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Fungal Systematics and Evolution: FUSE 3

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The present study introduces seven new species, one new combination, one new variety and several interesting taxonomical notes and/or geographical records. Most of the new taxa are Ascomycetes, but the study also includes a new variety of a Basidiomycete. Novel species include *Gyromitra khanspurensis* (Discinaceae, Pezizales, Pezizomycetes) from Pakistan growing near *Cedrus deoadara* and *Paramyrothecium guiyangense* and *Paramyrothecium verruridum* (Stachybotriaceae, Hypocreales, Sordariomycetes) both isolated from soil in China. New species from South Africa are *Sclerostagonospora elegiae* on culm litter of *Elegia equisetacea, Sclerostagonospora fusiformis* on culm litter of *Thamnochortus spicigerus, Sclerostagonospora pinguis* on culm litter of *Cannomois virgata* and *Sclerostagonospora sulcata* on culm litter of *Ischyrolepis subverticellata* (Phaeosphaeriaceae, Pleosporales, Dothideomycetes). *Hapalocystis berkeleyi* var. *kickxii* with its basionym *Hypoxylon kickxii* is shown to be a taxon on species level and thus recombined as *Hapalocystis kickxii* (Sydowiellaceae, Diaporthales, Sordariomycetes), and it is lecto- and epitypified. The new variety *Pluteus romellii* var. *luteoalbus* (Pluteaceae, Agaricales, Agaricomycetes) growing on a mossy fallen stem of a deciduous tree is described from Czech Republic. *Cortinarius scaurocaninus* (Cortinariaceae, Agaricales, Agaricomycetes) is new for Austria, *Humicola grisea* (Chaetomiaceae, Sordariales, Sordariomycetes) is an interesting new record for Chile. Two taxa are reported as new for Turkey: the lichenicolous fungus *Opegrapha parasitica* (Opegraphaceae, Arthoniales, Arthoniomycetes) growing partly immersed in the thallus of *Aspicilia* and the lichen *Rinodina zwackhiana* (Physciaceae, Teloschistales, Lecanoromycetes) from calcareous rock. Finally, *Xerula strigosa* (Physalacriaceae, Agaricales, Agaricomycetes), described from China, is confirmed to be present also in Pakistan.

Keywords: biodiversity, ITS barcodes, phylogeny, systematics.

The present paper is the third contribution in the Fungal Systematics and Evolution (FUSE) series. In this series new or rare taxa, interesting taxonomical notes, typifications, reference strains or specimens and interesting new records for a given geographical region are announced. Scientists wishing to contribute to future issues can e-mail submissions to the first author. FUSE is published yearly in Sydowia.

Materials and methods

Sample collection, isolation and specimen examination

For preparation and viewing methodology see Hernández-Restrepo et al. (2016) and below. Macroscopic descriptions of collected *Pluteus* and *Cortinarius* specimens are based on fresh basidiocarps. Colour abbreviations follow Küppers (1999), herbarium abbreviations are according to Thiers (2017). Authors of fungal names are cited according to the International Plant Names Index Authors website (http://www.ipni.org/ipni/authorsearchpage.do). Microscopic features are described from dried material mounted in KOH and Congo Red using an Olympus BX-50 light microscope with a magnification of 1000×. Abbreviations: avl = mean of basidiospore length; avw = mean of basidiospore width; Q = quotient of length and width in any one basidiospore; avQ = mean of basidiospore Q values. Taxonomic novelties were deposited in MycoBank (www.MycoBank.org; Crous et al. 2004).

Chinese specimens. They were collected from soil at the Huaxi district, Guiyang City, Guizhou province, Hechi City and Guangxi province in China (HGUP 2016-8001, HGUP 2016–8002, HGUP 2016–8006, HGUP 2016–8007). Cultures were obtained via the serial dilution method, as described in Xiang et al. (2003). Colony characters were observed and measured after two weeks. The fungi were examined under a Nikon ECLIPSE 80i microscope and photographed using a Canon DS126251 digital camera attached to the microscope. The images were processed using Adobe Photoshop CS6 13.0 version (Adobe Systems Inc., USA) and the Tarosoft® Image Frame Work program v. 0.9.7 was used for measurements. Type specimens and living cultures were deposited at the Herbarium of the Department of Plant Pathology, Guizhou University (HGUP).

Lichen specimens and collecting sites. Microscopical examination (incl. all measurements) of hand-made sections was done in water 10 % KOH. Air dried samples were observed and studied with Nikon Zeiss Stemi 2000-c stereomicroscope and a Zeiss Axio Imager.A2 light microscope. Macrophotographs and microphotographs were taken with the digital camera Zeiss AxioCam ERc5s. Samples were identified with Hawksworth (1983), Nash & al. (2001), Smith & al. (2009), and Fryday & Coppins (1997). The descriptions are based on Turkish specimens. Vouchers are stored at KTUB.

