neotype* (designated by Hsiao et al. 2022): TAIWAN. Nantou, 23.921944N, 120.697333E, 90 m alt., on *Ipomoea obscura*, 28 Mar 2021, *H.Y. Hsiao & Y.M. Shen* (TNM F0035015). Ex-neotype sequences: OM033351 (ITS); OM056701 (*TUB*).

Host range and distribution: On *Ipomoea* (*aquatica, obscura*); Asia (China, India, Taiwan, Thailand).

Notes: Erysiphe ipomoeae forms a highly supported species clade close to the *E. alphitoides* complex (FIG. 2). Pan et al. (2020) recorded the powdery mildew on *Ipomoea obscura* from China under *Erysiphe alphitoides*. Anamorphs of *E. convolvuli* and *E. ipomoeae* occur on *Ipomoea* spp. To reach unequivocal identifications of these species, sequence analyses are recommended.

Erysiphe izuensis (Y. Nomura) U. Braun & S. Takam., Schlechtendalia 4:9. 2000.

≡ *Microsphaera izuensis* Y. Nomura, Trans Mycol Soc Japan 25:479. 1984.

Holotype: JAPAN. PROV. SHIZUOKA: Ito, on *Rhododendron macrosepalum*, 31 Oct 1977, *Y. Nomura* (TNS-F-198228). Reference sequence: LC009950.1 [JAPAN. PREF. NARA: Mt. Nijo, on *Rhododendron macrosepalum*, 1 Nov 1998, *S. Takamatsu* (TNS-F-87410)].

Host range and distribution: On *Rhododendron* (*kaempferi, macrosepalum, mucronulatum, oomurasaki,*

pulchrum, reticulatum, simsii, yedoense); Asia (China, Japan, Korea, Russia [Far East]), introduced in Australia.

Notes: Tymon et al. (2022) included *Erysiphe izuensis* in comprehensive phylogenetic-taxonomic studies on *Erysiphe* spp. on *Rhododendron* spp. Sequences obtained from this species form a well-supported species clade. The type material of this species is relatively young and suitable for sequence analyses. Therefore, we propose, for the interim, a reference sequence retrieved from a Japanese sample on the type host.

Erysiphe juglandis-nigrae (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:10. 2000.

≡ *Microsphaera juglandis-nigrae* U. Braun, Mycotaxon 15:124. 1982.

Holotype: USA. KANSAS: Stockton, on *Juglans nigra*, 1 Sep 1908, *E. Bartholmew* [Fungi Columb 2637] (K(M) 169063). *Isotypes*: Barthol., Fungi Columb 2637 (e.g., BPI 556007, BPI 556008). *Epitype* (designated here, MBT10020090): USA. MASSACHUSETTS: Suffolk County, Boston, Arnold Arboretum, BBM5 quadrant, Blackwell foot path, on *Juglans nigra*, 1 Sep 2021, *M. Bradshaw* (FH01131067). Ex-epitype sequences: PP681100 (ITS+28S); PP720958 (*CAM*); PP720124 (*GAPDH*); PP720460 (*RPB2*); PP720041 (*TUB*).

Host range and distribution: On *Juglans nigra*; North America (USA, widespread). There are several North American records of "*M. alni*" on *Juglans cinerea, J. regia*, and *Juglans* sp. that might belong to the present species, but results of sequence analyses are necessary to prove the affinity of *Erysiphe* on these hosts.

Notes: Sequences retrieved from *Erysiphe juglandis-nigrae* form a well-supported species clade in the phylogenetic analyses. An *Erysiphe* specimen on *Carya ovata* (FH01131016) groups close to the *E. juglandis-nigrae* clade (FIG. 1), but this seems to represent a different species. Additional sequences are needed to clarify this taxon.

Erysiphe lathyrina U. Braun, M. Bradshaw & S. Takam., sp. nov.

MycoBank MB853742

Etymology: Epithet derived from the name of the host genus, *Lathyrus*, + Latin adjectival suffix *-ina* (belonging to).

Illustration: Abasova et al. (2018:37, FIG. 6).

Diagnosis: Phylogenetically and morphologically close to *Erysiphe cruchetiana*, but the wall of the chasmothecial appendages are somewhat thickened below, 1–2 µm wide, sometimes somewhat thickened up to the upper half, thinner toward the tip, aseptate or 1–3-septate in the lower half (vs. thin-walled throughout and pluriseptate). Furthermore, sequences retrieved from *E. lathyrina* form a well-supported species clade in sister position to *E. cruchetiana*.

Description: Mycelium on leaves, amphigenous, also on stems, petioles, and fruits, thin, white, effuse or in patches, subcircular in outline to irregularly shaped, evanescent to persistent; hyphae branched, mostly at right angles, septate, 2–7 µm wide, length of hyphal cells variable, 20–70 µm, thin-walled, hyaline, smooth; hyphal appressoria not very abundant, solitary or in opposite pairs, nipple-shaped or almost so to somewhat lobate, 2–6 µm diam; conidiophores (only a few have been observed) arising from the upper surface of hyphal mother cells, erect, straight, foot cells cylindrical, about 15–25 µm long and 5–7 µm wide, followed by 1–2 cells, about as long as the foot cells or shorter; conidia solitary, ellipsoid, 30–35 × 12–15 µm. Chasmothecia scattered, sometimes gregarious, (90–)95–150 µm diam; peridial cells polygonal to irregularly shaped, 8–23 µm diam, appendages numerous, in the lower half of the chasmothecia to equatorial, interlaced with each other or with hyphae, 0.3–1.3 times as long as the chasmothecial diameter (about 30–150 µm long), mostly rather short, 3–9(–11) µm wide, mycelioid, often irregularly branched, from the basal to the upper portion, sometimes strongly branched, giving the appendages a coral-like appearance, wall somewhat thickened below, 1–2 µm wide, sometimes somewhat thickened up to the upper half, thinner toward the tip, aseptate or 1–3-septate in the lower half, at first hyaline, later yellowish to medium brown from base to top, or paler toward the apex, smooth to rough; asci (3–)4–8, broad ellipsoid-ovoid, saccate, sessile or short-stalked, 45–65 × 30–40 µm, 4–6-spored, wall 1–2.5 µm wide, terminal oculum inconspicuous, about 8–12 µm diam; ascospores ellipsoid-ovoid, (12–)14–25 × (6–)9–14 µm, colorless.

Holotype: ARMENIA. PROV. SYUNIK [before 1995 "Megrinsky Rayon"], on *Lathyrus rotundifolius*, 18 Sep 1981, *S. Simonyan* (HAL 1356 F). Ex-holotype sequence: OQ266915 (ITS). *Paratype*: AZERBAIJAN. Tengalti vil., Quba, 41°21′35″N, 48°30′45″E, on *Lathyrus odoratus* L., 21 Jul 2016, *L.V. Abasova* (TNS-F-88325; BAK, Mycological Herbarium no. 10065). Ex-paratype sequence: LC270861 (ITS+28S).

Notes: Erysiphe lathyrina is a new powdery mildew species that is morphologically barely distinguishable from *E. viciae-unijugae*. Abasova et al. (2018) reported a collection made in Azerbaijan on *Lathyrus odoratus* and assigned it to *E. viciae-unijugae*. Owing to chasmothecia with frequently branched appendages, Braun and Cook (2012:402) identified powdery mildews on

Lathyrus species with frequently irregularly branched chasmothecial appendages as *E. pisi* var. *cruchetiana* and cited diverse species of this genus as hosts [*Lathyrus articulatus, L. cicer, L. clymenum, L. cyaneus, L. miniatus, L. odoratus, L. pratensis, L. rotundifolius*, and *L. tuberosus*]. *Lathyrus odoratus* and *L. rotundifolius* are two of the listed hosts of *E. pisi* var. *cruchetiana* that have been sequenced. These represent an undescribed species, sister to *E. cruchetiana*. However, it remains unclear whether the powdery mildews on all other so far not sequenced *Lathyrus* spp. also refer to this new species. Although morphologically very similar to *E. viciae-unijugae*, the powdery mildew collections on *Lathyrus* spp. cannot be assigned to the latter species. The sequences retrieved on these *Lathyrus* species form a small clade in sister position to the *E. cruchetiana* clade, distant from *E. viciae-unijugae. Erysiphe cruchetiana* on *Ononis* spp. is phylogenetically close to *E. lathyrina* but differs morphologically in having thin-walled, pluriseptate chasmothecial appendages. There are possibly additional differences in the asexual morphs of *E. cruchetiana* and *E. lathyrina*, which requires further examinations of the conidiophores and conidia, including the conidial germination pattern of the latter species. Details of the conidiophores and conidia, including germination, of *E. cruchetiana* have recently been published by Schmidt and Braun (2020), and led to the recognition of the *Ononis* powdery mildew as an independent species and not as a variety of *E. pisi*. This has been phylogenetically confirmed by Darsaraei et al. (2024) and in the present analyses.

Erysiphe lespedezae R.Y. Zheng & U. Braun, Mycotaxon 18:142. 1983.

≡ *Erysiphe glycines* var. *lespedezae* (R.Y. Zheng & U. Braun) U. Braun & R.Y. Zheng, Mycotaxon 22:88. 1985.

Holotype: CHINA. PROV. HEBEI: On *Lespedeza tomentosa*, 24 Sep 1950, *Zhao et al.* (HMAS 19344). *Isotype*: HAL 1448 F. Reference sequence: LC010091.1 [JAPAN. PROV. TOYAMA: Kosugi, on *Lespedeza thunbergii*, 27 Oct 1994, *Y. Sato* (TNS-F-87182)].

= *Erysiphe communis* f. *lespedezae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:257. 1927.

= *Erysiphe glycines* sensu Zheng and Chen (1981:278).

= *Oidium caesalpiniacearum* Hosag. & U. Braun, in Braun, Mycotaxon 25:267. 1986. [*Holotype*: INDIA. KARNATAKA: Bangalore, on *Bauhinia purpurea* (originally as *Bauhinia* sp.), 1984, *V.B. Hosagoudar* (HAL 1430 F).] Ex-holotype sequences: MG545902 (ITS +28S), PP680979 (ITS+28S); PP720896 (*CAM*); PP720304 (*GAPDH*); PP720535 (*GS*); PP720069 (*TUB*).

≡ *Pseudoidium caesalpiniacearum* (Hosag. & U. Braun) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):600. 2012.

Host range and distribution: On *Bauhinia* (*blakeana, variegata*, sp.), *Lespedeza* (*bicolor, buergeri, cuneata, cyrtobotrya, davurica, floribunda, hedysaroides, inschanica, intermixta, maximoviczii, pilosa, penduliflora, potaninii, striata, thunbergii* var. *obtusifolia, tomentosa, virgata*, sp.), *Ohwia caudata* (≡ *Desmodium caudatum*), *Uraria crinita*; Asia (China, India, Japan, Korea, Russia [Far East], Taiwan).

Notes: Erysiphe lespedezae is an Asian species of *Erysiphe* sect. *Erysiphe*. Type material has not yet been sequenced. For the interim, a sequence retrieved from Japanese material on *Lespedeza thunbergii* (LC010091.1) can serve as reference sequence for phylogenetic-taxonomic purposes. Sequences of *E. lespedezae* form a highly supported species clade, which is divided into two subclades with overlapping host ranges (Yeh et al. 2021). The second subclade encompasses sequences retrieved from *Bauhinia blakeana* [KP794928, China], *Lespedeza cuneata* [AB015921, Japan], *Ohwia caudata* [MW290429, Taiwan], and *Uraria crinita* [MT703848, Taiwan] (Yeh et al. 2021). Xu et al. (2018) sequenced type material of *Oidium caesalpiniacearum* and reduced this name to synonymy with *E. lespedezae*. Additional collections of this species on *Bauhinia* spp. and *Owia caudata* from Taiwan were sequenced by Xiao et al. (2020).

Erysiphe limonii L. Junell, Sv Bot Tidskr 61:225. 1967.

Holotype: GERMANY. NIEDERSACHSEN: Hannover, Langeoog, Gr. Sloop, on *Limonium vulgare*, 5 Aug 1938, *A. Ludwig* [Syd., Mycoth Germ 3296] (UPS). *Isotypes*: Syd., Mycoth Germ 3296 (e.g., B, FH, S). Reference sequence: LC010038.1 [UKRAINE. Crimea, on *Limonium* sp., 17 Feb 2002, *V.P. Heluta* (TNS-F-87863)].

= *Erysiphe communis* f. *statices* Poteb., Gribnye parasity vysshikh rasteny Kharkovskoy i smezhnykh guberny:230. 1916.

≡ *Erysiphe statices* (Poteb.) Heluta, Parazitnye griby stepnoy zony Ukrainy:165. 1987.

Host range and distribution: On diverse host species of the genus *Limonium*; Asia, Caucasus, Europe (for details, see Braun and Cook 2012).

Notes: Meeboon et al. (2021) analyzed diverse sequences obtained from *Erysiphe* collections on *Limonium* spp., including *E. limonii*, which formed a well-supported species clade. This result has been confirmed in the present analyses. The type collection of *E. limonii* is from 1938 and could be sequenced. Therefore, we propose, for the interim, a reference sequence for phylogenetic-taxonomic purposes.

Meeboon et al. (2021) discussed sequences of anamorphic specimens collected in Japan on *Limonium*

tetragonum as *Erysiphe* sp. The sequences group in sister position to the *E. acantholimonis* clade, but they form a separate clade, suggesting an undescribed species. The clarification of this taxon requires additional specimens and sequence analyses.

Erysiphe liriodendri Schwein., Trans Amer Philos Soc NS 4:269. 1834.

Holotype: USA. PENNSYLVANIA: Bethlehem, on *Liriodendron tulipifera*, herb. *Schweinitz* (PH01103554). *Isotype*: BPI 1052305. *Epitype* (designated here, MycoBank MBT10020091): USA. MASSACHUSETTS: Middlesex County, Cambridge, from the Experimental Garden behind the Farlow Herbarium at Harvard University, on *Liriodendron tulipifera*, 3 Sep 2021, *M. Bradshaw* (FH01131068). Ex-epitype sequences: PP681088 (ITS+28S); PP720974 (*CAM*); PP720330 (*GAPDH*); PP720560 (*GS*); PP720461 (*RPB2*); PP720042 (*TUB*).

= *Erysiphe communis* f. *liriodendri* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:249. 1927.

Host range and distribution: On *Liriodendron tulipifera*; Asia (introduced in Japan), North America (USA, widespread).

Notes: Sequences retrieved from *E. liriodendri* form a well-supported species clade. Meeboon and Takamatsu (2014) confirmed the occurrence of this species in Japan. *E. liriodendri* has recently also been found in Canada (Liu and Braun 2022; Melzer and Shan 2020).

Erysiphe longissima (M.Y. Li) U. Braun & S. Takam., Schlechtendalia 4:10. 2000.

≡ *Microsphaera longissima* M.Y. Li, Acta Microbiol Sin 17(2):96. 1977.

Holotype: CHINA. Beijing, Summer Palace, on *Caragana sinica*, 24 Oct 1975, *Li* 404 (Herbarium of the Laboratory of Plant Protection, Academy of Agricultural Science, Beijing).

Host range and distribution: On *Caragana* (*brevifolia, rosea, sinica*); Asia (China, endemic).

Notes: Erysiphe longissima is confirmed as a species in the phylogenetic analyses. The Chinese type material needs to be sequenced.

Erysiphe ludens (E.S. Salmon) U. Braun & S. Takam., Schlechtendalia 4:10. 2000.

≡ *Microsphaera alni* var. *ludens* E.S. Salmon, Mem Torrey Bot Club 9:154. 1900.

≡ *Microsphaera penicillata* var. *ludens* (E.S. Salmon) Sacc. & Trav., in Saccardo, Syll fung 20:88. 1911.

≡ *Trichocladia baeumleri* var. *ludens* (E.S. Salmon) Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:307. 1927.

≡ *Microsphaera ludens* (E.S. Salmon) S. Blumer, Beitr Krypt-Fl Schweiz 7(1):351. 1933.

≡ *Microsphaera penicillata* var. *ludens* (E.S. Salmon) W.B. Cooke, Mycologia 44:572. 1952.

Lectotype (designated by Braun 1987): USA. WYOMING: French Creek, on *Vicia americana*, Aug 1898, *Williams & Griffiths* (K(M) 169050). *Epitype* (designated here, MycoBank MBT10020092): USA. COLORADO: Palmer Lake on *Vicia americana*, 21 Aug 1925, *E. Bartholomew* (FH01122196). Ex-epitype sequences: PP680984 (ITS+28S); PP720902 (*CAM*); PP720307 (*GAPDH*).

Host range and distribution: On *Vicia* (*americana* and varieties, *cracca, faba, linearis, nigricans* subsp. *gigantea* [≡ *gigantea*], *ludoviciana, sparsifolia, truncata*, sp.); North America (Canada, USA).

Notes: Sequences retrieved from *E. ludens* on its type host form a well-supported species clade. The type material is likely too old to be successfully sequenced, so we have decided to propose an epitype with ex-epitype sequences.

Erysiphe magnifica (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:10. 2000.

≡ *Microsphaera magnifica* U. Braun, Mycotaxon 16 (2):418. 1983.

Holotype: USA. PENNSYLVANIA: northeast Erie County, Harrisburg, Bureau of Plant Industry, on *Magnolia acuminata*, 18 Oct 1920, *Cubbin* (BPI 558479). Reference sequences: PP681105 (ITS+28S); PP720972 (*CAM*); PP720332 (*GAPDH*); PP720558 (*GS*); PP720465 (*RPB2*); PP720046 (*TUB*). [USA. MASSACHUSETTS: Suffolk County, Boston, from the Arnold Arboretum Nursery on *Magnolia acuminata*, 21 Sep 2021, *M. Bradshaw* (FH01131075).]

Host range and distribution: On *Magnolia* (*acuminata*, ×*alba, ashei, compressa, cylindrica* [≡ *Yulania cylindrica*], *kobus, liliiflora* [≡ *Yulania liliiflora*], ×*loebneri, macrophylla, ovata, salicifolia*, ×*soulangeana* [≡ *Yulania* ×*soulangeana*], *sprengei, stellata* [≡ *Yulania stellata*], ×*thompsoniana, tripetala, wilsonii*) and *Nelumbo nucifera*; North America (USA: Alabama, Florida, Illinois, Maryland, Pennsylvania, Washington D.C.), South America (Argentina), Asia (Iran, Japan, Korea, Taiwan), introduced into Europe (Germany, Romania, Slovakia, Switzerland, UK, Ukraine).

Notes: Braun and Cook (2012) summarized the knowledge about the host range and distribution of this *E. magnifica*, including its introduction and spread in Europe. Since that time, numerous additional hosts have been reported, as well as first records from several countries (Chumak et al. 2012; Ondrušková et al. 2014;

Khodaparast et al. 2019; Wang et al. 2020, Choi et al. 2021; Chinan and Dascălu 2023). Chumak et al. (2012) reported infections on numerous *Magnolia* spp. in a botanical garden in Ukraine. Based on sequence analyses, Kirschner (2010) confirmed the occurrence of *E. magnifica* on *Nelumbo nucifera*, which is undoubtedly an unusual accidental infection. The holotype of *E. magnifica* is not too old for an attempt to sequence this material, but it has not yet been tried. Therefore, we prefer to propose a reference sequence for the interim.

Erysiphe malvae Heluta, Ukrayins'k Bot Zhurn 47(4):75. 1990.

Holotype: UKRAINE. CRIMEA: Yalta, Alupka, on *Malva erecta*, 16 Aug 1981, *V.P. Heluta* (KW). *Paratype*: KW.

Host range and distribution (Braun and Cook 2012): On *Lavatera cretica, Malva* (*ambigua, erecta, parviflora, sylvestris*); Asia (Iran, Israel, Nepal), Europe (Ukraine).

Notes: Erysiphe malvae is a phylogenetically unresolved species name. An ex-holotype sequence is not yet available. A sequence retrieved from a specimen on *Malva sylvestris* (MW581144.1) collected in Ukraine, which is probably representative for this name, falls within the *E. heraclei* clade. A sequence obtained from a specimen collected in Iran on *Malva* sp. groups together with ex-type sequences of *E. panacis* and *E. pavoniae. Erysiphe malvae* requires further phylogenetic analyses, when possible, based on a multilocus approach. It cannot be excluded that *E. heraclei* is able to cause occasional infections on *Malva* spp. *Erysiphe malvae* has recently been recorded from Nepal on *Malva sylvestris* (Adhikari 2021).

Erysiphe manihoticola (Hosag., Siddappa, Vijay. & Udaiyan) M. Bradshaw, M.G. Cabrera & Salcedo-Sarmiento, in Bradshaw et al., Sydowia 73:95. 2020.

≡ *Oidium manihoticola* Hosag., Siddappa, Vijay. & Udaiyan, Cryptog Bot 2(4):354. 1992.

Holotype: INDIA. TAMIL NADU: Nilgiris, Kotagiri, near Sundapatti, on *Manihot glaziovii*, 16 Feb 1991, *V.B. Hosagoudar & Siddapa* (HCIO30631). Reference sequence: MT106658.1 (ITS+28S) [ARGENTINA. CORRIENTES: Capital, Jardin de Fisiologia Vegetal de la Facultad de Ciencias Agrarias de la Universidad Nacional del Nordeste, on *Manihot esculenta* (cult.), 13 Aug 2019, *R.D. Medina & G. Cabrera* (WTU-F-72405)].

≡ *Pseudoidium manihoticola* (Hosag., Siddappa, Vijay. & Udaiyan) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):611. 2012.

Host range and distribution (Bradshaw et al. 2020b): On *Manihot* (*esculenta, glaziovii* [≡ *carthagenensis* subsp. *glaziovii*], *grahamii*); Asia (India), South America (Argentina, Brazil).

Notes: The phylogeny and taxonomy of *Erysiphe manihoticola* has been clarified and discussed in Bradshaw et al. (2020b). This species forms a highly supported species clade within the *E. diffusa* complex.

Erysiphe myoschili (Neger) U. Braun & S. Takam., Schlechtendalia 4:11. 2000.

≡ *Microsphaera myoschili* Neger, Ber Deutsch Bot Ges 17 (Ergänzungsheft):(241). 1900.

Lectotype (designated by Braun 1987): ARGENTINA. NEUQUÉN: "prope lacum argentinum dictum Quillen in Andibus Valdivianis vulgatissima," on *Myoschilos oblongum, F. Neger* (S). Reference sequence: LC010005.1 (ITS+28S) [ARGENTINA. PROV. RÍO NEGRO: San Carlos de Bariloche, Lago Gutierrez, on *Myoschilos oblongum*, 17 Apr 2001, *S. Takamatsu* (TNS-F-87752)].

Host range and distribution: On *Myoschilos oblongum*; South America (Argentina: Neuquén, Río Negro; Chile: Valdivia, Villarica).

Notes: As already shown in Takamatsu et al. (2015b), the ITS+28S sequence retrieved from the only sequenced collections of this species groups together with sequences obtained from *E. thaxteri*. Further multilocus sequence analyses are necessary to resolve this complex.

Erysiphe myzodendri (Speer & Oehrens) U. Braun & S. Takam., Schlechtendalia 4:11. 2000.

≡ *Microsphaera myzodendri* Speer & Oehrens, Sydowia 27:128. [1973] 1975.

Holotype: CHILE. VALDIVIA: Punahue, on *Misodendrum punctulatum* [= *Myzodendron imbricatum*], 9 Jan 1968, *Oehrens* (W). *Isotypes*: HFV 658 and HAL 1439 F. Reference sequence: LC009888.1 (ITS +28S) [ARGENTINA. PROV. RÍO NEGRO: Bariloche, Parque National Nahuel Huapi, Cerro Otto, on *Misodendrum linearifolium*, 16 Nov 1997, *M. Havrylenko* (TNS-F-87171, ex BCRU 04187)].

Host range and distribution: On *Misodendrum* (*linearifolium, punctulatum*); South America (Argentina, Chile).

Notes: Type material has not yet been sequenced. For the interim, a reference sequence for phylogenetic-taxonomic purposes is proposed (LC010005).

Erysiphe nemopanthi (Peck) U. Braun & S. Takam., Schlechtendalia 4:11. 2000.

≡ *Microsphaera nemopanthi* ("*nemopanthis*") Peck, Rep (Ann) New York Stat Mus Nat Hist 38:102. 1886.

Lectotype (designated here, MycoBank, MBT10022211): USA. NEW YORK: Albany Co., Karner, on *Ilex mucronata* (≡ *Nemopanthus mucronatus*, = *N. canadensis*), Sep./Oct. 1884, *C.H. Peck* (NY2941627). Isolectotypes: Ellis and Everh., N. Am. Fungi 1539, e.g., BPI958986, ILL98808, NY02941624-02941626, PH41547. Ex-syntype sequence (NYSf2056): PP680844 (ITS+28S); PP720519 (*RPB2*).

= *Microsphaera penicillata* f. *nemopanthi* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:348. 1927.

Host range and distribution (Braun and Cook 2012): On *Ilex* (*cassine, coriacea, decidua, glabra, mollis, montana, monticola, mucronata, verticillata, vomitoria*); North America (Canada; USA: Alabama, Florida, Illinois, North Carolina, New York, Pennsylvania, Wisconsin).

Notes: Sequences retrieved from *Erysiphe nemopanthi* form a well-supported species clade, including sequences obtained from collections on *Ilex verticillata*.

Erysiphe nomurae (U. Braun) U. Braun & S. Takam., Schlechtendalia 7:8. 2001.

≡ *Microsphaera nomurae* U. Braun, Feddes Repert 92:505. 1981.

Holotype: JAPAN. PREF. CHIBA: Taiei T., on *Symplocos sawafutagi* (= *S. chinensis* subsp. *pilosa*), 16 Nov 1978, *Nomura*, YNMH 4847-1 (HAL 1452 F). *Isotype*: TNS. Reference sequence: AB331648.1 [JAPAN. PREF. NIIGATA: Yahiko, on *Symplocos sawafutagi*, 18 Oct 1996, *S. Takamatsu* (TNS-F-87308)].

Host range and distribution: On *Symplocos* (*coreana, paniculata, sawafutagi*, sp.); Asia (China, Japan, Korea).

Notes: The holotype of this species has not yet been sequenced. For the interim, we propose to use AB331648.1 as reference sequence. This sequence groups in sister position to the *E. monascogera* clade.

Erysiphe oehrensii (Havryl.) U. Braun & S. Takam., Schlechtendalia 4:11. 2000.

≡ *Microsphaera oehrensii* Havryl., Mycotaxon 49:259. 1993, nom. cons. (Braun 2013).

= *Oidium robustum* U. Braun & Oehrens, Mycotaxon 25:268. 1986, nom. rej.

Holotype: ARGENTINA. PROV. RÍO NEGRO: Llao Llao, on *Maytenus magellanica*, 1993, *M. Havrylenko* 26 (LPS 45138). *Isotype*: BCRU 327. Reference sequence: LC010022.1 (ITS+28S) [ARGENTINA. PROV. NEUQUÈN: Dept. Los Lagos, La Angostura, on *Maytenus boaria*, 3 Mar 2004, *S. Takamatsu* (TNS-F-87831)].

Host range and distribution: On *Maytenus* (*boaria, magellanica*); South America (Argentina: Chubut, Neuquén, Río Negro).

Notes: Ex-type sequences are not yet available. Therefore, we propose a reference sequence (LC010022) for phylogenetic-taxonomic purposes.

Erysiphe orixae (U. Braun & Tanda) U. Braun & S. Takam., Schlechtendalia 4:12. 2000.

≡ *Microsphaera orixae* U. Braun & Tanda, Mycotaxon 25:260. 1986.

Holotype: JAPAN. PREF. KANAGAWA: Yamakita-machi, on *Orixa japonica*, 18 Oct 1984, *S. Tanda* (TUAMH 2613). *Isotype*: HAL 1454 F. Reference sequence: LC009907.1 (ITS+28S) [JAPAN. PREF. MIE: Mt. Fujiwara, on *Orixa japonica*, 23 Sep 1994, *S. Takamatsu* (TNS-F-87192)].

Host range and distribution: On *Orixa japonica*; Asia (Japan, endemic).

Notes: In the phylogenetic ITS+28S analyses (FIG. 2), *E. orixae* forms a well-supported species clade. Bradshaw et al. (2023c) included this species in comprehensive phylogenetic examinations of the *E. alphitoides* complex. Ex-type sequences are not yet available. For the interim, we propse to use LC009907.1 as reference sequence.

Erysiphe ovidiae (Havryl.) U. Braun & S. Takam., Schlechtendalia 4:12. 2000.

≡ *Microsphaera ovidiae* Havryl., Mycotaxon 49:260. 1993.

Holotype: ARGENTINA. PROV. RÍO NEGRO: Bariloche, Lago Frías, on *Ovidia andina*, Mar 1992, *M. Havrylenko* 100 (LPS 45137). *Isotype*: BCRU 328. Reference sequence: LC009882.1 (only 28S) [ARGENTINA. PROV. RÍO NEGRO: Bariloche, Lago Frias, on *Ovidia andina*, Mar 1992, *M. Havrylenko* (BCRU 328, TNS-F-87160)].

Host range and distribution: On *Ovidia andina*; South America (Argentina: Río Negro).

Notes: So far, only a single 28S sequence obtained from *E. ovidiae* is available, which groups together with sequences of *E. discariae* (only 28S), *E. ribicola*, and *Pseudoidium* sp. on *Schinus patagonicus* (LC010018.1, ITS+28S) [ARGENTINA. PROV. RÍO NEGRO: San Carlos de Bariloche, Nahuel Huapi Lake, Victoria Island, 29 Feb 2004, *S. Takamatsu* (TNS-F-87818)] in an insufficiently resolved South American complex (Takamatsu et al. 2015b). Additional sequences retrieved from *E. ovidiae* are necessary.

Erysiphe palczewskii (Jacz.) U. Braun & S. Takam., Schlechtendalia 4:12. 2000.

≡ *Microsphaera palczewskii* Jacz., Karmanny opredelitel' gribov Vyp 2 Muchnisto-rosjanye griby:339. 1927.

Lectotype (designated by Braun 1987): RUSSIA. PROV. YUZHNO-USSURIISK: Nikol'sk-Ussuriiskij District, on *Caragana arborescens*, 9 Jul 1912, *N.A. Naumov* (LE 34903). Reference sequence: LC010048.1 (ITS+28S) [UKRAINE. Zaporizhzhiya, on *Caragana arborescens*, 26 Sep 1997, *V.P. Heluta* (TNS-F-87874)].

= *Microsphaera subtrichotoma* U. Braun, Mycotaxon 22:90. 1985; type host: *Robinia pseudoacacia* (holotype: herbarium of Vladivostok State University; paratype: HMAS 39029).

≡ *Erysiphe subtrichotoma* (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:14. 2000.

= *Microsphaera caraganae* auct. p.p. (sensu Chen et al. 1987).

= *Microsphaera sophorae* auct. p.p. (sensu Tai 1936:23).

= *Microsphaera pseudolonicerae* auct. p.p. (sensu Wei 1942:112).

= *Microsphaera robiniae* auct p.p. (sensu Bunkina 1991; Shin 1988, 2000).

Host range and distribution (Braun and Cook 2012): On *Caragana* (*arborescens, boisii, brevispina, decorticans, frutex, fruticosa, korshinskii, manshurica, microphylla, mollis, pekinensis, sinica, sophorifolia, spinosa, ussuriensis*, sp.), *Colutea arborescens, Robinia* (*hispida, pseudoacacia*), *Styphnolobium japonicum*; Asia (China, Kazakhstan, South Korea, Russia [Siberia, Far East], Tajikistan), introduced into Europe (Austria, Byelorussia, Czech Republic, Estonia, Finland, Germany, Hungary, Latvia, Lithuania, Norway, Poland, Romania, Russia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Ukraine) and North America (Canada; USA: Idaho, North Dakota, Alaska).

Notes: Sequences obtained from *Erysiphe palczewskii* form a well-supported clade in the phylogenetic analyses. *Robinia* has been confirmed as host of *E. palczewsii* (Lee and Nguyen 2019; Takamatsu et al. 2015a). *Colutea arborescens* as a host of *E. palczewskii* was first reported by Schmidt and Scholler (2002) but requires phylogenetic confirmation. *Erysiphe palczewskii* on *Styphnolobium japonicum* has been reported from China and Czech Republic (Mieslerová et al. 2020; Xiong et al. 2017).

Erysiphe panacis R.L. Bai & W.C. Liu, Mycosystema 17 (2):119. 1998.

Holotype: CHINA. PROV. JILIN: Changchun, on *Panax ginseng*, 15 Jul 1985, *R.L. Bai* (Herbarium of the University of Agriculture and Animal Science, Chengchun, China, no. 8501). Reference sequence: KP676100.1 (ITS+28S) [KOREA. *Panax ginseng*].

Host range and distribution: On *Panax ginseng*; Asia (China, South Korea).

Notes: There is a single sequence (KP676100, ITS +28S) obtained from a specimen collected in South Korea. It groups with the ex-type sequence of *E. pavoniae* and a sequence obtained from *E.* "*malvae*" on *Malva* sp. in Iran in a strongly supported group, sister to the *E. heraclei* complex. The analysis favors *E. panacis* as a separate species. Cho et al. (2016) reported this powdery mildew from South Korea as *Erysiphe* sp. Stolberg (1996) published a record of *Erysiphe* sp. (with chasmothecia) on American ginseng (*Panax quinquefolius*) from Canada, and Avin et al. (2022) reported "*E. heraclei*" from Tennessee, USA, on this host, including an ITS sequence, which possibly pertains to *E. panacis*. Takamatsu et al. (1999) assigned a specimen collected on "*Panax ginseng*" from Japan to *E. heraclei*, but the cited sequence (AB000942), and the corresponding collection (MUMH73 = TNS-F-87227), refers to a Japanese sample on *Daucus carota*.

Erysiphe pavoniae (Bagyan. & U. Braun) M. Bradshaw, U. Braun & Pfister, comb. nov.
MycoBank MB853743

Basionym: Oidium pavoniae Bagyan. & U. Braun, Mycotaxon 27:61. 1986.

≡ *Pseudoidium pavoniae* (Bagyan. & U. Braun) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):614. 2012.

Holotype: INDIA. ANDHRA PRADESH: Hyderabad, on *Pavonia zeylanica*, 16 Dec 1984, *G. Bagyanarayana* (HAL 1432 F). Ex-holotype sequences: PP681000 (ITS +28S); PP720990 (*CAM*); PP720292 (*GAPDH*); PP720488 (*RPB2*); PP720071 (*TUB*).

Host range and distribution: On *Pavonia zeylanica*; Asia (India). Braun and Cook (2012) cited *Abutilon indicum* and *Sida rhombifolia* as additional host species in India, but these hosts are phylogenetically unconfirmed.

Notes: Ex-type sequences of *O. pavoniae* group together with *E.* "*malvae*" from Iran collected on *Malva* sp., also Malvaceae, and *E. panacis*, but at a separate branch, suggesting the status of this taxon as a well-supported species of *Erysiphe*.

Erysiphe peckii (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:12. 2000.

≡ *Microsphaera peckii* U. Braun, Mycotaxon 15:125. 1982.

Holotype: USA. COLORADO: Jefferson County ("Paroechia"), on *Campsis radicans* (= *Tecoma radicans*), 22 Oct 1968, *A.L. Welden* (K(M) 169082). Ex-holotype sequences: PP680975 (ITS+28S); PP720941 (*CAM*); PP720668 (*GS*); PP720500 (*RPB2*); PP720083 (*TUB*).

Host range and distribution: On *Campsis radicans*; North America (USA: Alabama, Colorado, Indiana, Kentucky, Maryland, Mississippi, Ohio, Texas, Virginia, Washington State, West Virginia).

Notes: Sequences retrieved from *E. peckii*, including an ex-holotype sequence, form a separate species clade, together with two sequences in sister position, identified as "*Erysiphe peruviana* on *Tecomaria capensis* (≡ *Tecoma capensis*)" (anamorph; Glawe et al. 2010). The identification of the causative agent of powdery mildew on *T. capensis* is very doubtful. Sequences retrieved from *E. peruviana* are not available for comparison. However, *E. peruviana* is a typical species of *Erysiphe* sect. *Uncinula*. Sequences of species belonging to this section fall within the "*Uncinula* lineage" of *Erysiphe* (Bradshaw et al. 2023b; Takamatsu et al. 2015b). Therefore, the identification as *E. peruviana* is undoubtedly wrong. The powdery mildew on *T. capensis* rather appears to represent an undescribed sister species of *E. peckii* or belongs to this species.

Erysiphe phyllanthi (Tanda & U. Braun) U. Braun & S. Takam., Schlechtendalia 4:12. 2000.

≡ *Microsphaera phyllanthi* Tanda & U. Braun, Trans Mycol Soc Japan 26:317. 1985.

Holotype: JAPAN. PREF. KUMAMOTO: Kahoku-cho, on *Phyllanthus flexuosus*, 20 Sep 1984, *T. Mogami* (TUAMH 2904). *Isotype*: HAL 1459 F. Reference sequence: LC009921.1 (ITS+28S) [JAPAN. PREF. MIE: Tsu, Mt. Shakujo, on *Phyllanthus flexuosus*, 14 Nov 1995, *S. Takamatsu* (TNS-F-87241)].

Host range and distribution: On *Phyllanthus flexuosus*; Asia (Japan, endemic).

Notes: The species status of *E. phyllanthi* has been confirmed in phylogenetic analyses (Takamatsu et al. 2015b; present analyses). Type material has not been sequenced.

Erysiphe pisi DC., Fl franç 2:274. 1805.

≡ *Alphitomorpha pisi* (DC.) Wallr., Ann Wetterauischen Ges Gesammte Naturk N F 4:241. 1819.

≡ *Ischnochaeta pisi* (DC.) Sawada, Special Publ Col Agric Natl Taiwan Univ 8:18. 1959, nom. inval. (Art. 35.1).

Neotype (designated by Braun 1987): On *Lathyrus oleraceaus* (= *Pisum sativum*), "*Erysiphe pisi*, herb. Léveillé", herb. *de Candolle* (G 00122107).

= ?*Oidium arachidis* Chorin, Bull Res Counc Israel Sect D Bot 10D:148. 1961.

Host range and distribution: On *Lathyrus* spp., including *L. oleraceus* [= *Pisum sativum*]; almost worldwide, wherever peas are cultivated. Further host range unclear.