Lichen samples were collected on 29–30 May 2015 and 8 August 2016 during a lichenological survey of the Bitlis and Muş regions. The Muş region (Bulanık districts) primarily encompasses vast areas of meadow, large plains, and steppe but no high mountains or canyons are seen (Baytop & Denizci 1963). Muş province, which encompasses vast areas of grassy meadows and steppe and high mountains with occasional to rare *Quercus* communities and *Salix* trees, has a climate characterized by very cold snowy winters, and short hot dry summers, with temperatures ranging from –29 to 37 °C. Mean annual rainfall is 733 mm (Baytop & Denizci 1963, Akman 1999).The other study areas in Bitlis region (Siirt-Bitlis main roadside) are mountainous with mostly *Quercus,* and *Populus* and *Salix* trees are sometimes seen in some places. In addition many rocks occur on mountain areas and also side of main road and riverside. So crustose and foliose lichens are predominantly seen (Baytop & Denizci 1963). Collecting localities are well-lit, windswept areas with trees and rocks on sloping terrain containing streams, and calcareous and siliceous rocks. The Bitlis has a conitinental climate with very cold winters and short hot dry summers. Mean annual temperature is 9.47 °C, while mean annual rainfall is around 1241 mm (Akman 1999).

Further descriptions of other fungi are based on dried specimens kept in the cited fungaria or on cultures maintained at the Westerdijk Fungal Biodiversity Centre in Utrecht, The Netherlands (CBS), the working collection of P. W. Crous (CPC), housed at CBS, and on strains originating from other laboratories as indicated in the text. For details on microscopy and morphological documentation of *Hapalocystis* see Voglmayr et al. (2017). Reference strains and specimens are maintained at the CBS, except as indicated otherwise (see Tab. 1 and Hernández-Restrepo et al 2016).

DNA isolation, amplification and analyses

Methods for DNA extraction, amplification and analysis follow either those presented in FUSE 2 (Hernández-Restrepo et al. 2016), Voglmayr et al. (2017) or are described below. Sequence data were

Tab. 1. Details of sequences and strains included in the molecular and morphological analysis for the new species and interesting reports.

Species	Strain accession no.[1] / herbarium voucher	Country	Locality	Substrate/ collection	Collector(s)/ Reference	GenBank/EMBL accession numbers[2]	
						ITS	LSU
Asterosporium asterospermum	CBS 112404	Italy			Tanaka et al. (2010)		AB553745
Cainiella johansonii	UPS F-567263 = Kruys 731	Sweden			Kruys & Castlebury (2012)	JF701922	JF701920
Calosporella innesii	BPI 840945 = AR 3639	Austria			De Silva et al. (2009), Kruys & Castlebury (2012)	JF681965	EU683071
Chapeckia nigrospora	CBS 125532 = AR 3897	USA			De Silva et al. (2009), Kruys & Castlebury (2012)	JF681957	EU683068
Coryneum depressum	BPI 843585 = AR 3897	Austria			De Silva et al. (2009)		EU683074
Coryneum modonium	BPI 749131 = AR 3558	Austria			De Silva et al. (2009)		EU683073
Coryneum umbonatum	BPI 872021 = AR 3541	Austria			De Silva et al. (2009)		EU683072
Gyromitra khanspurensis	CBS 118142 = CMW 18281	Pakistan	Khyber Pakhtunkhwa province	near *Cedrus deodara*	L. Choudry & A.N. Khalid	MF116159	
Cortinarius scaurocaninus	WU 13419	Austria	Gleichenberg, Kurpark	Near *Quercus*	W. Klofac	MG489871	
Hapalocystis berkeleyi	WU 24707	Germany	Tübingen	*Platanus ×hispanica*	W. Jaklitsch	MG548637	MG548637
Hapalocystis berkeleyi	WU 39959	United Kingdom	Kew Gardens	*Platanus ×hispanica*	H. Voglmayr	MG495968	MG495968
Hapalocystis kickxii	WU 39960	Austria	Botanical Garden of the University of Vienna	*Platanus orientalis*	H. Voglmayr	MG548638	MG548638
Hapalocystis kickxii	WU 39961	France	Gorge du Verdon near Rougon	*Platanus orientalis*	H. Voglmayr	MG548639	MG548639
Hapalocystis kickxii	WU 39962	France	Mirebeau-sur-Bèze	*Platanus orientalis*	A. Gardiennet	MG548640	MG548640
Hapalocystis occidentalis	WU 24705	USA	Tennessee, Cades Cove	*Platanus occidentalis*	W. Jaklitsch & H. Voglmayr	MG548641	MG548641
Humicola grisea	CCCT 17.02	Chile	Región Metropolitana, Santiago	decaying bark of unidentified Arecaceae	H. Madrid	KU705826	