Notes: Braun and Cook (2012) assigned to *E. pisi* (s. lat.) collections on numerous legume host genera, including *Aeschynomene, Arachis, Astragalus, Bituminaria, Dolichos, Dorycnium, Hymenocarpus, Lathyrus, Lens, Lotus, Lupinus, Medicago, Melilotoides, Melilotus, Onobrychis, Phaseolus, Pisum, Sophora, Trifolium, Trigonella*, and *Vicia*. However, the whole *E. pisi* complex requires a comprehensive phylogenetic-taxonomic revision, preferably based on a multilocus approach. *Erysiphe* on *Medicago* spp. has previously been assigned to *E. pisi* (s. lat., as widely circumscribed by Braun and Cook 2012). The description of *E. medicaginis* is an example that *E. pisi* s. lat. is undoubtedly heterogeneous. The currently available phylogenetic analyses confirm that sequences obtained from *E. pisi* on *Lathyrus oleraceus* (= *Pisum sativum*) form a highly supported species clade (Bradshaw et al. 2022a; Darsaraei et al. 2024; present analyses). Furthermore, diverse *Lathyrus* spp. undoubtedly belong to the host range of this species, which is not surprising since *Pisum* is nowadays reduced to synonymy with *Lathyrus* (legume tribe Fabeae), based on phylogenetic results (see Plants of the World Online, https://powo.science.kew.org/results?q=Pisum%20sativum). Within the *E. pisi* clade, there is a second group of sequences, obtained from the holotype of *E. baptisiicola* and from *Erysiphe* sp. on *Astragalus canadensis*, grouping together with moderate support, i.e., these taxa probably do not belong to the genuine *E. pisi* but need further phylogenetic examination.

Erysiphe platani (Howe) U. Braun & S. Takam., Schlechtendalia 4:12. 2000.

≡ *Microsphaera platani* Howe, Bull Torrey Bot Club 5:4. 1874.

Holotype: USA. NEW YORK: Yonkers, on *Platanus occidentalis*, undated, *E.C. Howe* (NYSf4474). *Epitype* (designated here, MycoBank MBT10020093): USA. DELAWARE: New Castle County, Mt. Cuba Botanical Garden, on *Platanus occidentalis*, 30 Sep 2021, *T.G. Potterfield* (FH01131087). Ex-epitype sequences: PP681091 (ITS +28S); PP720963 (*CAM*); PP720554 (*GS*); PP720470 (*RPB2*); PP720051 (*TUB*).

= *Microsphaera penicillata* f. *platani* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:359. 1927.

Host range and distribution: On *Platanus* (×*hispanica* [= ×*acerifolia*, ×*hybrida*], *occidentalis, orientalis, racemosa*); North America (Canada, USA, generally distributed, wherever plane trees are planted and throughout the entire ranges of the hosts), introduced in Africa (Algeria, Morocco, South Africa), Asia (China, Israel, Japan, South Korea, Syria, Turkey), Australia, Europe

(Austria, Belgium, Bulgaria, Croatia, Czech Republic, Denmark, France, Germany, Greece, Hungary, Italy, Montenegro, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, Switzerland, UK, Ukraine), South America (Brazil). Rarely on *Ailanthus altissima* (Beenken 2017; Marchica et al. 2020).

Notes: Sequences obtained from *Erysiphe platani* form a highly supported species clade in phylogenetic analyses. This species has been introduced to all continents. In Europe, it is now rather common in numerous countries. Scholler et al. (2012) documented the epidemic spread of this species in Germany and provided sequence data obtained from German collections. Pastirčáková et al. (2014) summarized the global distribution of this species and added first records for several countries.

Erysiphe polygoni DC., Fl franc 2:273. 1805, emend. Darsaraei et al. (2023).

≡ *Microsphaera polygoni* (DC.) Sawada, Special Rep Formosa Agric Exp Sta 9:52. 1914.

≡ *Ischnochaeta polygoni* (DC.) Sawada, Bull Gov Forest Exp Sta Meguro 50:115. 1951, and Special Publ Coll Agric Natl Taiwan Univ 8:19. 1959, nom. inval. (Art. 35.1).

Lectotype (designated by Braun 1987): FRANCE. Bagneux, on *Polygonum aviculare*, undated, herb. *de Candolle* (G 00122108). *Epitype* (designated by Darsaraei et al. 2023): GERMANY. SACHSEN-ANHALT: Landkreis Mansfeld-Südharz, Arnstein, OT Greifenhagen, on *Polygonum aviculare*, 10 Sep 1980, *U. Braun* (HAL 1356 F). Ex-epitype sequence: OP349645 (ITS+28S).

= *Alphitomorpha communis* η *polygonacearum* Wallr., Verh Ges Naturf Freunde Berlin 1(1):31. 1819.

= *Erysiphe* (as "*Erysibe*") *communis* var. *polygonearum* Link, Sp pl 4 6(1):107. 1824.

≡ *Erysiphe communis* x. *polygonearum* (Link) Fr., Syst mycol 3:242. 1829.

= *Erysiphe polygoni* Castagne, Cat pl Marseille:189. 1845, nom. illeg. (Art. 53.1), non *E. polygoni* DC., 1805.

= *Erysiphe polygoni* f. *muehlenbeckiae* O. Săvul. & Tud.-Băn., Lucr Grăd Bot Bucuresti 1966:278. 1967.

= *Erysiphe cichoracearum* f. *muehlenbeckiae* Nelen, Novisti Niszh Rast 3:133. 1966; type host: *Muehlenbeckia* sp. (type: LE 34535, examined by Braun 1987).

= *Oidium antigononis* B.S. Reddy, Khalis & Manohar., Curr Sci 51(16):793. 1982.

≡ *Pseudoidium antigononis* (B.S. Reddy, Khalis & Manohar.) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):597. 2012.

Host range and distribution: On *Antigonum leptopus, Muehlenbeckia* (*platyclada* [≡ *Homalocladium platycladum*], sp.), and diverse species of *Polygonum* s. lat.; almost circumglobal (Africa, Asia, Australia, Europe, North and South America). For details, see Braun and Cook (2012).

Notes: Darsaraei et al. (2023) published a comprehensive phylogenetic-taxonomic revision of *Erysiphe polygoni* s. lat. and confined this species to collections on *Antigonum, Muehlenbeckia*, and species of *Polygonum* s. lat. Collections on *Rumex* spp., except for species of *Rumex* subgen. *Acetosa*, proved to be a separate species, i.e., *E. rumicicola. Erysiphe polygoni* s. lat. on *Fagopyrum* and *Rheum* spp. are *E. rumicicola* as well.

Erysiphe pseudolonicerae (E.S. Salmon) U. Braun & S. Takam., Schlechtendalia 4:12. 2000.

≡ *Microsphaera alni* var. *pseudolonicerae* E.S. Salmon, Ann Mycol 6:4. 1908.

≡ *Microsphaera penicillata* var. *pseudolonicerae* (E.S. Salmon) Sacc. & Trott., Syll fung 22:24. 1913.

≡ *Microsphaera pseudolonicerae* (E.S. Salmon) S. Blumer, Beitr Krypt-Fl Schweiz 7(1):351. 1933.

≡ *Microsphaera pseudolonicerae* (E.S. Salmon) Homma, J Fac Agric Hokkaido Univ 38:393. 1937.

Lectotype (designated by Braun 1987): JAPAN. PREF. KŌCHI: Tosa, Hisato-mura, on *Cocculus trilobus*, Nov 1906, *T. Yoshinaga* (TNS-F-229734). *Epitype* (designated here, MycoBank MBT10020094): JAPAN. PREF. MIE: Tsu-shi, Misato, on *Cocculus trilobus*, 5 Nov 1994, *S. Takamatsu* (TNS-F-87234). Ex-epitype sequence: AB015915.1 (ITS+28S).

= *Microsphaera cocculi* Golovin & Bunkina, Bot Mater Otd Sporov Rast Bot Inst Komarova Akad Nauk SSSR 14:119. 1961; type host: *Cocculus trilobus*.

Host range and distribution: On *Cocculus* (*hirsutus, orbiculatus* [= *sarmentosus*], *trilobus*), *Cyclea barbata, Diploclisia affine, Menispermum dauricum, Pericampylus glaucus, Stephania* (*japonica, rotunda, tetrandra*); Asia (China, India, Indonesia, Japan, Korea, Russia [Far East], Taiwan, Thailand).

Notes: Sequences obtained from *E. pseudolonicerae* form a well-supported species clade. Meeboon and Takamatsu (2017) sequenced a collection of *E. pseudolonicerae* on *Cyclea barbata* from Thailand, and LC371311 is a sequence retrieved from a specimen of this species collected on *C. barbata* in Indonesia, which supports that this powdery mildew species has a wider host range amongst diverse host of the Menispermaceae.

Erysiphe quercicola S. Takam. & U. Braun, Mycol Res 111:819. 2007, nom. cons. (Braun 2013).

Holotype: JAPAN. PREF. NARA: Ikoma Mt., on *Quercus phillyraeoides*, 27 Nov 1999, *S. Takamatsu* (TNS-F87513 [previously MUMH 885]). *Isotype*: HAL 1969 F. Ex-holotype sequences: AB193591 (ITS); AB237813 (28S).

= *Oidium anacardii* Noack, Bol Inst Estado São Paulo 9(2):77. 1898.

≡ *Pseudoidium anacardii* (Noack) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):497. 2012.

= *Oidium mangiferae* Berthet, Bol Agric (São Paulo) 15:818. 1914.

≡ *Acrosporium mangiferae* (Berthet) Subram., Hyphomycetes (New Delhi):834. 1971.

≡ *Oidium erysiphoides* f. *mangiferae* (Berthet) J.M. Yen & Chin C. Wang, Rev Mycol 37(3):138. [1972] 1973.

= *Erysiphe cinnamomi* Sawada, Rep. Dept Agric Gov Inst Formosa 19:144. 1919.

≡ *Pseudoidium cinnamomi* (Sawada) U. Braun & R.T. A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):601. 2012.

= *Oidium bixae* Viégas, Bragantia 4(1–6):19. 1944.

= *Oidium nephelii* Hadiw., Landbouw (Landbouwkundig maandblad voor Indonesië) 22(5–6):253. 1950, nom. inval. (Art. 39.1).

≡ *Oidium erysiphoides* f. *nephelii* (Hadiw.) J.M. Yen, Rev Mycol 31(4):286. 1966, nom. inval. (Art. 35.1).

≡ *Oidium nephelii* Hadiw. ex U. Braun, Mycotaxon 25:267: 1986.

≡ *Pseudoidium nephelii* (Hadiw. ex U. Braun) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):613. 2012.

= *Oidium erysiphoides* f. *cinnamomi* J.M. Yen, Cah Pacifique 11:96. 1967.

≡ *Oidium cinnamomi* (J.M. Yen) U. Braun, Mycotaxon 25:266. 1986.

= *Oidium erysiphoides* f. *bixae* J.M. Yen, Cah Pacifique 11:88. 1967.

= *Oidium erysiphoides* f. *citri* J.M. Yen, Cah Pacifique 11:99. 1967.

≡ *Oidium citri* (J.M. Yen) U. Braun, Zentralbl Mikrobiol 137:323. 1982.

Host range and distribution: On *Quercus* (*crispula, glauca, mongolica, myrsinifolia, phillyraeoides, robur, rubra, salicinia, serrata*, sp.); Asia (China, India, Indonesia, Iran, Japan, Pakistan, South Korea, Thailand), Australia, Europe (France, UK, but probably widespread). Anamorphs on *Acacia* spp., *Ailanthus excelsa, Anacardium occidentale, Bauhinia purpurea, Bixa orellana, Cassia fistula, Cinnamomum camphora, Citrus* spp., *Clitoria fairchildiana, Durio zibethinus, Hevea brasiliensis, Mangifera indica, Murraya paniculata, Nephelium lappaceaum, Tamarindus indica, Ziziphus lotus*; widespread in tropical and subtropical Africa, Asia, and South America.

Notes: Since the introduction of the plurivorous name *E. quercicola* (Takamatsu et al. 2007), an increasing number of tropical-subtropical woody hosts have been found and confirmed by results of sequence analyses (Kirschner and Liu 2014; Siahaan et al. 2016; Azevedo Silva et al. 2021; Afshan et al. 2022a; etc.). Mougou et al. (2008) provided a detailed examination of this species in Europe, and Takamatsu et al. (2018) demonstrated that *E. quercicola* may also occur on species of *Quercus* subgen. *Cerris* sect. *Cyclobalanopsis*. Bradshaw et al. (2022e) provided a new phylogenetic analysis of the *E. alphitoides* complex on oaks and clarified the nomenclature of the names *E. alphitoides* and *E. quercicola*, which led to a proposal in the journal *Taxon* to maintain the traditional use of the two names (Braun et al. 2022).

Erysiphe radulescui Docea, Lucr Sti Inst Agron "N. Balcescu" Ser A 11:402. 1968.

Holotype: ROMANIA. "in foliis vivis Cleomi graveolentis Raf., in Horto Botanico Instituto Agronomico Bucarestiensis (R.S.R.)," 10 Sep 1956, *E. Docea* [type host probably *C. houtteana*] (BUAG). *Epitype* (designated by Bradshaw et al. 2024c): ROMANIA. Bucureşti, Botanical Garden, on *Cleome spinosa*, 15 Oct 1962, *E. Eliade* [Săvul., Herb Mycol Rom 1771] (I 111498). Ex-epitype sequences: OR427484 (*CAM*); OR427570 (*GADP*); OR427654 (*GS*); OR424974 (ITS+28S); OR427788 (*TUB*).

= *Erysiphe cruciferarum* var. *longispora* G.J.M. Gorter, Ann Univ Stellenbosch 3:21. 1988; type host: *Lepidium africanum* (holotype: PREM 47330).

= *Erysiphe cleomes* R.X. Li & D.S. Wang, Acta Mycol Sin 9:266. 1990; type host: *Cleome spinosa* (holotype: HMAS 58876).

= *Erysiphe cruciferarum* var. *cleomes* (as "*cleomae*") Y.S. Paul & V.K. Thakur, Indian Erysiphaceae:31. Jodpur 2006 [J Econ Taxon Bot Addn Ser 26:31. 2006], nom. inval. (Art. 40.6); type host: *Cleome spinosa* (type: DPDH 422).

= *Erysiphe cruciferarum* var. *chandra* Y.S. Paul & V. K. Thakur, Indian Erysiphaceae:31. Jodpur 2006 [J Econ Taxon Bot Addn Ser 26:31. 2006], nom. inval. (Art. 40.6); type host: *Capsella bursa-pastoris* (type: DPDH 374).

= *Erysiphe cruciferarum* var. *indica* Y.S. Paul & V.K. Thakur, Indian Erysiphaceae:29. Jodpur 2006 [J Econ Taxon Bot Addn Ser 26:29. 2006], nom. inval. (Art. 40.6); type host: *Lepidium latifolium* (type: DPDH 385).

= *Oidium brassicae* N. Ahmad, A.K. Sarbhoy, Kamal & D.K. Agarwal, Indian Phytopathol 59(2):219. 2006; type host: *Brassica napus* (holotype: HCIO 30154).

Host range and distribution (phylogenetically proven host genera for *E. radulescui*): Brassicaceae (*Arabidopsis, Brassica, Camellina, Diplotaxis, Eutrema, Isatis, Lepidium, Orychophragmus, Sinapis, Sisymbrium*), Cleomaceae (*Cleome*), Papaveraceae (*Papaver*).

Host range and distribution (based on Braun and Cook 2012): On numerous host species of various genera of the Brassicaceae (*Arabis, Armoracia, Barbarea, Biscutella, Brassica, Bunias, Camelina, Capsella, Cardamine, Cardaria, Cheiranthus, Cochlearia, Coronopus, Crambe, Dentaria, Descurainia, Diplotaxis, Dontostemon, Draba, Eruca, Erucaria, Erucastrum, Erysimum, Fibigia, Hesperis, Hirschfeldia, Hymenophysa, Iberis, Isatis, Kernera, Lepidium, Lobularia, Lunaria, Malcomia*, ?*Matthiola, Morisia, Nasturtium, Neotorularia, Neslia, Peltaria*, ×*Raphanobrassica, Raphanus, Rapistrum, Rorippa, Sinapis, Sisymbrium, Sterigmostemum, Thlaspi, Turritis, Vellea*), on Cleomaceae (*Cleome* spp., including *dodecandra* [*graveolens*], *hassleriana, spinosa* [*pungens*], *viscosa*).

Notes: Bradshaw et al. (2024c) published a phylogenetic-taxonomic revision of the *E. cruciferarum* complex and split it into three species, viz., *E. cruciferarum* s. str. on *Alyssum* (s. lat.) spp. and *Berteroa incana, E. alliariicola* on *Alliaria petiolata*, and *E. radulescui*, which is a plurivorous species on a wide range of Brassicaceae, but also on hosts of other plant families.

Erysiphe ravenelii (Berk.) U. Braun & S. Takam., Schlechtendalia 4:13. 2000.

≡ *Microsphaera ravenelii* Berk., Grevillea 4:160. 1876.

Lectotype (designated by Braun 1987): USA. "in foliis Gledischiae, Aiken, S. Carolina," on *Gleditsia triacanthos* (K(M) 169042). *Epitype* (designated here, MycoBank MBT10020095): USA. SOUTH CAROLINA: Aiken County, on *Gleditsia triacanthos*, 14 Oct 1924, *E. Bartholomew* (FH01122210). Ex-epitype sequences: PP680980 (ITS+28S); PP720942 (*CAM*); PP720270 (*GAPDH*); PP720739 (*GS*); PP719999 (*TUB*).

= *Microsphaera penicillata* f. *gledischiae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:358. 1927.

Host range and distribution: On *Gleditsia triacanthos*; North America (USA, widespread).

Notes: In the phylogenetic analyses, sequences obtained from *E. ravenelii* form a strongly supported species clade (FIG. 4). Since the type material is very old and not available for sequencing attempts, an epitype with ex-epitype sequence is designated.

Erysiphe ribicola (Havryl.) U. Braun & S. Takam., Schlechtendalia 4:13. 2000.

≡ *Microsphaera ribicola* Havryl., Mycotaxon 49:262. 1993.

Holotype: ARGENTINA. PROV. RÍO NEGO: Bariloche, cerro Catedral, on *Ribes magellanicum*, May 1990, *M. Havrylenko* 12 (LPS 45136). *Isotype*: BCRU 329. Reference sequence: LC009885.1 (ITS+28S) [ARGENTINA. PROV. RÍO NEGO: Nahuel Huapi, on *Ribes magellanicum*, 2 Apr 1996, *M. Havryleno* (BCRU 03850, TNS-F-87168)].

Host range and distribution: On *Ribes magellanicum*; South America (Argentina: Río Negro).

Notes: An available sequence retrieved from *E. ribicola* falls in an insufficiently resolved complex together with sequences of *E. discariae* (LC010007.1, only 28S), *E. ovidiae* (LC009882.1, only 28S), and *Pseudoidium* sp. on *Schinus patagonicus*, LC010018.1 (ITS+28S) [ARGENTINA. PROV. RÍO NEGRO: San Carlos de Bariloche, Nahuel Huapi Lake, Victoria Island, 29 Feb 2004, *S. Takamatsu* (TNS-F-87818)] (Takamatsu et al. 2015b). Further phylogenetic research on this complex, including additional sequences, is necessary.

Erysiphe robiniicola U. Braun & S. Takam., Schlechtendalia 4:13. 2000.

≡ *Microsphaera robiniae* F.L. Tai, Bull Torrey Bot Club 73:118. 1946, non *E. robiniae* Grev., 1824.

≡ *Erysiphe robiniae* var. *chinensis* U. Braun, Taxonomic Manual of the Erysiphales (Powdery Mildews):500. 2012.

Holotype: CHINA. PROV. GANSU: Tiensuei, on *Robinia pseudoacacia*, 10 Oct 1943, *Siang* 197 (HMAS 05523). Reference sequences: MT309808 (ITS); MT420266 (28S) [CHINA. on *Robinia* sp., QHU2016095].

Host range and distribution: On *Robinia* (*hispida, pseudoacacia*); Asia (China).

Notes: Ex-holotype sequences are not available, although this material is not too old for sequencing attempts. Therefore, for the interim, we propose reference sequences (MT309808, MT420266), which were deposited under *E. robiniae* var. *chinensis* in GenBank. They group far away from sequences of *E. robiniae*, which belong to the *E. trifoliorum* complex, supporting that a separate species being involved, for which the name *Erysiphe robiniicola* is available.

Erysiphe russellii (Clinton) U. Braun & S. Takam., Schlechtendalia 4:13. 2000.

≡ *Microsphaera russellii* Clinton, in Peck, Rep (Ann) New York Stat Mus Nat Hist 26:80. 1874.

≡ *Trichocladia russellii* (Clinton) Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:299. 1927.

Lectotype (designated by Braun 1987): USA. NEW YORK: Buffalo, on *Oxalis* sp., undated, *G.W. Clinton* (NYSf4401). *Isolectotypes*: BPI 558793, NY02942199, NY02942227. Former syntype: USA. NEW YORK: N. Greenbush, on *Oxalis* sp., *C.H. Peck* (NYSf4402).

= *Oidium oxalidis* McAlpine, Proc Roy Soc Victoria NS 6:219. 1894.

≡ *Acrosporium oxalidis* (McAlpine) Subram., Hyphomycetes (New Delhi):838. 1971.

≡ *Pseudoidium oxalidis* (McAlpine) U. Braun & R.T. A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):502. 2012.

Host range and distribution (Braun and Cook 2012): On *Oxalis* [incl. *Xanthoxalis*] (*corniculata* [= *repens*], *corymbosa, dillenii, rosea, stricta* [*europaea, fontana*], *suksdorfii, violacea*, sp.); North America (Canada; USA: mainly from Maine to West Virginia, westward to Kansas, Minnesota), introduced into various parts of the world, Africa (Ethiopia, Morocco, South Africa, Uganda), South America (Argentina), Asia (India, Israel, Japan, Korea, Nepal, Sri Lanka), Australia, Caucasus (Georgia), Europe (Czech Republic, Denmark, France, Germany, Hungary, Poland, Romania, Russia, Ukraine, UK), New Zealand.

Notes: Sequences retrieved from *E. russellii* form a highly supported species clade (FIG. 4). We refrain from designating an epitype until attempts can be made to sequence the holotype.

Erysiphe salmoniana M. Bradshaw & J.K. Mitch., sp. nov. FIG. 7

MycoBank MB853850

Etymology: Epithet dedicated to E. S. Salmon (1871–1959), North American pioneer of powdery mildew taxonomy.

= *Trichocladia diffusa* f. *apios* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:313. 1927.

= *Microsphaera diffusa* auct.

Diagnosis: Differs from the phylogenetically closely allied *Erysiphe diffusa* in having much shorter chasmothecial appendages, 0.7–1.3(–1.5) times as long as the chasmothecial diameter [vs. (1–)1.5–2.5(–3) times as long as the chasmothecial diameter in var. *diffusa*, even much longer in var. *elongata*]; distinct from *E. vignae* by being 3–5(–6)-spored [vs. 5–7-spored]. Furthermore, phylogenetically different from all allied species by forming a separate species clade.

Description: Mycelium foliicolous, amphigenous, thin, effuse or patchy; hyphal appressoria slightly lobed. Anamorph not yet observed. Chasmothecia scattered to gregarious, subglobose to somewhat depressed, 105–150(–160) µm diam; peridium cells irregularly polygonal to daedaleoid, 10–23(–28) × 7–16(–20) µm diam, but occasionally much larger and very irregularly shaped; appendages 7–18, arising ±equatorially, occasionally somewhat from the upper half, appendages stiff, 0.7–1.3(–1.5) times as long as the chasmothecial diameter, base about 9–11 µm wide, 2–3-septate with one septum basal and another near the base, sometimes with an additional septum usually closer to the middle of the appendage, pigmented at the base until the second septum, pigmentation rarely extending significantly further, walls faintly reticulated from base to tip, but more evident in the pigmented region; apices 3–5 times branched, lax, diffuse to dichotomous, divergent particularly in earlier branches, tips straight, not recurved; asci 2–7(–9), ellipsoid-obovoid (exceptionally subglobose), saccate, (40–)46–58 × 28–41(–50) µm, sessile or short-stalked, 3–5(–6)-spored; ascospores ellipsoid-ovoid to subglobose, 12–21 × 10–15 µm, colorless.

Holotype: USA. TENNESSEE: Knox County, Cherokee Drive, on *Apios americana*, Oct 1938, *R. Zuck & F. Zuck* (FH01122166). Ex-holotype sequences: PP681008 (ITS+28S); PP720900 (*CAM*); PP720279 (*GAPDH*); PP720528 (*GS*).

Host range and distribution: On *Apios americana*; North America (USA: Georgia, Tennessee, Wisconsin).

Notes: This North America powdery mildew has previously been assigned to *Erysiphe* (*Microsphaera*) *diffusa*, but sequence analyses have shown that a different, undescribed species is involved. Sequences obtained from *E. diffusa* s. lat. on *Apios americana* form a highly supported species clade in sister position to *E. diffusa* s. str. The cited distribution data only refer to phylogenetically proven specimens. *Erysiphe salmoniana* is probably widespread in North America, with older records hidden under *Microsphaera diffusa*, such as records from Indiana (Anonymous 1960) and Ohio (Ellett 1966).

Erysiphe santalicola M. Bradshaw, S.H Wagh, M.B. Kanade & S.V. Thite, sp. nov. FIG. 8

MycoBank MB853745

Etymology: Epithet composed of the name of the host genus, *Santalum*, + *cola* (dweller).

Diagnosis: Morphologically very similar to *Erysiphe santali*, but different in having straight, cylindrical to often curved-sinuous conidiophore foot cells. Genetically quite different and unrelated, sequences forming a well-supported clade distant from *E. santali*.

Description: Mycelium amphigenous, forming circular to irregular thin white patches or effuse; hyphae colorless, branched, septate, thin-walled, smooth,

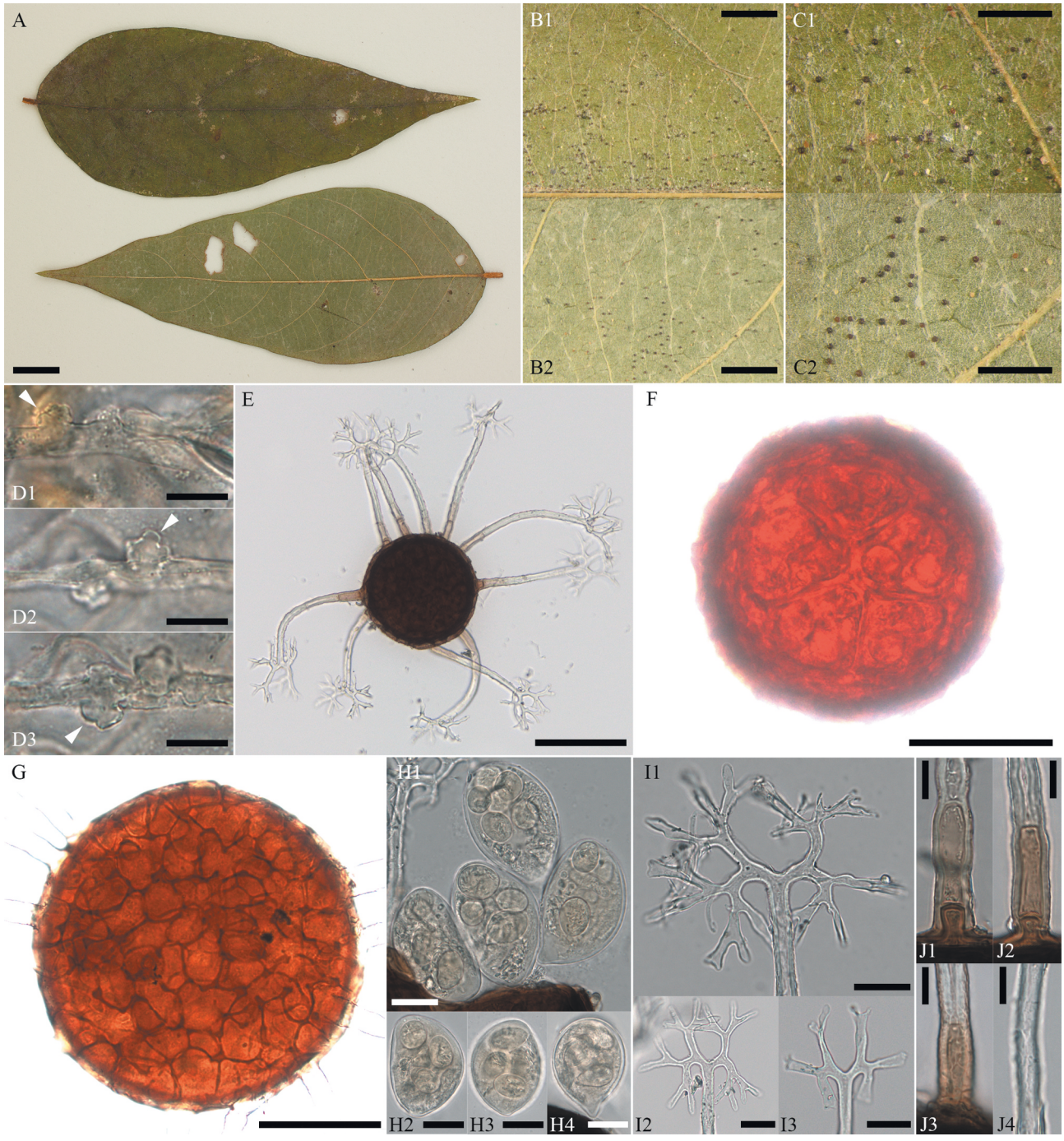

Figure 7. Morphological details of the mycelium and sexual morph (chasmothecia) of *Erysiphe salmoniana*, sp. nov., on *Apios americana* [= *tuberosa*]. All images derived from the holotype (FH01122166). (A–C) Infected leaves and chasmothecia including upper (A, B1, C1) and lower (A, B2, C2) leaf surfaces. (D) Hyphae with appressoria on the leaf surface. (E) Chasmothecium with appendages. (F) Arrangement of five asci within an intact chasmothecium in top view. (G) Excipular cell arrangement in the peridium in frontal view. (H) Asci released from broken chasmothecia with ascospores. (I) Appendage tips showing variation in branching. (J) Appendages showing variation. (J1–J2) Septa near brown base of appendages. (J3) Detail of reticulation on appendage base. (J4) Detail of reticulation near middle of appendage. Water after KOH pretreatment: D–G, I–J. KOH: H. Bars: A = 1 cm; B = 2 mm; C = 1 mm; D, J = 10 µm; E = 100 µm; F–G = 50 µm; H–I = 20 µm.

hyphal cells 40–60 µm long and 2–8 µm wide; hyphal appressoria solitary, occasionally in opposite pairs, almost nipple-shaped, slightly to multilobate, ca. 3–8 µm diam; a single or occasionally two conidiophores arise from the upper surface of hyphal mother cells, position mostly toward one septum, i.e., not in the middle of the mother cell, erect, ca. 40–80 µm long (without conidia), foot cells straight to curved-sinous,

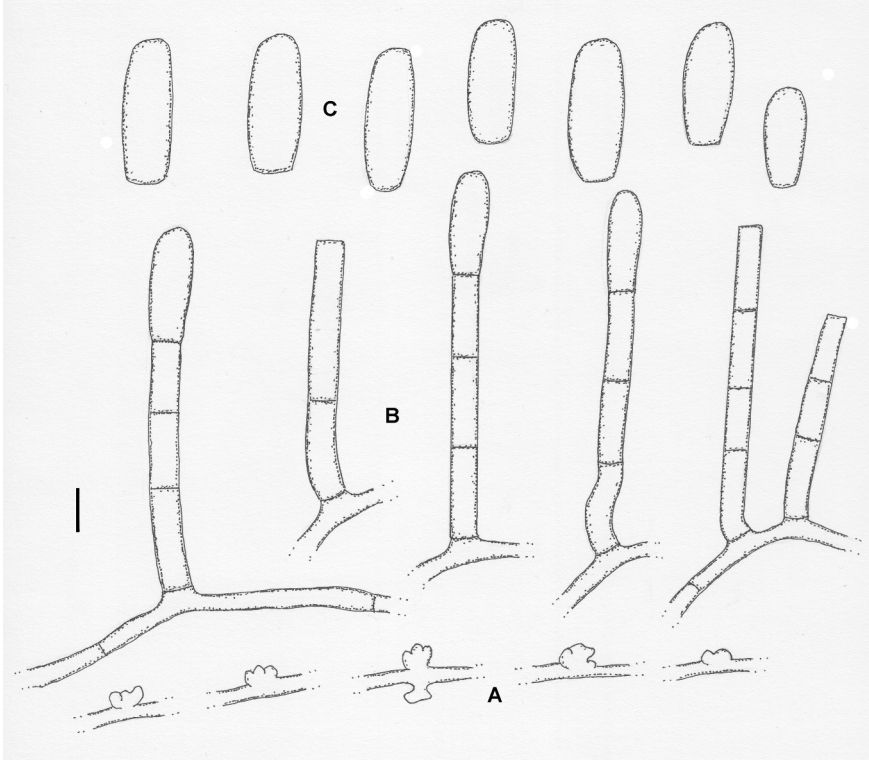

Figure 8. Morphological details of the asexual morph of *Erysiphe santalicola*. (A) Hyphal appressoria. (B) Conidiophores. (C) Conidia. Bar = 10 µm.

15–30 × 6–9 µm, followed by (1–)2(–3) cells, shorter than the foot cell, about as long as the foot cell or occasionally somewhat longer, 8–25 µm; conidia formed singly, ellipsoid-cylindrical, (20–)25–38 × 10–15 µm.

Holotype: INDIA. MAHARASHTRA: Ambegaon, Shinoli, on *Santalum album*, Dec 2020, *S.H. Wagh, M. B. Kanade & S.V. Thite* (HAL 3497 F). *Isotype*: NCSLG24449. Ex-holotype sequence: PP681085 (ITS+28S).

Host range and distribution: On *Santalum album*; Asia (China, India).

Notes: Bradshaw et al. (2024a) sequenced type material of *Oidium santalacearum*, described from India, and confirmed that this anamorphic species represents a species in the genus *Erysiphe*. The ex-type sequence is in a basal position to the the *Erysiphe aquilegiae* complex. The new name *Erysiphe santali* was introduced, since the epithet "*santalacearum*" was preoccupied in *Erysiphe*. Li et al. (2023) sequenced Chinese powdery mildew specimens collected on *Santalum album* and assigned them to *Pseudoidium santalacearum*. However, our own sequence analyses revealed that two unrelated, but morphologically similar anamorphic powdery mildew species occur in Asia on *Santalum album*. Sequences of the second species, described herein as *E. santalicola*, group quite distant from *E. santali* and close to *E. palczewskii* and the *E. trifoliorum* complex. In any case, the Chinese specimens examined by Li et al. (2023) pertain to *E. santalicola*. There are some differences between the described morphology of the Indian type specimen and the Chinese collection. Li et al. (2023) described very long conidiophores (83.5–127.3 × 6.6.–7.6 µm), somewhat longer and much wider conidiophore foot cells (24.8–44.6 × 8.2–11.7 µm), and somewhat longer conidia (31.3–41.2 × 11.3–13.7 µm). The conidia agree well with the India type material. The described conidiophores are unusually long, but it is unclear what Li et al. (2023) included in their measurements. The given width of the conidiophores (6.6.–7.6 µm) coincides with the Indian type. However, the cited width of the foot cells in the Chinese sample (8.2–11.7 µm) cannot be correct, and it is in conflict with the given width of the conidiophore.

Erysiphe schizandrae (Sawada) U. Braun & S. Takam., Schlechtendalia 4:13. 2000.

≡ *Microsphaera schizandrae* Sawada, Bull Gov Forest Exp Sta Meguro 50:123. 1951.

Neotype (designated by Braun and Cook 2012): JAPAN. Sapporo, on *Schisandra chinensis*, 28 Sep

1894, *K. Miyabe* (BPI 556588). Reference sequence: LC010049.1 [RUSSIA. Far East, on *Schisandra chinensis*, 21 Sep 1989, *V.P. Heluta* (TNS-F-87875)].

= *Microsphaera penicillata* f. *schizandrae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:357. 1927.

≡ *Microsphaera schizandrae* (Jacz.) Golovin, Trudy Bot Inst Akad Nauk SSSR Ser 2 Sporov Rast 10:350. 1956, nom. illeg. (Art. 53.1).

= *Microsphaera paederiae* Tanda, Y. Nomura & U. Braun, Mycotaxon 25:262. 1986; type host: *Schisandra repanda* [not *Paederia*] (holotype: TUAMH 0045).

= *Microsphaera schizandrae* f. *breviseta* Tanda & Y. Nomura, Trans Mycol Soc Japan 33(2):219. 1992, and in Nomura, Taxonomical study of Erysiphaceae of Japan:130. 1997; type host: *Schisandra chinensis* (holotype: TUAMH 3513).

Host range and distribution: On *Schisandra* (*chinensis, nigra, repanda*); Asia (China, Japan, Korea, Russia [Far East]).

Notes: Sequenced specimens from Japan, useful as epitype, are not yet available. Therefore, we recommend, for the interim, LC010049.1 as reference sequence for phylogenetic-taxonomic purposes.

Erysiphe sydowiana (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:14. 2000.

≡ *Microsphaera sydowiana* U. Braun, Mycotaxon 15:139. 1982.

Holotype: USA. WASHINGTON: Deer Lake, on *Ceanothus velutinus*, 15 Aug 1906, *Bonser* (FH00965537). Ex-holotype sequences: PP681031 (ITS +28S); PP720891 (*CAM*); PP720125 (*GAPDH*); PP720562 (*GS*); PP720416 (*RPB2*); PP719975 (*TUB*).

Host range and distribution (Braun and Cook 2012): On *Ceanothus* (*americanus* [= *sanguineus*], *spinosus, velutinus*), *Colubrina triflora* [= *Ceanothus arboreus*]; North America (USA, widespread).

Notes: The ex-holotype sequence of *E. sydowiana* falls in a sister position to the *E. ceanothi* clade. However, additional sequences obtained from *E. sydowiana* are urgently necessary.

Erysiphe syringae Schwein., Trans Amer Philos Soc 4:270. 1834.

≡ *Microsphaera syringae* (Schwein.) Magnus, Ber Deutsch Bot Ges 16:67. 1898.

Lectotype (designated here, MycoBank MBT10020097): USA. PENNSYLVANIA: Bethlehem (and New York), on *Syringa* sp., s.d., *Schweinitz*, s.n. (BPI 1052310). *Epitype* (designated here, MycoBank MBT10020096): USA. Suffolk County, from the Arnold Arboretum on *Syringa oblata* subsp. *dilatata* (host accession 316-96-A), 26 Aug 2021, *M. Bradshaw* (FH01131095). Ex-epitype sequences: PP681102 (ITS +28S); PP720984 (*CAM*); PP720335 (*GAPDH*); PP720671 (*GS*); PP720472 (*RPB2*); PP720053 (*TUB*).