Tab. 1. Continued

Species	Strain accession no.[1] / herbarium voucher	Country	Locality	Substrate/ collection	Collector(s)/ Reference	GenBank/EMBL accession numbers[2]	
						ITS	LSU
Paramyrothecium guiyangense	HGUP 2016-8001	China	Guizhou Province, Guiyang City	soil		KY126417	KY196208
Paramyrothecium guiyangense	HGUP 2016-8002	China	Guizhou Province, Guiyang City	soil		KY126418	KY196209
Paramyrothecium guiyangense	HGUP 2016-8007	China	Guizhou Province, Guiyang City	soil		KY126423	KY196214
Paramyrothecium verruridum	HGUP 2016-8006	China	Guangxi province, Hechi City	soil		KY126422	KY196213
Opegrapha parasitica	KTUB–2457	Turkey	Muş: Bulanık	on *Aspicilia* cf. *calcarea*	K.Yazici, A. Aslan, A. Aptroot		
Rinodina zwackhiana	KTUB–2459	Turkey	Bitlis: Center	on calcareous rock	K.Yazici, A. Aslan, A. Aptroot		
Pluteus cervinus	BRNM 788200	Czech Republic	Brno, Panská 9, in the garden	root of *Ailantuhs*	Vlašín M.	LT838193	
Pluteus chrysophaeus	BRNM 747557	Czech Republic	Lanžhot, Ranšpurk	dead deciduous trunk	H. Ševčíková	LT838192	
Pluteus cinereofuscus	BRNM 751705	Czech Republic	Mladá Boleslav	mixed forest with *Tilia*	S. Tutka	LT838187	
Pluteus cinereofuscus	BRNM 751723	Czech Republic	Habrůvecká bučina	fallen trunk of *Fagus*	H. Ševčíková	LT838188	
Pluteus fenzlii	BP 88763	Hungary	Vas, Hosszúpereszteg	heap of sawdust	P. Serediuk	LT838183	
Pluteus cf. insidiosus	BRNM 781263	Czech Republic	Kulatý dub	fallen *Quercus*	H. Ševčíková	LT838189	
Pluteus leoninus	BRNM 766775	Czech Republic	Brno, Baba	heap of branches of *Tilia*	J. Hrabáková & H. Ševčíková	LT838184	
Pluteus leoninus	BRNM 788272	Czech Republic	Brno, Baba	heap of branches of *Tilia*	J. Hrabáková & H. Ševčíková	LT838185	
Pluteus romellii	BRNM 788197	Czech Republic	Brno, Bystrc, Jelení žlíbek	deciduous wood	H. Ševčíková	LT838191	
Pluteus romellii var. luteoalbus	BRNM 788199	Czech Republic	Brno, Kanice, Zadní Hády	fallen mossy stem of deciduous tree	P. Ševčík & H. Ševčíková	LT838190	

Tab. 1. Continued

Species	Strain accession no.[1] / herbarium voucher	Country	Locality	Substrate/ collection	Collector(s)/ Reference	GenBank/EMBL accession numbers[2]	
						ITS	LSU
Pluteus variabilicolor	BRNM 788273	Republic of Korea	Taean Peninsula, Deoksung	dead trunk of *Castanea*	V. Antonín	LT838186	
Pluteus variabilicolor	BRNM 788274	Slovakia	Snina, Hrb	heap of sawdust	J. Pavlík	LT838182	
Pluteus romellii	AJ232 (LOU)	Spain			Justo & al. (2011)	HM562062	
Pluteus romellii	AJ215 (LOU)	Spain			Justo & al. (2011)	HM562054	
Pluteus romellii	TNSF12387	Japan			Justo & al. (2011)	HM562123	
Pluteus romellii	24198112 (SIU)	USA			Justo & al. (2011)	HM562105	
Pluteus romellii	LE 217944	Russia			Justo & al. (2011)	FJ774073	
Pluteus romellii	AJ857	USA			Menolli & al. (2015)	KM983701	
Pluteus romellii	AJ864	USA			Menolli & al. (2015)	KM983700	
Pluteus galeroides	G. Consiglio 17-Oct-2002	Italy			Osmundson & al. (2013b)	JF908609	
Pluteus galeroides	G. Consiglio 17-Oct-2002	Italy			Osmundson & al. (2013b)	JF908610	
Pluteus chrysophlebius	AJ45 (MA)	Spain			Justo & al. (2011)	HM562064	
Pluteus chrysophlebius	TNSF12388	Japan			Justo & al. (2011)	HM562088	
Pluteus chrysophlebius	SF10 (BPI)	USA			Justo & al. (2011)	HM562180	
Pluteus chrysophlebius	SF11 (SIU)	USA			Justo & al. (2011)	HM562181	
Pluteus aurantiorugosus	AJ219 (LOU)	Spain			Justo et &. (2011)	HM562041	
Pluteus aurantiorugosus	G. Consiglio 17-Oct-2002	Italy			Osmundson & al. (2013b)	JF908608	
Pluteus aurantiorugosus	TNSF12391	Japan			Justo & al. (2011)	HM562121	
Pluteus aurantiorugosus	ILLS42433	USA			Justo & al. (2011)	HM562081	
Pluteus aurantiorugosus var. aurantiovelatus	TO AVPP212	Italy			Vizzini & Ercole (2011)	HQ654908	
Rossmania ukurunduensis	BPI 747566 = AR 3484	Russia			De Silva et al. (2009)		EU683075