= *Microsphaera friesii* var. *syringae* Cooke & Peck, J Bot 10:12. 1872.

= *Microsphaera syringae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby: 337. 1927, nom. illeg. (Art. 53.1), non *M. syringae* (Schwein.) Magnus, 1898.

≡ *Microsphaera jaczewskii* U. Braun, Feddes Repert 92:510. 1981.

= *Microsphaera fraxini* U. Braun, Mycotaxon 14:372. 1982; type host: *Fraxinus americana* (holotype: PH00041546).

= *Microsphaera penicillata* f. *forestieri* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:357. 1927.

= *Microsphaera penicillata* f. f. *ligustri* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:357. 1927.

= *Microsphaera penicillata* f. *syringae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:357. 1927.

Host range and distribution (Braun and Cook 2012): On ?*Chionanthus virginicus, Forestiera acuminata, Fraxinus* (*americana, ornus*, sp.), *Ligustrum* (*medium, vulgare*, sp.), *Syringa* (*amurensis* [≡ *reticulata* subsp. *amurensis*], ×*chinensis*, ×*hyaciniflora, oblata* subsp. *dilatata*, ×*persica, tomentella, vulgaris*, sp.); North America (Canada, USA, widespread), South America (Argentina), introduced into Europe (Belgium, England, France, Germany, Hungary, Italy, Lithuania, Portugal, Romania, Russia, Spain, Slovakia, Switzerland, former Yugoslavia), probably also in Asia (Russia, Siberia) and Australia.

Notes: The lectotypification designated by Braun (1987) was in error. It may be superseded, since it is in serious conflict with the protolog [Art. 9.19(c)]. Schweinitz (1834) cited "Bethlehem" as the only locality in the protolog of *E. syringae*, which is not mentioned on the label of the "lectotype" deposited as PH00062389 (only "New York" is cited). Therefore, another lectotype is designated. Sequences retrieved from *Erysiphe syringae* form a well-supported species clade. Previously, *E. syringae* and *E. syringae-japonicae* have been confused. Seko et al. (2008, 2011) and Takamatsu et al. (2016) clarified the phylogenetic-taxonomic status of *E. syringae* and confirmed that *E. syringae-japonicae* represents a separate species. In our phylogenetic analyses, we showed that *E. syringae* and *E. syringae-japonicae* are not closely allied (the latter species is treated in Bradshaw et al. 2024a). Seko et al. (2011) analyzed collections on *Ligustrum* and *Syringa* spp. from Asia, Europe, and North and South America and showed that Asian collections on *Ligustrum* spp., genetically close to *E. syringae-japonicae* but

morphologically different, must be assigned to *E. ligustri*, in contrast to North America samples on *Ligustrum* spp., which pertain to *E. syringae*. In our present analyses (FIG. 1), a sequence retrieved from a collection of *Erysiphe* on *Chionanthus virginicus* groups close to but outside the *E. syringae* clade, suggesting that this host might harbor an undescribed cryptic sister species, but additional sequences obtained from powdery mildew on this host are needed for final conclusions. Therefore, the taxonomic status of *Microsphaera penicillata* f. *chionanthi* Jacz. remains open, at least for the interim.

Erysiphe thaxteri (Havryl. & U. Braun) U. Braun & S. Takam., Schlechtendalia 4:14. 2000.

≡ *Microsphaera thaxteri* Havryl. & U. Braun, Nova Hedwigia 66:414.1998.

Holotype: ARGENTINA. PROV. RÍO NEGRO: Bariloche, Mt. Tronador, on *Berberis microphylla* [= *B. buxifolia*], 14 Apr 1996, *M. Havrylenko* 359 (BCRU 01614). Reference sequence: LC010017.1 [ARGENTINA. PROV. RÍO NEGRO: San Carlos de Bariloche, Victoria Island, Nahuel Huapi Lake, on *Berberis darwinii*, 29 Feb 2004, *S. Takamatsu* (TNS-F-87817)].

Host range and distribution: On *Berberis* (*darwinii, microphylla, trigona* [= *linerifolia*]); South America (Argentina: Neuquén, Río Negro, Tierra del Fuego; Chile).

Notes: Type material of *E. thaxteri* has not yet been sequenced. As already shown in Takamatsu et al. (2015b), sequences retrieved from collections of this species group together with a single available sequence obtained from a non-type collection of *E. myoschili*. Further sequence analyses are needed to clarify the phylogeny and taxonomy of the two South American species.

Erysiphe thermopsidis R.Y. Zheng & G.Q. Chen, Sydowia 34:287. 1981.

Holotype: CHINA. PROV. QUINGHAI: Xining, on *Thermopsis lanceolata*, 22 Aug 1959, *Ma & Xing* 1481 (HMAS 40171). Reference sequences: MT309725 (ITS); MT309801 (28S) [CHINA. on *Thermopsis lanceolata* (QHU2018034)].

= *Erysiphe communis* f. *thermopsidis* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:263. 1927.

= *Trichocladia diffusa* f. *thermopsidis* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:316. 1927.

≡ *Microsphaera diffusa* var. *thermopsidis* (Jacz.) T.Z. Liu, Mycosystema 17:299. 1998.

= *Microsphaera thermopsidis* U. Braun, Mycotaxon 20:491. 1984; type host: *Thermopsis lanceolata* (holotype: LE 34548).

≡ *Erysiphe thermopsidis* (U. Braun) U. Braun & S. Takam., Schlechtendalia 4:14. 2000, nom. illeg. (Art. 53.1), non *E. thermopsidis* R.Y. Zheng & G.Q. Chen, 1981.

≡ *Erysiphe shinii* U. Braun, Schlechtendalia 8:34. 2002.

Host range and distribution (Braun and Cook 2012): On *Genista tinctoria, Melilotus suaveolens, Thermopsis* (*lanceolata, lupinoides*); Asia (China, Russia [Siberia, Far East]), Caucasus (Armenia), Europe (Lithuania).

Notes: Sequences obtained from a single Chinese specimen of this species are available and confirm the status as independent species. They can currently be used as reference sequences for this species, but the type material is not too old for sequencing attempts. The complicated nomenclature and taxonomy of this species have been discussed in detail by Liu and Braun (2009) and Braun and Cook (2012). The various names were based on collections with chasmothecia in different developmental stages, either with simple or with branched appendages.

Erysiphe umbilici (Kom.) U. Braun & S. Takam., Schlechtendalia 4:15. 2000.

≡ *Microsphaera umbilici* Kom., Bot Zap 4:270. 1895.

Lectotype (designated by Braun and Cook 2012): TAJIKISTAN ["Turkestan"]. "ad fluvium Seravschan superior," on *Clementsia semenovii* [≡ *Rhodiola semenovii*], Aug 1893, *Komarov* [Jacz. et al., Fungi Ross Exs 29] (LEP). *Isolectotypes*: Jacz. et al., Fungi Ross Exs 29 (e.g., BPI 558977, FH00965543 & 00972923, K, LEP, S). Ex-isolectotype sequences: PP680982 (ITS+28S); PP720319 (*GAPDH*); PP719976 (*TUB*).

= *Microsphaera umbilici* f. *sedi* Pospelov, in Pospelov et al., Grib Fl Kirgiz SSR 1:96. 1957.

≡ *Microsphaera sedi* (Pospelov) Y.N. Yu, Acta Microbiol Sin 21(7):12. 1981.

Host range and distribution: On *Clementsia semenovii, Rhodiola rosea, Hylotelephium ewersii, Sedum* (*rubrotinctum*, sp.); Asia (China, Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan).

Notes: The status of *E. umbilici* as a species has been confirmed based on an ex-type sequence, obtained from an isolectotype deposited at (FH00965543).

Erysiphe vaccinii, see below (*Erysiphe vaccinii* complex).

Erysiphe viciae-unijugae (Homma) U. Braun, Feddes Repert 92(7–8):499. 1981.

≡ *Microsphaera viciae-unijugae* Homma, J Fac Agric Hokkaido Univ 38:400. 1937.

≡ *Ischnochaeta viciae-unijugae* (Homma) Sawada, Bull Gov Forest Exp Sta Meguro 50:115. 1951, nom. inval. (Art. 35.1).

Holotype: JAPAN. PREF. OKAYAMA: Okayama, on *Vicia unijuga*, 2 Dec 1929, *S. Igata* (SAPA). *Epitype* (designated by Darsaraei et al. 2024): JAPAN. PREF. OSAKA: Yao, Toyama, on *Vicia unijuga*, 6 Oct 1986, *Y. Sato* (TNS-F-87175). Ex-epitype sequence: LC010086.1 (ITS+28S).

= *Erysiphe cruchetiana* var. *hyalina* R.Y. Zheng & G. Q. Chen, Sydowia 34:288. 1981; type host: *Vicia amoena* (holotype: HMAS 40119).

Host range and distribution: On *Vicia* (*amoena, amurensis, bifolia, cracca, faba, japonica, pseudorobus, sepium, unijuga, venosa, villosa*); Asia (China, Japan, Russia [Siberia, Far East]).

Notes: In a recently published phylogenetic-taxonomic treatment of *Erysiphe* spp. on Fabaceae, Darsaraei et al. (2024) epitypified *M. viciae-unijugae* and demonstrated that this species is confined to hosts of the genus *Vicia*. Morphologically similar collections on *Lathyrus* spp. phylogenetically represent an undescribed sister species, which is described herein as *E. lathyrina*.

Erysiphe vignae L. Kelly, L. Kiss & Vaghefi, in Kelly et al., Phytopathology 111(7):1200. 2021, emend. FIG. 9

Holotype: AUSTRALIA. QUEENSLAND: Toowoomba, on *Vigna radiata*, 22 Mar 2019, *L. Kelley* (BRIP 71005). Ex-holotype sequences: MT628282 (ITS); MT228017 (28S).

Description (teleomorph): Chasmothecia scattered to gregarious, both foliicolous and caulicolous, depressed globose, 135–185 µm diam; peridium cells irregularly polygonal, 13–28 × 10–19 µm; appendages 11–37, arising ±equatorially, appendages ±stiff but often geniculate, about 0.5–1.1 times as long as the chasmothecial diameter, 8–11.5(–13.5) µm wide, with 0–4 septa in the stem, almost always with one ±basal septum, others usually in the bottom half of the stem and occasionally additional septa in the branching apex, hyaline or faintly to strongly pigmented at the base, pigmentation disappearing by the middle of the stalk if not much earlier, walls reticulated, particularly visible at the base, but smooth at the tip branches, thick toward the base but thinning above, apices 3–6 times branched, mostly richly branched but rather loose, diffuse, often deeply cleft, sometimes forking even at the appendage base, sometimes diverging at the first bifurcation, tips straight, not recurved; asci 4–11, ellipsoid-obovoid, saccate, 70–85(–95) × 35–55 µm, sessile or short-stalked, 5–7-spored; ascospores ellipsoid-ovoid, 18–24 × 12–15 µm, colorless.

Host range and distribution (phylogenetically proven hosts): On *Phaseolus vulgaris, Strophostyles leiosperma* [= *pauciflora*], *Vigna* (*mungo, radiata, unguiculata*); Australia, Asia (China), North America (USA). Probably widespread on *Phaseolus* and *Vigna* spp.

Notes: The recently described *E. vignae* has a wide distribution on diverse host species of the legume subtribe Phaseolinae, including *Phaseolus, Strophostyles*, and *Vigna* (e.g., Deng et al. 2022; present analyses). The teleomorph of this species was unknown and had not yet been described, so that the present description constitutes an emendation. The present description is based on: "USA. OKLAHOMA: Ottawa Co[unty], 2 mi [les] E[ast] of Picher, on *Strophostyles leiosperma* [as *pauciflora*], 9 Oct 1943, *D.A. Preston* (FH01122172)." The general characteristics of the chasmothecia agree well with those of *E. diffusa*, as expected due to the phylogenetic affinity to the latter species. However, chasmothecia of *E. vignae* differ from those of *E. diffusa* in having much shorter appendages, about 0.5–1.1 times as long as the chasmothecial diameter [vs. (1–)1.5–2.5(–3) times as long as the chasmothecial diameter in var. *diffusa*, even much longer in var. *elongata*].

Further species of the "Microsphaera lineage" *with available ex-type sequences as reference sequences*

Erysiphe acantholimonis J.G. Song, B. Xu & H.D. Shin

Holotype: HMUT00821 (China, on *Acantholimon hedinii*). *Isotype*: KUS-F29047. Ex-holotype sequences: KU554537 (ITS); KU554536 (28S).

Notes: This species was introduced by Song et al. (2016). Braun and Cook (2012) treated *Erysiphe communis* f. *acantholimonis* Koshk. [Bot Mater Otd Sporov Rast Bot Inst Komarova Akad Nauk SSSR 14:124. 1961], described from Turkmenistan on *Acantholimon avenaceum* (type: LE 34543), as synonym of *E. limonii*. This forma might be a synonym of *E. acantholinonis*, but this requires confirmation by results of sequence analyses.

Erysiphe alliariicola M. Bradshaw & U. Braun

Holotype: GLM-F62492 (Germany, on *Alliaria petiolata*). Ex-holotype sequences: OR427409 (*CAM*); OR427505 (*GADPH*); OR427592 (*GS*); OR424895 (ITS +28S); OR427672 (*RPB2*); OR427778 (*TUB*).

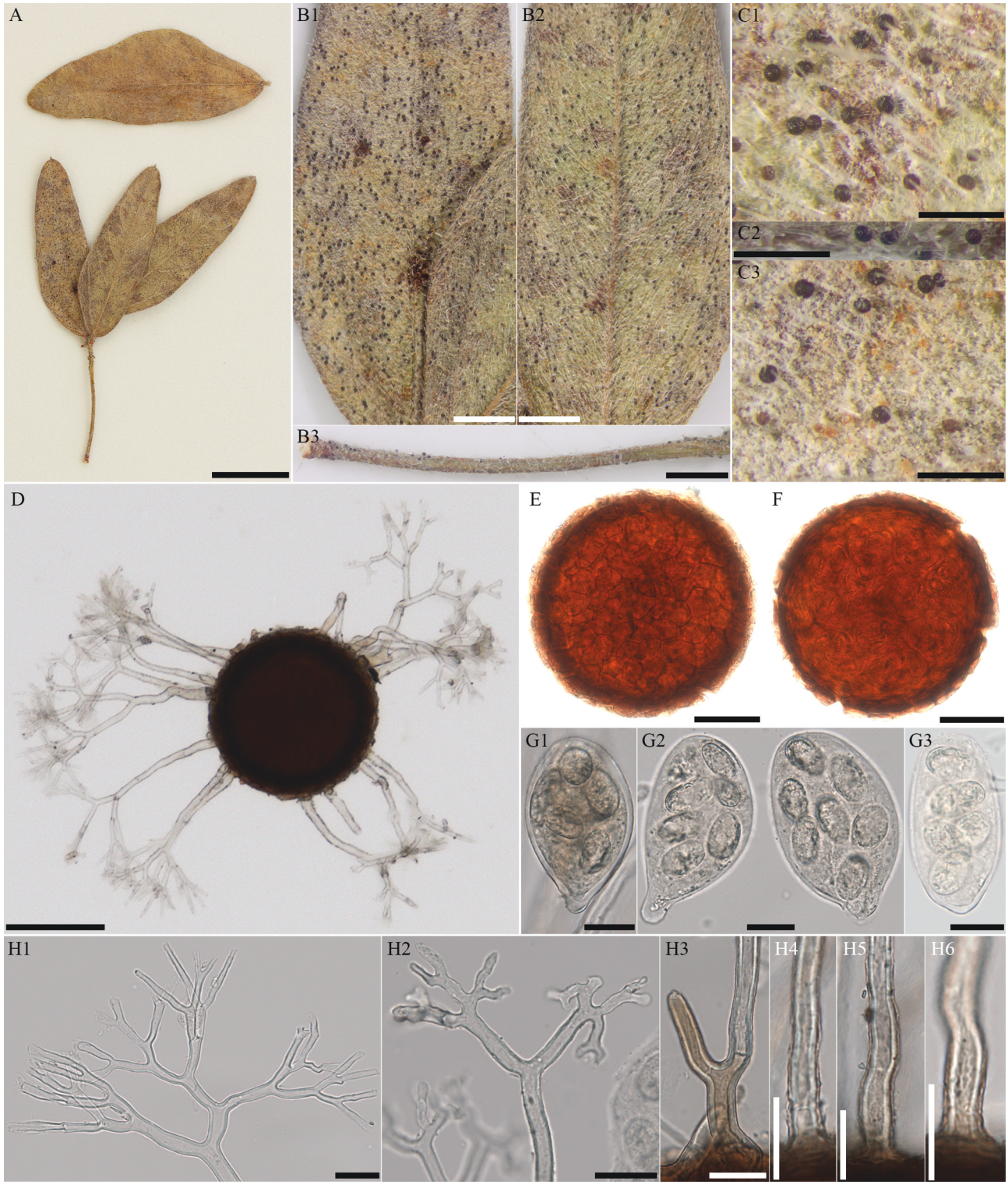

Figure 9. Morphological details of the mycelium and sexual morph (chasmothecia) of *Erysiphe vignae* on *Strophostyles leiosperma* [= *pauciflora*]. All images derived from FH01122172. (A–C) Infected plant material and chasmothecia including upper (A, B1, C1) and lower (A, B2, C3) leaf surfaces and stem (A, B3, C2). (D) Chasmothecium with appendages. (E) Excipular cell arrangement in the peridium. (F) Arrangement of 10 asci within an intact chasmothecium. (G) Asci released from broken chasmothecia with ascospores. (H) Details of appendages. (H1–H2) Details of appendage tips. (H3) Near-basal bifurcation in appendage, with septa in the branches. (H4) Detail of basal septum in appendage. (H5–H6) Detail of reticulation at base of appendage. Water after KOH pretreatment: D–H. Bars: A = 1 cm; B = 2 mm; C = 0.5 mm; D = 100 µm; E–F = 50 µm; G–H = 20 µm.

Notes: This species has recently been described in Bradshaw et al. (2024c). It belongs to the *E. cruciferarum* complex but forms a separate highly supported clade. It is widespread in Asia (India, Iran, Kazakhstan), the Caucasus region (Armenia, Georgia), and Europe (Bulgaria, Czech Republic, France, Germany, Greece, Hungary, Italy, Poland, Romania, Russia, Slovakia, Sweden, Switzerland, Ukraine).

Erysiphe baliensis Siahaan & S. Takam

Holotype: TNS-F-61949 (Indonesia, on *Gliricidia sepium*). *Isotype*: BO 22736. Ex-holotype sequence: LC060727 (ITS+28S).

Notes: The description of this species was based on anamorphs. Chasmothecia are not yet known. This species is known from Indonesia and Japan on *Gliricidia sepium* and *Wisteria japonica*.

Erysiphe digitata (A.J. Inman & U. Braun) A.J. Inman & U. Braun

≡ *Microsphaera digitata* A.J. Inman & U. Braun.

Holotype: E 83207 (Belgium, on *Rhododendron mekongense* var. *melinanthum*). Ex-holotype sequence: OK636218 (ITS).

Notes: Tymon et al. (2022) provided an ex-holotype sequence of this species, clarified the phylogenetic affinity, and demonstrated that this species with Asian origin has been introduced in the USA on evergreen *Rhododendron* spp.

Erysiphe eschscholziae Pastirč. & Jankovics

Holotype: G 111708 (Switzerland, on *Eschscholzia californica*). Ex-holotype sequence: KT588626 (ITS). *Paratype*: G 111709 (Switzerland, *Eschscholzia californica*). Ex-paratype sequences: KT588627 (ITS); KU672354 (28S).