Tab. 1. Continued

Species	Strain accession no.[1] / herbarium voucher	Country	Locality	Substrate/ collection	Collector(s)/ Reference	GenBank/EMBL accession numbers[2]	
						ITS	LSU
Sclerostagnospora elegiae	CBS 118142 = CMW 18281	South Africa	Western Cape province, Kirstenbosch	culm litter of *Elegia equisetacea*	S. Marincowitz	DQ286766	DQ286770
Sclerostagnospora fusiformis	CBS 118152 = CMW 18025	South Africa	Western Cape province, Kirstenbosch	culm litter of *Thamnochortus spicigerus*	S. Marincowitz	DQ286767	DQ286771
Sclerostagnospora pinguis	CBS 118146 = CMW 17948	South Africa	Western Cape province, Jonkershoek	culm litter of *Cannomois virgata*	S. Marincowitz	DQ286765	DQ286769
Sclerostagnospora sulcata	CBS 118224 = CMW 18063	South Africa	Western Cape province, Kirstenbosch	culm litter of *Ischyrolepis subverticellata*	S. Marincowitz	DQ286768	DQ286772
Sillia ferruginea	CBS 126567	Austria			De Silva et al. (2009), Kruys & Castlebury (2012)	JF681959	EU683076
Sydowiella fenestrans	CBS 125530	Russia			De Silva et al. (2009), Kruys & Castlebury (2012)	JF681956	EU683078
Xerula strigosa	LAH 240806	Pakistan	Khyber Pakhtunkhwa, Khanspur	moist ground, mixed forest	A. Razaq	LK932286	

[1] AJ C.I.T.A.-Xunta de Galicia, Pontevedra Spain; BP Hungarian Natural History Museum, Budapest, Hungary; BPI U.S. National Fungus Collections, USDA-ARS; BRNM Moravian Museum, Brno, Czech Republic; CBS: CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands; CCCT Colección Chilena de Cultivos Tipo-CCCT/UFRO, Universidad de La Frontera, Chile; CMW: Culture collection of the Forestry and Agricultural Biotechnology Institute (FABI) of the University of Pretoria, Pretoria South Africa; HGUP Herbarium of the Department of Plant Pathology, Guizhou University, China; ILLS: Herbarium of the Illinois Natural History Survey, Champaign, Illinois, USA; KTUB herbarium of the Department of Biology at Karadeniz Technical University, Turkey; LAH: Herbarium of the Botany Department, at the University of the Punjab, Lahore, Pakistan; LE V. L. Komarov Botanical Institute, Saint Petersburg, Russia ; SF Universidad Nacional del Litoral, Esperanza, Santa Fe, Argentina; SIU Southern Illinois University , Carbondale, Illinois, U.S.A. ; TNSF National Museum of Nature and Science, Tsukuba, Japan; TO University of Turin, Torino, Italy; UPS Museum of Evolution, Uppsala, Sweden; WU University of Vienna, Wien, Austria;

[2] ITS: internal transcribed spacer regions 1 & 2 including 5.8S nrRNA gene; LSU: 28S large subunit of the nrRNA gene

deposited in GenBank (Tab. 1) and the alignments and trees in TreeBASE (http://www.treebase.org).

Genomic DNA was extracted from growing mycelium on PDA. The genomic DNA was obtained using an EZgene™ Fungal gDNA Kit (GD2416) (The Inventor of EZgene™ and ViraTrap™ Systems, Biomiga, Inc., CA, USA) following the manufacturer's instructions. PCR were performed on a ProFlex™ Base (Applied Biosystems®, Life Technologies Pt. Ltd., Singapore) using primer pairs: cmdA (Carbone & Kohn 1999, Groenewald et al. 2013), ITS (White et al. 1990), LSU (Rehner & Samuels 1995, Vilgalys & Hester 1990), *rpb*2 (O'Donnell et al. 2007), *tef*1 (Carbone & Kohn 1999, O'Donnell et al. 1998) and *tub*2 (Glass & Donaldson 1995). The amplification reaction (25-µl volume) contained 1 µL DNA, 12.5 µL 2× Taq PCR MasterMix, 1 µl of each primer and 9.5 µL ddH_2O. The PCR conditions were as described in Lombard et al. (2015). PCR products were visualized by 1% agarose gel electrophoresis (TsingKe Biological Technology Limited Company, China). The sequence of each locus was assembled in Bioedit using the closest matches within the NCBI database (BLASTn). The *rpb*2 gene was absent in some strains. The other gene sequences were as described in Lombard et al. (2016). Sequence alignments were done in MAFFT (http://www.ebi.ac.uk/Tools/msa/mafft/).

The combined multi-gene phylogenetic analyses of *Paramyrothecium* were performed using cmdA, ITS, LSU, *rpb*2, *tef*1 and *tub*2 sequence data of 49 taxa downloaded from GenBank. *Alfaria ossiformis* (CBS 324.54) was used as outgroup. The combined sequence alignment was obtained from Molecular Evolutionary Genetics Analysis (MEGA, Kumar et al. 2012). Ambiguously aligned regions were excluded, and gaps were treated as missing data. Alignments were checked visually and manually adjusted for errors. The partition homogeneity test (PHT) was used to test the congruence and combinability of the individual datasets with 1,000 heuristic search replicates in PAUP v. 4.0b10 (Farris et al. 1995a, b; Swofford 2003). The genealogical analyses were generated on Bayesian inference (BI), Maximum Likelihood (ML) and Maximum Parsimony (MP) using each gene and combined genes of cmdA, ITS, LSU, *rpb*2, *tef*1 and *tub*2.

For each gene, MrModeltest software (v. 2.2) (Nylander 2004) was used to determine the optimum model for Bayesian inference. Four Markov Chain Monte Carlo (MCMC) chains for Bayesian analyses were run from random trees for 5,000,000 generations and sampled every 100 generations. The temperature value was lowered to 0.15, burn-in was set to 0.25, and the run was automatically stopped as soon as the average standard deviation of split frequencies reached less than 0.01.

Using RAxML (v. 8.0.9) (Stamatakis 2014), maximum likelihood datasets were run through the platform of CIPRES website (http://www.phylo.org). RAxML evaluated the robust analysis automatically with determined bootstrap support (ML-BS).

In addition, maximum parsimony (MP) analyses were performed using Phylogenetic Analysis Using Parsimony (PAUP) (v. 4.0 b10) (Swofford 2003). Gaps were treated as missing data, and ambiguously aligned regions were excluded. The heuristic search option was used to infer the tree on TBR branch swapping with 1,000 random sequence additions replicates. Maxtrees were set up to 2,000, the zero length branches were collapsed, and all most parsimonious trees were saved. The most parsimonious tree [MPT] was calculated with descriptive tree statistics, including tree length [TL], consistency index [CI], retention index [RI], relative consistency index [RC] and homoplasy index [HI]. The trees were printed in TreeView (v.1.6.6) (Page 1996).

The resulting trees were viewed in FigTree (v. 1.4.0) (http://tree.bio.ed.ac.uk/software/figtree/). Sequences derived from this study were deposited in GenBank and alignments were saved in TreeBASE (www.treebase.org, submission ID: 20663).

For *Pluteus* nuclear DNA was extracted from a dry piece of the basidioma (Tab. 1) using the NucleoSpin® Plant II extraction kit (Macherey-Nagel) according to the manufacturer's instructions. Alternatively, NaOH extraction method was used (Osmundson & al. 2013a). ITS rDNA region (ITS1, 5.8S, and ITS2 sequences) was amplified with the primer pair ITS1F-ITS4B under PCR conditions described in Borovička & al. (2011). When necessary, sequencing was based on semi-nested PCR product obtained with the primer pair ITS1F-ITS4 in the second step. Amplicons were purified by isopropanol precipitation and both strands were sequenced at Macrogen Europe. Sequences were edited in BioEdit (Hall 1999) and submitted to the EMBL Nucleotide Sequence Database (EMBL-Bank, http://www.ebi.ac.uk/ena). Appropriate sequences (species of subsect. *Eucellulodermini* or similarly looking yellowish *Pluteus* spp., Tab. 1) were downloaded from the public database GenBank (https://www.ncbi.nlm.nih.gov/genbank) and aligned in BioEdit using ClustalW algorithm (Hall 1999). The evolutionary history was inferred by using the Maximum Likelihood method based on the Kimura 2-parameter model (Kimura 1980) which was selected as the

Fig. **1.** *Gyromitra khanspurensis*. Ascomata, holotype, LAH35074, bar 0.5 cm.

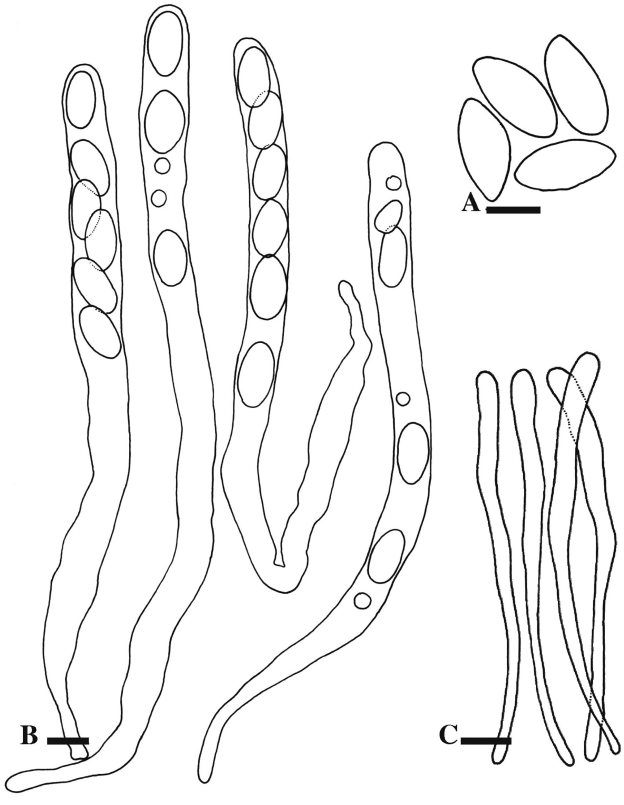


Fig. 2. *Gyromitra khanspurensis*, holotype, LAH35074. **A.** Ascospores. **B.** Asci. **C.** Paraphyses. Scale bars 10 µm.

best-fit substitution model by MEGA7 software (Kumar & al. 2016). The tree with the highest log likelihood (-2461.2532) is shown and the bootstrap support values are shown next to the branches. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 35 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 496 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.