Notes: This species was reported from North America as *Erysiphe cruciferarum* on *Eschscholzia californica* (Glawe 2006), and from Mexico, including phylogenetic confirmation (Camacho-Tapia et al. 2018). Records of "*Erysiphe communis*" on *Eschscholzi californica* from Japan, Romania, and the USA (Amano 1986) belong possibly to *E. eschscholziae*.

Erysiphe euphorbiae-cotinifoliae Fern.-Pav. & S. Takam

Holotype: TNS-F-95888 (Mexico, on *Euphorbia cotinifolia*). Ex-holotype sequence: OR438205 (ITS+28S).

Notes: This recently described species (Bradshaw et al. 2024c) is, as far as known, confined to its type host. Sequences form a species clade in sister position to *E. euphorbiicola*.

Erysiphe hypogena S. Takam. & U. Braun

Holotype: TNS-F-87778 (Japan, on *Quercus acutissima*). *Isotype*: HAL 1994 F. Ex-holotype sequence: AB292723 (ITS+28S).

Notes: This species is known from Japan on *Quercus acutissima* and *Q. variabilis*, and it possibly also occurs in China.

Erysiphe iranica Darsaraei, Khodap. & Pirnia

Holotype: GUM 1805 (Iran, on *Onobrychis caput-galli*). Ex-holotype sequences: OL709413 (ITS); OL709411 (28S).

Notes: So far, this species, recently described by Darsaraei et al. (2022), is only known from Iran, but a wider distribution can be expected. Additional sequences, including those from other *Onobrychis* spp., are necessary.

Erysiphe lupini M. Bradshaw

Holotype: HAL 3378 F (USA, Washington, on *Lupinus* sp.). Ex-holotype sequence: MZ265170 (ITS+28S).

Notes: This species was described in Bradshaw et al. (2022a). Sequences form a highly supported species clade. This species is known from North America (western USA) on *Lupinus* (*lepidus, polyphyllus, Lupinus* sp.).

Erysiphe medicaginis L. Kiss, L. Kelly & Vaghefi

Holotype: BRIP 70957 (Australia, on *Medicago polymorpha*). Ex-holotype sequences: MT160214 (ITS); MT248412 (28S).

Notes: Sequences of *E. medicaginis* form a highly supported species clade. The exact host range of this species is still unknown. It can be expected that this species has a wide, almost worldwide distribution on diverse *Medicago* species. Records of *Erysiphe* on *Medicago* spp. are known from Africa, Asia, Europe, and North and South America (Amano 1986). Khodaparast et al. (2003) provided a sequence retrieved from *Erysiphe* on *Medicago sativa* from Iran (AB104519). On the other hand, proven sequences retrieved from collections on *Baptisia australis* (LC009967, Japan, TNS-F-87515, originally identified as *Pseudoidium* sp.) and *Sophora flavescens* (LC009919, Japan, TNS-F-87236, originally identified as *Pseudoidium* sp.), belonging to the *E. medicaginis* clade, suggest a much wider host range amongst legumes.

Erysiphe monascogera Shiroya, C. Nakash. & S. Takam

Holotype: TNS-F-15700 (Japan, on *Styrax japonicus*). Ex-holotype sequence: AB331646 (ITS+28S).

Notes: This is a very unusual species, with usually a single ascus per chasmothecium, as in *Podosphaera*, but nevertheless phylogenetically pertaining to *Erysiphe*.

Erysiphe rumicicola Darsaraei, Khodap., Afshan & U. Braun

Holotype: IRAN 16527 F (Iran, *Rumex crispus*). Ex-holotype sequences: OP326702 (ITS); OP326704 (28S).

Notes: In a phylogenetic-taxonomic revision of *Erysiphe polygoni* s. lat., Darsaraei et al. (2023) pointed out that *Erysiphe* collections on *Rumex* spp. (excluding species of *Rumex* subgen. *Acetosa*) pertain to a species on its own, *E. rumicicola*, phylogenetically and morphologically distinct from *E. polygoni* s. str. on *Polygonum* spp. Species of the genera *Fagopyrum* and *Rheum* belong also to the host range of *E. rumicicola*.

The Erysiphe alphitoides *complex*

In the comprehensive phylogenetic examination of the "*Microsphaera* lineage" of the genus *Erysiphe*, Takamatsu et al. (2015a) identified a complex of taxa around *Erysiphe alphitoides*, which was insufficiently resolved in ITS+28S analyses, and classified it as "*E. alphitoides* clade." We prefer the name "*E. alphitoides* complex." The whole complex has recently been reexamined by multilocus analyses in which high resolutions were achieved on the species level (Bradshaw et al. 2023c), which confirmed almost all taxa included in this complex, including *E. alphitoides, E. aucubae, E. euonymicola, E. ipomoeae, E. menispermi* var. *dahurica, E. orixae, E. pseudolonicerae, E. sinomenii*, and *E. wallrothii*.

Erysiphe akebiae (Sawada) U. Braun & S. Takam., Schlechtendalia 4:5. 2000.

≡ *Microsphaera akebiae*, Sawada, Bull Gov Forest Exp Sta Meguro 50:116. 1951.

Lectotype (designated by Braun 1987): JAPAN. PROV. IWATE: Asagishi, on *Akebia quinata*, 2 Oct 1906, *Yamada* (FH00965525). *Syntype*: IUM.

Host range and distribution: On *Akebia* (*quinata, trifoliata*); Asia (China, Japan, Korea), Europe (introduced in the Netherlands and UK).

Notes: E. akebiae is morphologically close to *E. alphitoides* but differs in forming cylindrical conidia, vs. usually doliiform conidia in the latter species. ITS+28S sequences of the two species are not clearly different. In the *RPB2* tree, *E. akebiae* and *E. wallrothii* form a strongly supported clade. In the concatenated tree published by Bradshaw et al. (2023c), two sequences retrieved from specimens of *E. akebiae* collected in Japan and the USA group close to a highly supported *E. wallrothii* clade (Bradshaw et al. 2023c). However, the relation of the Japanese and North American collections is not clear and requires additional multilocus sequences of specimens of *E. wallrothii* and *E. akebiae*.

Erysiphe alphitoides (Griff. & Maubl.) U. Braun & S. Takam., Schlechtendalia 4:5. 2000.

≡ *Microsphaera alphitoides* Griff. & Maubl., Bull Soc Mycol France 28:103. 1912.

[*Holotype*: FRANCE. Gard, on *Quercus petraea* (= *Q. sessiliflora, Q. robur* p.p.), Dec 1911, *G. Arnaud* (FH00965519); ex-holotype sequence: OM436186.] Proposed conserved type (Braun et al. 2022): SWITZERLAND, Neuchâtel, on *Quercus robur*, 4 Apr 1999, *S. Takamatsu* (TNS-F-87437 [previously MUMH 631]). Duplicate: HAL 1946 F. Ex-type sequence: AB292708 (ITS+28S).

= *Oidium alphitoides* Griff. & Maubl., Bull Soc Mycol France 26:132. 1910.

= *Microsphaera dentatae* Liou, Contr Lab Bot.Natl Acad Peiping 1:19. 1931.

≡ *Microsphaera alni* var. *dentatae* (Liou) F.L. Tai, Bull Chin Bot Soc 1:22. 1935.

= *Microsphaera quercus* Sawada, Bull Gov Forest Exp Sta Meguro 50:122. 1951.

Host range and distribution (for details, see Braun and Cook 2012): On *Castanea* (*crenata, sativa*), *Castanopsis* (*cuspidata, sieboldii*), *Fagus* (*ferruginea, sylvatica*), and very numerous *Quercus* spp.; infections occasionally on *Cotinus* and *Mangifera* [Anacardiaceae], *Aesculus* [Hippocastanaceae] (Braun and Cook 2012), *Paeonia* [Paeoniaceae] (Bolay 2005, as "*E. hypophylla*"; Takamatsu et al. 2007), and *Piptanthus* and *Wisteria* [Fabaceae] (Bolay et al. 2021); almost circumglobal, origin probably in Asia, but nowadays introduced and widespread in Africa, Australia, Caucasus, Europe, North and South America, and New Zealand.

Notes: Bradshaw et al. (2022e) traced holotype material of *E. alphitoides* at FH, sequenced it, and pointed out that this material belongs to the powdery mildew species that has so far been referred to as *E. quercicola*. To avoid a total confusion around the names *E. alphitoides* and *E. quercicola*, a proposal to maintain the customary application of *E. alphitoides* with conserved type has been submitted (Braun et al. 2022). *Erysiphe alphitoides* is part of the eponymous complex. Several additional powdery mildew species pertain to this complex, and the ITS+28S sequences of these taxa are not sufficiently different from *E. alphitoides* sequences. The clarification and resolution of this complex required multilocus analyses, which have recently been performed and published (Bradshaw et al. 2023c). The results led to the

confirmation of *E. alphitoides* as a species of its own, as demonstrated in a concatenated tree.

Erysiphe aucubae S. Takam. & Siahaan, in Siahaan & Takamatsu, Mycoscience 57(4):252. 2016.

Holotype: JAPAN. PREF. SHIGA: Maibara-shi, Ikesita, Green Park Santo, on *Aucuba japonica*, 14 Oct 2015, *S. Takamatsu & S.A.S. Siahaan* (TNS-F-65454). *Isotypes*: MUMH 6474 and HAL 2984 F. Ex-holotype sequence: LC121921 (ITS+28S).

Host range and distribution: On *Aucuba japonica*; Asia (Japan).

Notes: Siahaan and Takamatsu (2016) described the anamorphic powdery mildew species *E. aucubae* from Japan, based on numerous collections. This species belongs to the *E. alphitoides* complex, but sequences form a well-supported species clade. Furthermore, this species differs from *E. alphitoides* in having longer conidia with a length/width ratio higher than 2.0. It is confirmed as an independent species in phylogenetic multilocus analyses (Bradshaw et al. 2023c).

Erysiphe euonymicola U. Braun, in Braun and Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):461. 2012.

Holotype: FRANCE. Pays de la Loir, Dépt. de la Vendée, La Mothe-Archard, on *Euonymus japonicus*, 19 Nov 2002, *J. Gaborit* (HAL 2360 F).

= *Oidium leucoconium* var. *euonymi-japonici* Arcang., Atti Soc Tosc Sci Nat Pisa Processi Verbali 12:108. 1900.

≡ *Oidium euonymi-japonici* (Arcang.) Sacc., in Salmon, Ann Mycol 3:1. 1905.

≡ *Acrosporium euonymi-japonici* (Arcang.) Sumst., Mycologia 5(2):58. 1913 [as "(E.S. Salmon) Sumst."].

≡ *Microsphaera euonymi-japonici* (Arcang.) Hara, Bull Agric Soc Shizuoka Pref 282:29. 1921.

≡ *Uncinula euonymi-japonici* (Arcang.) Hara, Dendropathology:22. 1922.

≡ *Microsphaera euonymi-japonici* (Arcang.) Herter, Estad Bot Reg Urug, Florula Uruguayensis, Plantes Avasculares:33. 1933.

≡ *Pseudoidium euonymi-japonici* (Arcang.) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):461. 2012.

Pseudonyms: Microsphaera euonymi-japonici Vienn.-Bourg., nom. illeg. (Art. 53.1), auct.; *Erysiphe euonymi-japonici* U. Braun & S. Takam. (as "(Vienn.-Bourg.) U. Braun & S. Takam."), auct.

Host range and distribution (Braun and Cook 2012): On *Euonymus* (*fortunei* var. *fortunei* and var. *radicans* [≡ *radicans*], *japonicus*); almost circumglobal, native in Asia and distributed wherever the hosts are cultivated [Africa (Canary Islands, Ethiopia, Libya, Malawi, Morocco, Mozambique, Sudan, Tanzania, Uganda), Asia (China, India, Iran, Israel, Japan, Jordan, Kazakhstan, Korea, Kyrgyzstan, Lebanon, Nepal, Pakistan, Saudi Arabia, Sri Lanka, Tajikistan, Turkey, Uzbekistan), Australia, Caucasus (Armenia, Georgia), all Europe, North America (Canada, USA) and West Indies, South America (Argentina, Brazil, Chile, Colombia, Uruguay, Venezuela), New Zealand].

Notes: This species pertains to the *E. alphitoides* complex. It forms a well-supported species clade in ITS+28S analyses and was confirmed as a distinct species in phylogenetic multilocus analyses (Bradshaw et al. 2023c). The complicated, confused nomenclature of this species has been discussed by Braun and Cook (2012). Previously, this powdery has mostly been referred to as *Microsphaera euonymi-japonici* Vienn.-Bourg., 1968, nom. illeg. (non (Arcang.) Hara, 1921). Braun and Takamatsu (2000) introduced the "new combination" *Erysiphe euonymi-japonici*, based on the illegitimate name *Microsphaera euonymi-japonici* Vienn.-Bourg., so that *E. euonymi-japonici* must be considered a new name ascribed to Braun and Takamatsu. Type material of *M. euonymi-japonici* Vienn.-Bourg. is not preserved, but the chasmothecia described and illustrated in Viennot-Bourgin (1968) are quite distinct from chasmothecia of the common *Erysiphe* on *Euonymus japonicus* and allied species, which resemble those of *E. alphitoides*, so Braun (in Braun and Cook 2012) introduced a new description under the name *E. euonymicola*, sp. nov., with a holomorphic holotype from France.

Erysiphe menispermi var. *dahurica* (U. Braun & Y. Nomura) U. Braun & S. Takam., Schlechtendalia 4:11. 2000.

≡ *Microsphaera menispermi* var. *dahurica* U. Braun & Y. Nomura, Mycotaxon 22:88. 1985.

Holotype: JAPAN. PREF. KANAGAWA: Oenohara Town, on *Menispermum dauricum*, 23 Sep 1981, *Y. Nomura*, YNMH 6758-2 (HAL 1382 F). *Isotype*: TNS. Reference sequence: LC009940.1 [JAPAN. PREF. NIIGATA: Mt. Yahiko, on *Menispermum dauricum*, 18 Oct 1996, *S. Takamatsu* (TNS-F-87311)].

Host range and distribution: On *Menispermum dauricum*; Asia (China, Japan, Korea, Russia [Siberia, Far East]).

Notes: Sequences retrieved from *Erysiphe menispermi* var. *dahurica* fall within the *E. alphitoides* complex. In the analyses published by Siahaan and Takmatsu (2016), sequences retrieved from *E. menispermi* var. *dahurica* and *E. sinomenii* formed a well-supported clade within

this complex. This taxon has been confirmed in phylogenetic multilocus analyses (Bradshaw et al. 2023c). However, the taxonomic status of *Erysiphe* on *Menispermum dahuricum* can currently not be clarified. Sequences obtained from *Erysiphe menispermi* (var. *menispermi*) on *Menispermum canadense* in North America are required to reach a conclusion. An ex-holotype sequence is not yet available. For the interim, we propose to use LC009940 as reference sequence.

Erysiphe sinomenii (Y.N. Yu) U. Braun, Taxonomic Manual of the Erysiphales (Powdery Mildews):506. 2012.

≡ *Microsphaera sinomenii* Y.N.Yu, Acta Microbiol Sin 21(1):10. 1981.

≡ *Microsphaera menispermi* var. *sinomenii* (Y.N. Yu) U. Braun, Mycotaxon 22:88. 1985.

≡ *Erysiphe menispermi* var. *sinomenii* (Y.N. Yu) U. Braun & S. Takam., Schlechtendalia 4:11. 2000.

Holotype: CHINA. PROV. SICHUAN: Dabashan, on *Sinomenium acutum*, 21 Oct 1958, *Y.S. Xing* 282 (HMAS 24958). Reference sequence: LC009936.2 (ITS +28S) [JAPAN. PREF. NIIGATA; Oyashirzu, Itoigawa, on *Sinomenium acutum*, 20 Oct 1996, *S. Takamatsu* (TNS-F-87300)].

Host range and distribution: On *Sinomenium acutum*; Asia (China, Japan).

Notes: In the analyses published by Siahaan and Takmatsu (2016), sequences retrieved from *E. menispermi* var. *dahurica* and *E. sinomenii* formed a well-supported clade within this complex, suggesting a sister position of the two taxa. *E. sinomenii* has been confirmed in phylogenetic multilocus analyses as a separate species (Bradshaw et al. 2023c). The Chinese holotype is not too old to be sequenced. Therefore, only a reference sequence is proposed until ex-type sequences will be available.

Erysiphe wallrothii (U. Braun & Tanda) U. Braun & S. Takam., Schlechtendalia 4:15. 2000.

≡ *Microsphaera wallrothii* U. Braun & S. Tanda, Mycotaxon 25:262. 1986.

Holotype: JAPAN. PREF. MIE: Tsu-shi, on *Vaccinium hirtum*, 1 Nov 1977, *Abiko* (TUAMH 2782). Reference sequence: LC010088.1 [JAPAN. PREF. FUKUI: Maruoka, Kamitakedo, on *Vaccinium hirtum*, 25 Oct 1994, *Inoue* (TNS-F-87178)].

Host range and distribution: On *Eubotryoides grayana* (≡ *Leucothoe grayana*), *Vaccinium* (*hirtum* var. *hirtum, hirtum* var. *pubescens* [= *usunoki*], *smallii* [= *versicolor*]); Asia (Japan, endemic).

Notes: Sequences obtained from *E. wallrothii* fall within the *E. alphitoides* complex. ITS+28S sequences resemble those of *E. alphitoides*. However, *E. wallrothii* is well supported in the *GAPDH* tree and in the concatenated analysis. In the *RPB2* tree, sequences obtained from *E. akebiae* and *E. wallrothii* group together in a well-supported clade (Bradshaw et al. 2023c). Morphologically, *E. wallrothii* differs from *E. alphitoides* in having relatively few chasmothecial appendages, 3–12, few asci (3–)4–6(–7) that are (3–)5–6(–7)-spored (Braun and Cook 2012). Ex-holotype sequences of *Erysiphe wallrothii* are currently not available. For the interim, we propose to use multilocus sequences retrieved from TNS-F-93371 for reference.

North America Erysiphe *spp. on oaks*

North America *Erysiphe* spp. on oaks belong to the "*Microsphaera* lineage," which are treated in the present work. Based on morphology, Braun and Cook (2012) recognized and treated the following North American species: *Erysiphe abbreviata* (Peck) U. Braun & S. Takam., *E. calocladophora* (G.F. Atk.) U. Braun & S. Takam., *E. extensa* (Cooke & Peck) U. Braun & S. Takam. var. *extensa*, and *E. extensa* var. *curta* (U. Braun) U. Braun & S. Takam. Recently performed phylogenetic multilocus examinations of the North American oak *Erysiphe* complex revealed a high species diversity, including many cryptic, undescribed species (Bradshaw et al. 2024b). However, the treatment of this complex requires a publication of its own. Therefore, the species of this complex are left out in the present publication.

The Erysiphe trifoliorum *complex*

In phylogenetic examinations of the "Microsphaera lineage" of the genus *Erysiphe*, Takamatsu et al. (2015a) identified a complex of taxa around *Erysiphe trifoliorum*, which was insufficiently resolved in ITS +28S analyses, and classified it as the "*E. trifoliorum* clade." We prefer to name this "clade" the *Erysiphe trifoliorum* complex, particularly since this assemblage of taxa and sequences encompasses smaller species clades, such as the *E. euonymi* clade. In our analysis, it is evident that the *E. trifoliorum* complex is in need of further phylogenetic multilocus analyses.