Taxonomy

Gyromitra khanspurensis Jabeen & Khalid, **sp. nov.** – Figs. 1–2
MycoBank no.: MB 821408

Description.– Ascomata up to 3.4 cm high, hymenium free from the stipe; irregular, up to 2 cm high; 3.5 cm wide at the widest point; yellowish brown (5YR7/12) to brown (2.5YR5/10); surface smooth to wrinkled, becoming more wrinkled with age. – Stipe 3.5 × 1 cm; base slightly wider up to 1.3 cm, off-white, surface smooth. – Ascospores 14–17 × 7–8.5 µm, Q = 1.5–2, avQ = 1.8; smooth, ellipsoid, guttulate, apiculus short. – Asci up to 220 × 10 µm; 8-spored; cylindrical with a long narrow base; hyaline. – Paraphyses up to 140 × 6.5 µm,

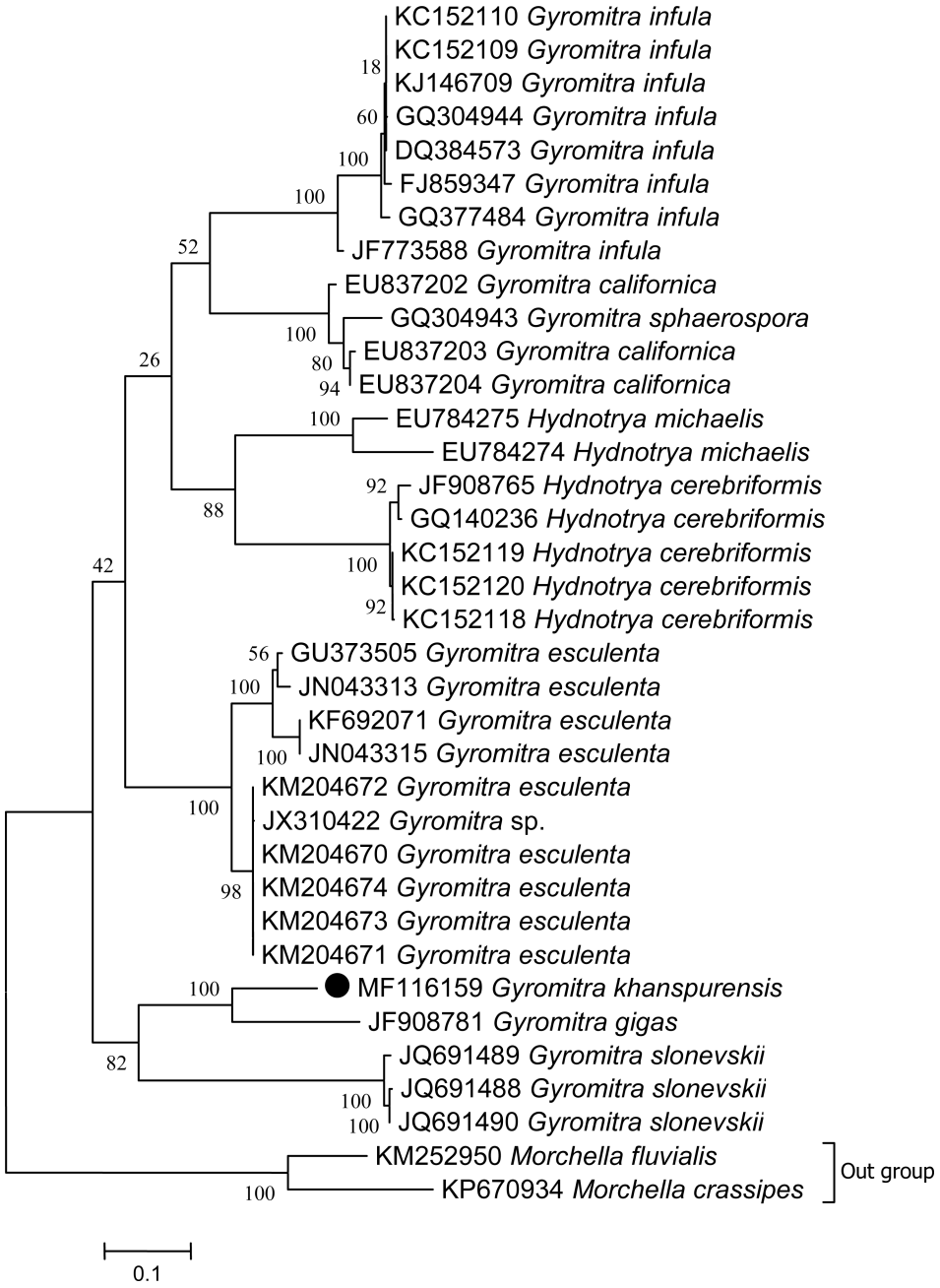


Fig. 3. Molecular genetic analysis of *Gyromitra khanspurensis* based on ITS sequences. The evolutionary history was inferred by the Maximum Likelihood method using Jukes-Cantor model in MEGA6. The analysis involved 36 nucleotide sequences. There were a total of 1337 positions in the final dataset. Sequence generated from LAH35074 marked with ●.

clavate, narrowing towards base; hyaline. All tissues observed in 5 % KOH.

Etymology. – Named after Khanspur, the site of collection in Khyber Pakhtunkhwa province, Pakistan.

Holotypus. – PAKISTAN. Khyber Pakhtunkhwa province, Abbottabad district, Khanspur, near *Cedrus deodara* (Roxb. ex D. Don) G. Don (*Pinaceae*), 19 May 2014, *leg.* L. Choudry & A.N. Khalid, holotype SJ95 (LAH35074), ITS sequence GenBank MF116159.

Notes. – *Gyromitra khanspurensis* is characterized by its yellowish brown wrinkled hymenium free from the stipe, long clavate asci, and ellipsoid, hyaline ascospores. Morphologically it is closely re-

lated to *G. gigas* (Krombh.) Cooke, but differs by smaller ascospores than in *G. gigas* (26–40 × 11.5–15 µm) (Kuo 2012). Type material of *G. gigas*, which is the oldest name and has priority, is absent and there is some confusion regarding the spore size. Abbott & Currah (1997) synonymised the North American *G. korfii* (Raitv.) Harmaja and *G. montana* with *G. gigas* and consider the latter to have a broad range of ascospore size. The North American *G. korfii* is represented by a type specimen having an irregularly wrinkled hymenium borne on a ribbed stipe. *Gyromitra khanspurensis* bears more convoluted hymenium with a smooth stipe in comparison with *G. korfii*. *Gyromitra khanspurensis* also differs from *G. korfii* by the lack of an apiculus, which is prominent in *G. korfii* at mature stages (Methven et al. 2013). Morphologically, *G. khanspurensis* is also distinct from *G. slonevskii* V.P. Heluta. *Gyromitra slonevskii* bears a chestnut brown to liver coloured hymenium and white to brownish, rough and ribbed, slightly compressed stipe. Ascospore size is also comparatively larger (27–35 × 11–15 µm) in *G. slonevskii* (Hetula 2001). Molecular genetic sequence comparisons of the ITS also suggest *G. khanspurensis* as a distinct taxon (Fig. 3).

Authors: S. Jabeen & A.N. Khalid

Hapalocystis kickxii (Westend.) Voglmayr, **comb. nov.** – Fig. 4

MycoBank no.: MB 823505

Basionym. – *Hypoxylon kickxii* Westend., Bull. Acad. R. Sci. Belg., Cl. Sci. 19(3): 112 (1852).

Synonyms. – *Aglaospora kickxii* (Westend.) Kuntze, Revis. gen. pl. (Leipzig) 3(2): 441 (1898).

Hapalocystis berkeleyi var. *kickxii* (Westend.) M.E. Barr, Mycol. Mem. 7: 193 (1978).

Prosthecium hapalocystis var. *kickxii* (Westend.) Wehm., Revision of *Melanconis*, *Pseudovalsa*, *Prosthecium* & *Titania*: 107 (1941).

Pseudovalsa kickxii (Westend.) Sacc., Syll. fung. (Abellini) 2: 139 (1883).

Valsa kickxii (Westend.) J. Kickx f., Fl. Crypt. Flandres (Paris) 1: 322 (1867).

Description. – Pseudostromata 1–1.6 mm diam., immersed in the outermost layer of the bark of dead branches, flat or slightly convex, circular, separate, gregarious, sometimes confluent, perithecial outlines sometimes translucent through bark. Stromatic tissues sparse, consisting of loose light brown hyphae growing between bark and perithecia. – Perithecia 4–12 per stroma, black, pyriform, strongly depressed to lenticular, (250)300–600(750) µm diam., 130–170 µm high, monostichous, circinately arranged, with ostiolar necks of perithecia fused in a single central ostiole. – Ostiole (93)105–135(145) µm diam. (n=20), dark, not projecting, with hyaline, filamentous periphyses embedded in a gel matrix. – Paraphyses of broad bands 4–9 µm wide, septate, deliquescent at maturity. – Asci detached from the perithecial wall at maturity, (119)133–183(224) × (45)47–56(62) µm (n=28), broadly fusoid, with a 5–70 µm long stipe and an inconspicuous apical ring, containing 4 (rarely 1–2) ascospores. – Ascospores (42)48–61(91) × (14)17–23(33) µm, l/w = (2.3)2.5–2.9(3.2) (n=80), subhyaline to olive brown when fresh, dark brown with age, ellipsoid to slightly obovoid, asymmetric, rarely straight to usually distinctly curved, (3)4–5 septate, strongly constricted at the primary and strongly to not constricted at the secondary septa, with broadly rounded ends, with tubular gelatinous, slightly tapering appendages (18)23–31(37) × (5)6–7.5(9) µm long at each end; cells of unequal size, multiguttulate when vital; wall ca. 1–1.5 µm thick, finely verruculose, hyaline when young, becoming olive to dark brown at maturity, swelling, surrounded by a sharply delimited, irregularly swelling, up to 6 µm thick subhyaline to brownish gelatinous sheath.