Erysiphe baeumleri (Magnus) U. Braun & S. Takam., Schlechtendalia 4:5. 2000.

≡ *Microsphaera baeumleri* Magnus, Ber Deutsch Bot Ges 17:148. 1899.

Holotype: CZECH REPUBLIC. Prenčov, on *Vicia sylvatica, Kmet*, herb. *J.A. Baeumler* (HBG, s.n.). *Isotype*: K(M) 169040. *Epitype* (designated by Bradshaw et al. 2022a): GERMANY.

BRANDENBURG: Mittelmark, Potsdam, Botanical Garden, on *Vicia sylvatica*, 16 Sep 1999, *V. Kummer* (HAL 3360 F). Ex-epitype sequence: MZ265152 (ITS).

≡ *Trichocladia baeumleri* (Magnus) Neger, Krypt-Fl Mark Brandenburg 7(1):123. 1905.

≡ *Ischnochaeta baeumleri* (Magnus) Sawada, Bull Gov Forest Exp Sta Meguro 50:112. 1951, nom. inval. (Art. 35.1).

= *Microsphaera marchica* Magnus, Ber Deutsch Bot Ges 17:149. 1899. [*Lectotype* (designated by Bradshaw et al. 2022a): CZECH REPUBLIC. Prenčov, on *Vicia cassubica*, 29 Jul 1885, *Kmet* (HBG, s.n.). *Epitype* (designated by Bradshaw et al. 2022c): GERMANY. BRANDENBURG: Mittelmark, Bergholz, Leisberge, on *Vicia cassubica*, 23 Aug 2009, *M. Ristow* (HAL 3355 F).] Ex-epitype sequence: MZ265154 (ITS+28S).

Host range and distribution (for details, see Braun and Cook 2012): On numerous *Vicia* spp.; Asia, Caucasus, Europe, North America, South America (Argentina, Chile).

Notes: The phylogenetic-taxonomic status of *Erysiphe baeumleri*, a species in the *E. trifoliorum* complex, is currently unclear (see also Bradshaw et al. 2022a). Phylogenetic analyses suggest that *E. baeumleri*, as currently widely circumscribed, does not represent a single species. The ex-epitype sequence of *E. baeumleri* falls within the *E. trifoliorum* complex. Other sequences obtained from collections of *E. baeumleri* also fall within the *E. trifoliorum* complex but separate from the epitype, suggesting that they could pertain to the genuine *E. trifoliorum*. However, the available *E. baeumleri* sequences are not sufficient to make any conclusions.

Erysiphe euonymi DC., Fl franç 6:105. 1815.

≡ *Microsphaera euonymi* (DC.) Sacc., Syll Fung 1:11. 1882.

≡ *Trichocladia euonymi* (DC.) Neger, Krypt-Fl Mark Brandenburg 7:124. 1905.

Lectotype (designated by Braun 1987): FRANCE. "*Erysiphe Euonymi* No. 231. *Erysiphe euonymi europaei* Hedw.," on *Euonymus europaeus*, herb. *de Candolle* (G 00122099). Reference sequence: LC010050.1 [UKRAINE. Poltava, on *Euonymus europaeus*, 14 Jun 2002, *V.P. Heluta* (TNS-F-87876)].

≡ *Alphitomorpha comata* Wallr., Verh Ges Naturf Freunde Berlin 1(1):40. 1819, nom. illeg. (nom. superfl., Art. 52.1).

≡ *Erysiphe comata* (Wallr.) Ficinus & C. Schub., Fl Gegend Dresden 2:XIX. 1823, nom. inval. (Art. 6.10).

≡ *Calocladia comata* (Wallr.) Lév., Ann Sci Nat Bot Sér 3 15:157. 1851, nom. inval. (Art. 6.10).

≡ *Microsphaera comata* (Wallr.) Cooke, Handb Brit Fung 2:649. 1871, nom. inval. (Art. 6.10).

≡ *Podosphaera comata* (Wallr.) Quél., Mém Soc d'Emul Montbéliard Sér 2 5:534(106). 1875, nom. inval. (Art. 6.10).

= *Alphitomorpha euonymi* Wallr., Ann Wetterauischen Ges Gesammten Naturk N F 4:245. 1819; type host: *Euonymus europaeus* (STR, herb. *Wallroth*, without any further data, lectotype, designated by Braun and Cook 2012).

≡ *Erysiphe penicillata* e. *euonymi* (Wallr.) Fr., Syst mycol 3:244. 1829.

Host range and distribution: On *Euonymus* (*atropurpureus, europaeus, latifolius, maakii, verrucosus*); North America (Delaware, Kansas, Nebraska, New York, West Virginia, Wisconsin), Asia (China, Central Asia, Turkey), Caucasus (Armenia), all Europe.

Notes: Erysiphe euonymi belongs to the *E. trifoliorum* complex, but sequences retrieved from specimens of this species form a well-supported species clade. Sequences obtained from specimens collected in Asia (China; *Euonymus maackii*), Europe, and North America confirm the distribution of this species in the whole Northern hemisphere.

Erysiphe hyperici (Wallr.) S. Blumer, Beitr Krypt-Fl Schweiz 7(1):106. 1933.

≡ *Alphitomorpha hyperici* Wallr., Ann Wetterauischen Ges Gesammte Naturk N F 4:239. 1819.

Lectotype (designated by Braun and Cook 2012): GERMANY. Alter Stolberg, on *Hypericum hirsutum*, herb. *Wallroth* (STR), as "*Alphitomorpha communis* γ *hypericacearum*."

≡ *Microsphaera hypericacearum* U. Braun, Nova Hedwigia 34:686. 1981, nom. nov. (non *M. hyperici* Y. N. Yu & Y.Q. Lai, 1981).

= *Erysiphe communis* d. *hypericearum* Fr., Syst mycol 3:240. 1829.

= *Erysiphe communis* f. *hyperici* Potebn., Gribnye parazity vysshikh rasteny Kharkovskoy i smezhnykh guberny:228. 1915.

Host range and distribution (for details, see Braun and Cook 2012): On diverse *Hypericum* spp.; Asia (Central Asia, China, Iran, Russia, Siberia), Caucasus (Armenia), all Europe, North America (Canada, USA).

Notes: Sequences retrieved from specimens of *E. hyperici* fall within the *E. trifoliorum* complex together with core *E. trifoliorum* sequences. They do not form a discernible species clade. Multilocus analyses are necessary for final conclusions about the genuine phylogenetic and taxonomic status of *E. hyperici*, which is morphologically close to *E. trifoliorum* but differs in having consistently straight conidiophore foot cells and cylindrical conidia.

Erysiphe robiniae Grev., Fl edin:460. 1824.

Holotype: UK. SCOTLAND: Garden Foxhall, on *Robinia viscosa*, Sep 1822, herb. *Greville* (E00456438).

= *Microsphaera caraganae* Magnus, Ber Deutsch Bot Ges 17:150. 1899. [*Lectotype* (designated by Braun and Cook 2012): GERMANY. Berlin, Wannsee, on *Caragana arborescens*, Aug 1898, *P. Magnus* [Rehm, Ascomyc 1350] (HAL 267 F). *Isolectotypes*: Rehm, Ascomyc 1350 (e.g., B, FH00965530, MICH-Fungi 308596, PAD).] Ex-isolectotype sequences: PP680991 (ITS+28S); PP720924 (*CAM*); PP720321 (*GAPDH*); PP719973 (*TUB*).

≡ *Trichocladia caraganae* (Magnus) Neger, Krypt-Fl Mark Brandenburg 7(1):121. 1905.

= *Erysiphe polygoni* f. *robiniae-hispidae* Nann., Rivista Patol Veg Ser 2 14(9–10):173. 1924. [*Lectotype* (designated by Braun and Cook 2012): ITALY. "in horto botanico Senensis," on *Robinia hispida*, Oct 1924, *Nannizzi* (BPI 565340).]

= *Trichocladia robiniae* Tschern., Mater Mikol Fitopatol 5(2):172. 1926; type host: *Robinia pseudoacacia.*

Host range and distribution: On *Caragana arborescens, Robinia* (*hispida, pseudoacacia, viscosa*); Asia (China, India, Japan, Korea, Russia [Far East], Turkey), Caucasus, Europe (Austria, Bulgaria, Czech Republic, Estonia, Lithuania, Finland, France, Germany, Hungary, Italy, Netherlands, Poland, Romania, Russia in Europe, Sweden, UK), North America (USA).

Notes: Braun (1987, 1995) treated *Erysiphe robiniae* as synonym of *E. trifoliorum* (= *Microsphaera trifolii*). Later, Braun and Cook (2012) preferred to maintain *E. robiniae* as an independent species and treated *Microsphaera caraganae* as synonym, particularly since the two taxa are morphologically indistinguishable and biologically not differentiated. Buchheim (1928, 1929) demonstrated that the powdery mildew on *Caragana arborescens* was able to infect *Robinia pseudoacaia*. Braun and Cook (2012) emphasized that this taxonomy can only be regarded to be tentative, pending molecular examinations. The present analyses showed that sequences retrieved from *E. caraganae* and *E. robiniae* (Japanese specimen) fall within the *E. trifoliorum* complex, so that the taxonomic status of *E. robiniae* in the sense of Braun and Cook (2012) remains doubtful. It is completely possible that *E. caraganae* and *E. robiniae* are rather synonyms of *E. trifoliorum*, possibly representing biological races of the latter species. This would not be surprising, particularly since *E. trifoliorum* undoubtedly constitutes a complex of biological races (Braun and Cook 2012). The current multilocus analyses seem to support this assumption. Support values of smaller groups of sequences might suggest the involvement of genetically fixed biological races that are now treated as "formae" (see Bradshaw et al. 2024 and present work under *E. vaccinii* complex). However, final conclusions are currently not possible. The available sequences in this respect are insufficient.

Erysiphe sesbaniae Wolcan & U. Braun, Mycotaxon 112:181. 2010.

Holotype: ARGENTINA. BUENOS AIRES PROV.: La Plata, in a nursery, on leaves of young trees of *Sesbania punicea*, Oct 2009, *N. Acosta* (HAL 2330 F). *Isotype*: LPS 48291. Ex-holotype sequence: OQ266917 (ITS+28S).

Host range and distribution: On *Sesbania punicea*; Asia (Iran), South America (Argentina).

Notes: Two sequences retrieved from *E. sesbaniae* are currently available, viz., an ex-holotype sequence and one from a specimen collected in Iran, which falls within the *E. trifoliorum* complex. This result indicates that *E. sesbaniae* might be a synonym of *E. trifoliorum*, but multilocus sequence examination is necessary for final conclusions. There are some morphological differences between the two taxa.

Erysiphe trifoliorum (Wallr.) U. Braun, Mycotaxon 112:175. 2010.

≡ *Alphitomorpha trifoliorum* Wallr., Ann Wetterauischen Ges Gesammte Naturk N F 4:238. 1819.

Lectotype (designated by Braun et al. 2010): On *Trifolium medium* (= *T. flexuosum*), herb. *Wallroth*, without any further data (STR), as "*Alphitomorpha communis* α *leguminosarum, A. leguminosarum* and *Erysibe trifolii-flexuosi*." Reference sequence: LC009955 (ITS +28S) [HUNGARY. Budapest, on *Trifolium arvense*, 7 Sep 1999, without collector (TNS-F-87455)].

= *Erysiphe trifolii* Grev., Fl edin:459. 1824; type host: *Trifolium medium* (holotype: E).

≡ *Microsphaera trifolii* (Grev.) U. Braun, Nova Hedwigia 34:685. 1981.

= *Erysiphe lathyri* Grev., Fl edin:460. 1824; type host: *Lathyrus pratensis* (holotype: E).

= *Erysiphe martii* Lév., Ann Sci Nat Bot Sér 3 15:166. 1851 nom. illeg. (nom. superfl., Art. 52.1) [sensu Blumer 1933, 1967].

≡ *Microsphaera martii* (Lév.) Y.S. Paul & V.K. Thakur, Indian Erysiphaceae:53. Jodhpur 2006, nom. inval. (Art. 6.10) [sensu Paul and Thakur 2006].

≡ *Microsphaera paulii* Hosag. & D.K. Agarwal, Powdery mildews of India—check list:25. New Delhi 2009, nom. illeg. (Art. 52.1).

= *Erysiphe acaciae* Erikss., Die Pilzkrankheiten der Kulturgewächse II Teil:224. Stuttgart 1928, nom. illeg. (Art. 53.1), non *E. acaciae* S. Blumer 1926.

Host range and distribution (of *E. trifoliorum* s. lat.; see Braun and Cook 2012): On numerous host species of diverse genera of legumes, Fabaceae; almost worldwide.

Notes: The phylogenetic-taxonomic circumscription of *E. trifoliorum* is far from being well understood. Currently, hosts of numerous genera of the Fabaceae are assigned to this species (Braun and Cook 2012). As far as anamorph and chasmothecial characters, such collections are morphologically rather uniform. Furthermore, anamorphs found on diverse genera of legumes have been proven to be assigned to the *E. trifoliorum* complex by sequence analyses, such as *Aeschynomene, Albizia, Lotus*, and *Melilotus* in Japan (Takamatsu et al. 2015a). However, in the latter publication, anamorphs on hosts of other plant families have also been confirmed to fall within the *E. trifoliorum* complex, including *Mirabilis* (Nyctaginaceae) and *Eustoma* (Gentianaceae). A corresponding powdery mildew on *Eustoma grandiflorum* has been reported from Argentina under *Oidium* sp. (Cabrera et al. 2009). The anamorph on *Mirabilis* has previously been described as *Oidium nyctaginacearum*. Later, Meeboon and Takamatsu (2017) reassigned *O. nyctaginacearum* to *Erysiphe*. In our examination, a sequenced anamorph on *Acanthus* (Acanthaceae), collected in the USA, has been found to be part of the *E. trifoliorum* complex. These unusual host records suggest possible host jumps among members of the *E. trifoliorum* complex. In the phylogenetic ITS+28S tree published by Takamatsu et al. (2015a), a group of sequences retrieved from *E. trifoliorum* on *Trifolium* spp. and *Melilotus* was highlighted as "*E. trifoliorum* s. str.?." *Melilotus* and *Trifolium* both belong to the legume tribe Trifolieae. However, the assumption that all sequences obtained from specimens collected on *Trifolium* spp. group together could not be confirmed in the analyses published by Bradshaw et al. (2022a). The resolution of the *E. trifoliorum* complex requires comprehensive multilocus analyses. Initial multilocus analyses have been performed (FIG. 4), but they are insufficient to resolve such a large worldwide complex. In any case, these multilocus analyses revealed the existence of smaller, well-supported groups within this complex. However, based on the currently limited data, the interpretation of these results remains unclear. The observed smaller genetic groups might reflect cryptic species within the *E. trifoliorum* complex or biological races, or even mixtures of genuine species and biological races.

Erysiphe nyctaginacearum (Hosag.) Meeboon & S. Takam., Trop Plant Pathol 42:489. 2017.

≡ *Oidium nyctaginacearum* Hosag., Indian Phytopathol 43:217. 1990.

≡ *Pseudoidium nyctaginacearum* (Hosag.) U. Braun & R.T.A. Cook, Taxonomic Manual of the Erysiphales (Powdery Mildews):613. 2012.

Holotype: INDIA. TAMIL NADU: Coimbatore, Southern Circle, Experimental Garden of the Botanical Survey of India, on *Mirabilis jalapa*, 6 Jan 1989, *V.B. Hosagoudar* (HCIO 40607).

Host range and distribution: On *Mirabilis jalapa*; Asia (India, Thailand).

Notes: Sequences retrieved from *Oidium nyctaginacearum* fall within the *E. trifoliorum* complex (Meeboon and Takamatsu 2017; present analyses). The sequences are not clearly different from other sequences of this complex, including those obtained from *E. hyperici*. Multilocus analyses are necessary to clarify the phylogenetic-taxonomic status of *E. nyctaginacearum*.

The Erysiphe vaccinii *complex*

Erysiphe vaccinii Schwein., Trans Amer Philos Soc 4:270. 1834.

≡ *Microsphaera vaccinii* (Schwein.) Cooke & Peck, J Bot NS 1:13. 1872.

≡ *Microsphaera alni* var. *vaccinii* (Schwein.) E.S. Salmon, Mem Torrey Bot Club 9:149. 1900.

≡ *Trichocladia vaccinii* (Schwein.) Jacz., Karm Opred Grib Vyp 2 Muchn-rosj griby:295. 1927.

≡ *Microsphaera penicillata* var. *vaccinii* (Schwein.) W.B. Cooke, Mycologia 44:573. 1952.

Lectotype (designated by Braun 1987): [USA. PENNSYLVANIA: Berks County, on *Vaccinium pensylvanicum*.] Data given on the label of the lectotype collection in herbarium Schweinitz: "Pennsylvania, Berks, Furnace, marsh, without date and collector" (PH00062390). *Isolectotype*: FH00781085. *Epitype* (designated by Tymon et al. 2022): USA. WASHINGTON: Seattle, Washington State Arboretum, on *Vaccinium parvifolium*, 23 Aug 2018, *M. Bradshaw* (WTU F 073138). Ex-epitype sequence: OK959861 (ITS+28S).

= *Microsphaera elevata* Burrill, Bull Illinois State Lab Nat Hist 1:58. 1876. [*Lectotype* (designated by Braun 1987): On *Catalpa bignonioides*, Burrill (l.c., Pl. 2, FIGS. 4–5).]

≡ *Erysiphe elevata* (Burrill) U. Braun & S. Takam., Schlechtendalia 4:8. 2000.

= *Trichocladia vaccinii* f. *andromedae* Jacz., Karm Opred Grib Vyp 2 Muchn-rosj griby:297. 1927.

= *Trichocladia vaccinii* f. *epigaeae* Jacz., l.c.
= *Trichocladia vaccinii* f. *gaylussaciae* Jacz., l.c.
= *Trichocladia vaccinii* f. *kalmiae* Jacz., l.c.
= *Trichocladia vaccinii* f. *lyoniae* Jacz., l.c.

Host range and distribution (Braun and Cook 2012): On *Andromeda* (*glaucophylla, polifolia*, sp.), *Chiogenes hispidula, Epigaea repens, Gaultheria* (*procumbens, shallon*), *Gaylusaccia* (*baccata, dumosa, frondosa, resinosa*, sp.), *Kalmia polifolia, Ledum glandulosum, Lyonia ligustrina, Menziesia* (*ferruginea, pilosa*), *Rhododendron* (*calendulaceum, catawbiense, japonicum, molle, nudiflorum, occidentale*, sp.), *Vaccinium* (*alaskaense, angustifolium, arboreum, ashei, atrococcum, australe, canadense, corymbosum, corymbosum × pensylvanicum, macrocarpon, myrtilloides, myrtillus, oxycoccos, pallidum, parvifolium, pensylvanicum, stamineum, tenellum, vacillans, virgatum*, sp.); North America (Canada, USA, incl. Alaska, widespread). Also occurring on *Catalpa* (*bignonioides, bungei*, ×*erubescens, ovata, speciosa*, sp.) and ×*Chitalpa tashkentensis* [*Catalpa speciosa* × *Chilopsis linearis*); North America (Canada; USA: Massachusetts to Alabama, Texas, Nebraska, New Jersey), introduced in Asia (South Korea, Turkey) and Europe (Bulgaria, Czech Republic, France, Germany, Hungary, Montenegro, Poland, Romania, Slovakia, Switzerland, UK). Additional hosts are *Eucalyptus* spp. (Myrtaceae), *Cerbera manghas, Plumeria* spp., and *Tabernaemontana divaricata* (Apocynaceae) in Asia (China, Indonesia, Taiwan, Thailand).

Notes: Tymon et al. (2022) included *Erysiphe vaccinii* in phylogenetic-taxonomic examinations of *Erysiphe* spp. on rhododendron. Based on analyses of ITS+28 sequences, *E. elevata* on *Catalpa* spp. is indistinguishable from *E. vaccinii*. The two species have been tentatively maintained as separate species, emphasizing that phylogenetic multilocus analyses are required to clarify the taxonomy of the two taxa. The necessary multilocus analyses have recently been performed by Bradshaw et al. (2024). These analyses revealed that the *E. vaccinii* clade is divided into several highly supported subclades on different *Vaccinium* species, some of them with overlapping host ranges, including one subclade comprising sequences retrieved from powdery mildew on *Catalpa* spp. and an additional one encompassing sequences retrieved from specimens on *Eucalyptus* in Asia. These subclades reflect biological races, without obvious morphological differentiation. A corresponding treatment of *E. vaccinii* has recently been published by Bradshaw et al. (2024d). In this paper, the detected subclades have been considered genetically fixed biological races that are identifiable by molecular methods. The formal introduction of the new formae has not been proposed in Bradshaw et al. (2024d) and is presented here. In addition, a discussion about the advantages of the official rank "forma," which is ruled by the Code (ICNafp) over the unregulated, unofficial category "forma specialis," is discussed in the following section.

Division of Erysiphe vaccinii *into formae*

Erysiphe vaccinii f. *vaccinii*

Lectotype, epitype, and homotypic synonyms: See above under the species' circumscription.

Host range and distribution (phylogenetically proven hosts): *Gaultheria shallon*, Ericaceae subfam. Vaccinioideae tribe Gaultherieae; *Vaccinium* (*angustifolium* [= *pensylvanicum*], *corymbosum, pallidum* [= *vacillans*], *parvifolium*), Ericaceae subfam. Vaccinioideae tribe Vaccinieae; North America (USA: Massachusetts, New Jersey, North Carolina, Virginia, Washington, probably widespread in North America).

Erysiphe vaccinii* f. *convertibilis M. Bradshaw & U. Braun, f. nov.
MycoBank MB853746

Etymology: "*convertibilis*" (confusable), referring to the identical host range as in the case of f. *vaccinii-corymbosi*.

Holotype: USA. NORTH CAROLINA: Raleigh, North Carolina State University, Fox Greenhouse, on *Vaccinium angustifolium* × *Vaccinium virgatum*, 19 Apr 2022, *S. Moparthi* (FH00941976). Ex-holotype sequences: PP680928 (ITS+28S); PP720851 (*CAM*); PP720244 (*GAPDH*); PP720574 (*GS*); PP720412 (*RPB2*); PP719969 (*TUB*).

Diagnosis: Morphologically indistinguishable from other formae of *E. vaccinii*, but forming a strongly supported subclade in phylogenetic multilocus analyses (see ex-type sequences), clearly separated from all other subclades.

Host range and distribution: On *Vaccinium corymbosum*; natural distribution unknown, but probably following the native range of the host in North America (eastern Canada to central and eastern USA), so far known from the USA (North Carolina and likely introduced in California) and introduced in Mexico and Asia (China). This forma is only known from the anamorph.

Erysiphe vaccinii* f. *elevata (Burrill) M. Bradshaw & U. Braun, comb. et stat. nov.
MycoBank MB853747

Basionym: Microsphaera elevata Burrill, Bull Illinois State Lab Nat Hist 1:58. 1876.

Lectotype (designated by Braun 1987): On *Catalpa bignonioides*, Burrill (l.c., pl. 2, figs. 4–5). *Epitype* (designated here, MycoBank MBT10020098): USA.

MASSACHUSETTS: Cambridge, experimental garden behind the Farlow Herbarium, on *Catalpa speciosa*, 26 Aug 2021, *M. Bradshaw* (FH01131059). Ex-epitype sequences: PP681058 (ITS+28S); PP720800 (*CAM*); PP720257 (*GAPDH*); PP720618 (*GS*); PP720453 (*RPB2*); PP720034 (*TUB*).

≡ *Erysiphe elevata* (Burrill) U. Braun & S. Takam., Schlechtendalia 4:8. 2000.

Host range and distribution: On *Catalpa* (*bignonioides, bungei*, ×*erubescens, ovata, speciosa*, sp.), ×*Chitalpa tashkentensis* [*Catalpa speciosa* × *Chilopsis linearis*], Bignoniaceae; North America (Canada; USA: Massachusetts to Alabama, Texas, Nebraska, New Jersey), introduced in Asia (South Korea, Turkey) and Europe (Bulgaria, Czech Republic, France, Germany, Hungary, Montenegro, Poland, Romania, Slovakia, Switzerland, UK).

Notes: In ITS+28S analyses, sequences retrieved from *E. elevata*, including those obtained from specimens on *Eucalypus* spp. and apocynaceous hosts, and *E. vaccinii* are indistinguishable and form a single large species clade (Tymon et al. 2022). All reports of *Erysiphe elevata* on *Eucalyptus* and apocynaceous hosts have been confirmed by ITS(+28S) sequences. Meeboon and Takamatsu (2017) assigned a specimen on *Eucalyptus camaldulensis* from Thailand to *E. elevata*. At that time, sequences retrieved from *E. vaccinii* were not available for comparison. Later, Tymon et al. (2022) generated sequences from specimens of *E. vaccinii* on *Vaccinium* spp., which revealed that they are indistinguishable from those of *E. elevata*. Nevertheless, the two species have been tentatively maintained as separate species pending multilocus analyses. The analyses confirm that *E. elevata* must be reduced to synonymy with *E. vaccinii*. Previously assumed differences in the anamorphs of *E. elevata* and *E. vaccinii* (Braun and Cook 2012) are not confirmed (Tymon et al. (2022). However, in multilocus analyses, sequences from specimens of *E. elevata* form a well-supported subclade within the *E. vaccinii* clade.

Meeboon and Takamatsu (2017) assigned a specimens on *Eucalyptus camaldulensis* from Thailand to *E. elevata*, followed by records on *E. pellita* from Indonesia (Oliveira et al. 2023) and *E. urophylla* × *E. camaldulensis* in China (Yi et al. 2023). These sequences form a well-supported sister clade, which is recognized as a separate forma (see f. *eucalyptorum*). Within the "*elevata*" subclade, there are further well-supported smaller groups of sequences that probably reflect populations and do not warrant a further taxonomic splitting.

Multilocus sequence data retrieved from apocynaceous host are not available [*Catharanthus roseus* (Meeboon and Takamatsu 2017), *Cerbera manghas* (Mukhtar et al. 2022), *Plumeria rubra* (Yeh et al. 2019; Wu et al. 2019), and *Tabernaemontana divaricata* (Xu et al. 2020); Asia (China, Indonesia, Taiwan, Thailand)]. ITS+28S sequences are not different from sequences of *E. vaccinii* (including *E. elevata*). Multilocus sequences obtained from apocynaceous host are needed to clarify the affinity to f. *elevata* and f. *eucalyptorum*. An additional cryptic forma on apocynaceous hosts cannot be excluded.

Suarez et al. (2017) reported *Erysiphe* sp. on *Plumeria pudica* in the USA. The affinity of this powdery mildew remains unclear. Yeh et al. (2019) discussed the sequence concerned and emphasized that this sequence had only a similarity of 97% to the sequence obtained from *Plumeria rubra* in Taiwan. However, this sequence was found to be of questionable quality.

Erysiphe vaccinii* f. *epigaeae (Jacz.) M. Bradshaw & U. Braun, comb. nov.
MycoBank MB853748
Basionym: Trichocladia vaccinii f. *epigaeae* Jacz., Karm Opred Grib Vip 2 Muchn-rosj griby:424. 1927.

Neotype (designated here, MycoBank MBT10020099): USA. MASSACHUSETTS: Worcester County, Lunenberg, on *Epigaea repens*, 11 Jul 1903, *F.L. Sargent* (FH01122266). Ex-neotype sequences: PP681041 (ITS+28S); PP720787 (*CAM*); PP720175 (*GAPDH*); PP720617 (*GS*); PP720434 (*RPB2*); PP720012 (*TUB*).

Host range and distribution (phylogenetically proven hosts): *Epigaea repens*, principal host, Ericaceae subfam. Ericoideae tribe Phyllodoceae; *Gaylussacia baccata* and *Vaccinium angustifolium*, Ericaceae subfam. Vaccinioideae tribe Vaccinieae; North America (Canada; USA: New Hampshire, New York, Massachusetts, Wisconsin), probably widespread in North America.

Notes: Jaczewski (1927) introduced *Trichocladia vaccinii* f. *epigaeae* for powdery mildew on *Epigaea repens* in North America, without a description and without any type details, undoubtedly based on hosts cited in Salmon (1900) under *Microsphaera alni* var. *vaccinii*. Nevertheless, *T. vaccinii* f. *epigaeae* is a recognized, valid "host forma" sufficiently differentiated by a particular host. *Epigaea repens* seems to be the main host of this forma, although the sequences retrieved from specimens on *Gaylussacia baccata* and *Vaccinium angustifolium* that fall in the "*epigaeae*" clade suggesting occasional infections of this forma on hosts of tribe Vaccinieae. Misidentifications and confusions between *Epigaea repens* and *Gaylussacia baccata* as well as *Vaccinium angustifolium* can likely be excluded because

these plants and their leaves are morphologically easily differentiated.

Erysiphe vaccinii* f. *eucalyptorum M. Bradshaw & U. Braun, f. nov.
MycoBank MB853749

Etymology: "*eucalyptorum*" is derived from the name of the host genus, *Eucalyptus*, in genitive plural.

Holotype: THAILAND. Chiangmai, Doi Suthep, on *Eucalyptus camaldulensis*, 9 Nov 2013, *J. Meeboon* (TNS-F-40300). *Isotype*: TNS-F-88224. Ex-holotype sequences: LC177376 (ITS+28S); PP720784 (*CAM*); PP720194 (*GAPDH*); PP720573 (*GS*); PP720521 (*RPB2*); PP720108 (*TUB*).

Diagnosis: Morphologically indistinguishable from other formae of *E. vaccinii*, but forming a well-supported subclade in phylogenetic multilocus analyses, clearly separated from all other subclades.

Host range and distribution: On *Eucalyptus* (*camaldulensis, pellita, urophylla* × *camaldulensis*), Myrtaceae; Asia (China, Indonesia, Thailand) [Meeboon and Takamatsu 2017; Oliveira et al. 2023; Yi et al. 2023].

Notes: Based on ITS(+28S) sequences, powdery mildew on *Eucalyptus* spp. in Asia has previously been assigned to *Erysiphe elevata*. In our phylogenetic multilocus analyses, sequences retrieved from specimens on *Eucalyptus* spp. form a well-supported subclade within the *E. vaccinii* clade in a sister position to the "*E. elevata* subclade," and as such it warrants to be considered to be a forma.

Erysiphe vaccinii* f. *principalis M. Bradshaw & U. Braun, f. nov.
MycoBank MB853750

Etymology: "*principalis*" (primordial), referring to the placement of sequences in a subclade at the very base of the *E. vaccinii* clade.

Holotype: USA. NEW JERSEY: Newfield, on *Vaccinium corymbosum*, <1905. *J.B. Ellis* (NYSd14155.3). Ex-holotype sequences: PP680931 (ITS+28S); PP720807 (*CAM*); PP720192 (*GAPDH*); PP720734 (*GS*); PP720517 (*RPB2*); PP720104 (*TUB*).

Diagnosis: Morphologically indistinguishable from other formae of *E. vaccinii*, but forming a strongly supported subclade in phylogenetic multilocus analyses and in single-locus trees (*CAM* and *GS*), clearly separated from all other subclades.

Host range and distribution: On *Vaccinium* (*corymbosum*, sp.); North America (USA: New Jersey), natural range unknown, but probably more widespread in eastern North America.

Notes: The two available sequences form a subclade in basal position, strongly supported in multilocus analyses, but also in the *CAM* and *GS* single-locus trees. The type specimen had no collection date but was collected by Ellis who died in 1905. It is likely they were collected around the same time as the other *E. vaccinii* f. *principalis* specimen on *Vaccinium* sp. in 1879. As such, these specimens were collected from the late 1800s.

Erysiphe vaccinii* f. *vaccinii-corymbosi M. Bradshaw & U. Braun, f. nov.
MycoBank MB853751

Etymology: Derived from the name of the host species, *Vaccinium corymbosum*.

Holotype: USA. MASSACHUSETTS: Suffolk County, Boston. Collected from the Arnold Arboretum (accession number 197-2006-A), on *Vaccinium corymbosum* "Earl Blue," 13 Sep 2021, *M. Bradshaw* (FH00941201). Ex-holotype sequences: ON073869 (ITS+28S); ON101655 (*CAM*); PP720142 (*GAPDH*); ON075687 (*GS*); ON119159 (*RPB2*); PP719951 (*TUB*).

Diagnosis: Morphologically indistinguishable from other formae of *E. vaccinii*, but forming a strongly supported subclade in phylogenetic multilocus analyses (see ex-type sequences), clearly separated from all other subclades.

Host range and distribution: On *Vaccinium corymbosum*; natural range unknown, but probably following the native range of the host in North America (eastern Canada to central and eastern USA), so far known from the USA (Massachusetts, New York, North Carolina) and introduced in South America (Peru), Europe (Portugal), and Africa (Morocco).

Notes: Within the subclade representing f. *vaccinii-corymbosi*, there are further well-supported, smaller groups of sequences, such as a group of sequences retrieved from specimens collected in Massachusetts. This likely reflects a lower level of diversity, such as populations. Interestingly, the specimens in the clade collected from North Carolina, Peru, Portugal, and Morocco only contain the anamorph. The clades that only bear the anamorph have been reported to appear earlier in the season and require increased control compared with the ones that contain the teleomorph (Bradshaw et al. 2024d).

DISCUSSION

This second part of an overview of species of the genus *Erysiphe* comprises species belonging to the "*Microsphaera* lineage," a term coined by Takamatsu et al. (2015a). This lineage is too large to be treated in a single paper because corresponding phylogenetic analyses would be too large and complex. Therefore, the treatment of this lineage has been split into two parts. The present part continues the work of Bradshaw et al.

(2024a) and is composed of phylogenetic-taxonomic treatments of numerous *Erysiphe* spp., including the new species *Erysiphe acetosae, E. acmisponis, E. lathyrina*, and *E. salmoniana*. The new species are form well-supported clades in the phylogenetic trees. The same applies to the introduced new combinations, *E. biuncinata, E. dahurica*, and *E. pavoniae*. In general, most species treated here of the "*Microsphaera* lineage" are strongly supported in the phylogenetic ITS+28S trees, confirming result of numerous previous works. These works showed that most powdery mildew species of this group are well supported and readily identifiable by ITS +28S analyses. Furthermore, these results suggest a high degree of host specificity and coevolution between powdery mildew species, host genera, and in some cases host species. To facilitate the phylogeny, taxonomy, and identification study of *Erysiphe* species of the "*Microsphaera* lineage," we paid special attention to the typification of the species, including reference to ex-type sequences that should be generally used to authenticate identifications.

The second half of the "*Microsphaera* lineage" encompasses large assemblages of species, including the "*Erysiphe alphitoides* complex on oaks" and the "*E. trifoliorum* complex," two groups without sufficient resolution at the species level in ITS+28S analyses. The two complexes require phylogenetic multilocus analyses for satisfactory resolutions. Initial attempts have been made in connection with the inadequately examined complex of *Erysiphe* spp. on oaks in North America (Bradshaw et al. 2023c). These analyses revealed a tremendous diversity, including numerous cryptic or undetected species. Recently, phylogenetic multilocus analyses have also been performed with species involved in the *E. alphitoides* complex (Bradshaw et al. 2023c).

The "*E. trifoliorum* complex" is still insufficiently examined. The phylogeny and taxonomy of *Erysiphe* species on legumes are, in general, extremely complex (Darsaraei et al. 2024). *Erysiphe trifoliorum* s. lat. has a wide host range and an almost worldwide distribution. Multilocus analyses are needed, and they should be based on specimens from all parts of the world and on hosts of diverse genera. *Erysiphe euonymi* is, so far, the only species within this complex with sequences that form a well-supported species clade in ITS+28S analyses, i.e., the status as an independent species has been confirmed. The circumscription of *E. trifoliorum* and potential synonyms, including *E. baeumleri, E. robiniae*, and *E. sesbaniae*, is yet to be clarified.

The taxonomic status of *Erysiphe elevata* on *Catalpa* spp. and *E. vaccinii* on ericaceous host species and the affinity of the two species raised an additional problem. Tymon et al. (2022) retrieved ITS+28S sequences from *E. vaccinii* specimens, which enabled us to assess the relation between this species and *E. elevata*. These authors showed that powdery mildews on *Catalpa* and *Vaccinium* species are indistinguishable based in ITS data alone. These results led to a revision of the *E. vaccinii*/*E. elavata* complex, based on a multilocus approach (Bradshaw et al. 2024d). The multilocus analyses revealed a strongly supported species clade, including sequences obtained from *Catalpa* spp. (*E. elevata*). This result confirmed ITS analyses and supported the reduction of *E. elevata* to synonymy with *E. vaccinii*. The multilocus analyses yielded additional information. The *E. vaccinii*/*E. elevata* species clade is divided into several highly supported subclades reflecting genetically established and verifiable biological races. The naming of these races posed a problem. Such biological races have previously been referred to as "formae speciales." However, the term "forma specialis" is not covered and ruled by the International Code of Nomenclature for algae, fungi, and plants (ICNafp), i.e., there are no binding rules for the introduction of such names and as such they do not have types and ex-type sequences that make such names verifiable. "Formae speciales" were usually introduced based on the results of local inoculation experiments. Inoculation experiments often did not include details of the experiment, causing replications to be difficult. As such, it is not surprising that results by different authors have often been contradictory, difficult to understand, and hard to repeat. For example, cross-inoculation tests with *Erysiphe neolycopersici* (L. Kiss) H.Y. Hsiao & Y.M. Shen have revealed contradictory results. Shin et al. (2019; as *Pseudoidium neolycopersici*) provided a discussion of this issue. However, the present case of biological races differentiated based on virulence and host range preferences represents a unique situation because these results are based on sequence analyses of many collections on a wide range of hosts from a wide range of intercontinental regions. The biological races are genetically established in well-supported clades/subclades in phylogenetic analyses. This renders these races objectively verifiable. In addition, the genetic differences are found to be accompanied by corresponding ecological differences (host preferences). Therefore, the naming in such cases warrants the application of an official rank covered by the Code. Using a name covered by the Code has the advantage in that holotype collections with ex-type sequences as reference sequences for phylogenetic-taxonomic purposes are available. We propose using the taxonomic rank "forma" for such cases, which follows an old tradition often

applied in the premolecular time, mostly in the second half of the 19th century and the first half of the 20th century, when "formae" were often introduced in plant-pathogenic fungi for collections found on new host genera. Jaczewski (1927) was the first author in powdery mildews who used the rank "forma" extensively. Nowadays, it is recommended to introduce new "formae" for biological races only in genetically well-examined cases, based on larger samplings from a wider geographic range, and only when the races concerned are reflected in well-supported clades/subclades and are accompanied by corresponding ecological and/or chemical data.

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