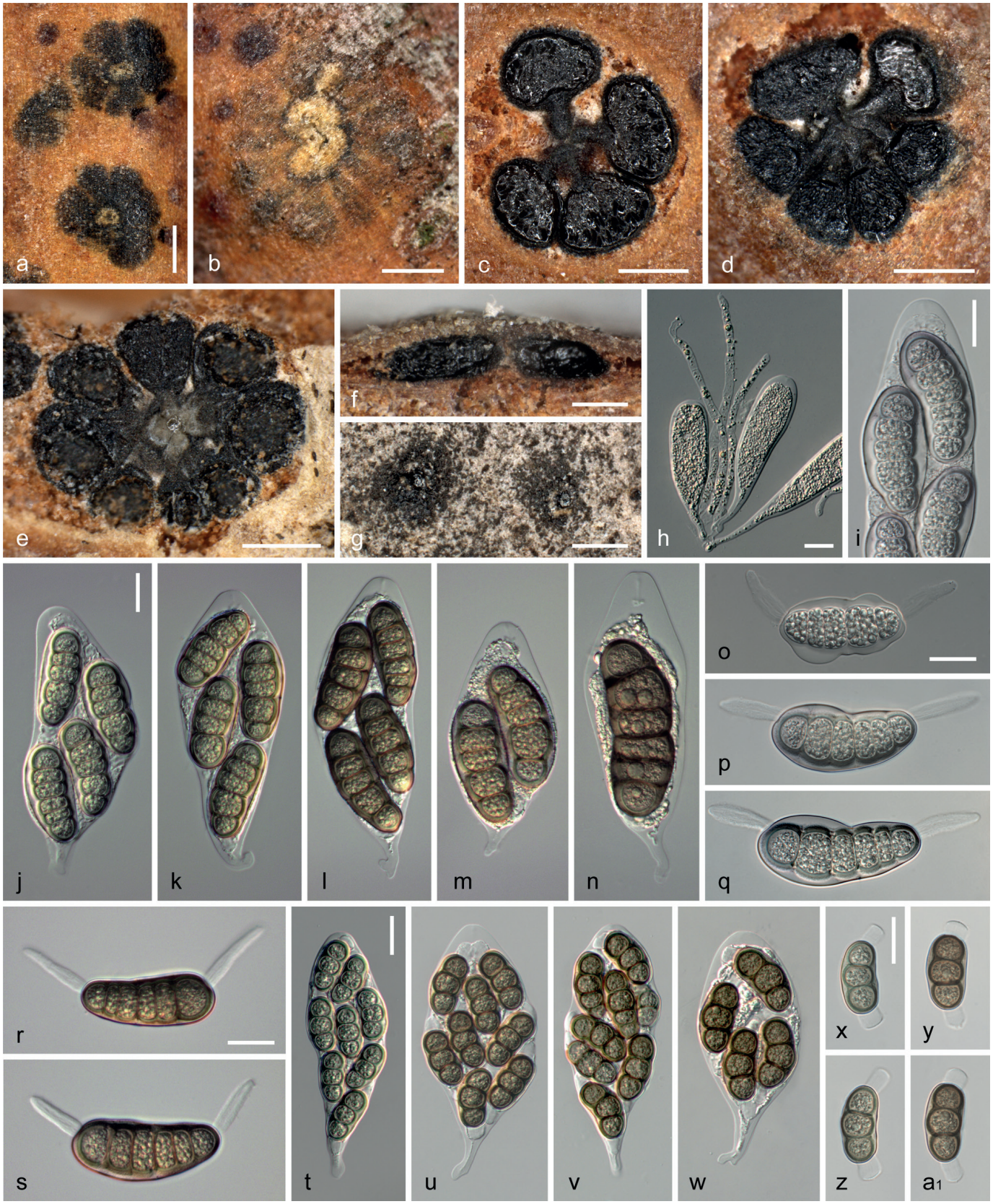
Asexual morph not observed.

Habitat. – On dead corticated branches of *Platanus* spp. (*P.* ×*hispanica*, *P. orientalis*).

Distribution. – Widely distributed in Europe; known e.g. from Austria, Belgium, Germany, France, Greece, Netherlands, Spain, United Kingdom.

Material examined. – ***Hapalocystis kickxii***: AUSTRIA. Wien, Landstraße, Botanical Garden of the University of Vienna (HBV), on corticated branches of *Platanus orientalis* and *P.* ×*hispanica*, 3 March 2008, *leg.* H. Voglmayr (WU 39960, epitype of *Hypoxylon kickxii* here designated; ex epitype culture D75 = CBS 123818; MBT379570) ibid., 10 November 2017, *leg.* H. Voglmayr (WU 39964); Währing, Türkenschanzpark, on corticated branches of *Platanus* ×*hispanica*, 11 November 2017, *leg.* H. Voglmayr (WU 39965). BELGIUM. Courtrai, Saint George park, on branches of *Platanus orientalis*, without date

Fig. 4. *Hapalocystis kickxii* (**a**–**s**). **a, b.** Stromata on dead corticated branch of *Platanus orientalis*, showing the translucent black perithecia; **c–e.** Transverse sections of pseudostromata, showing the perithecia with fusing perithecial necks; **f.** Vertical section of a pseudostroma showing the strongly depressed perithecia; **g.** Two ostiolar openings surrounded by discharged dark brown ascospores; **h.** Young asci with paraphyses; **i.** Ascus apex; **j–n.** Asci (**m.** two-spored, **n**. one-spored); **o–s.** Immature (**o**), almost mature (**p, q**) and fully mature (**r, s**) ascospores; *Hapalocystis berkeleyi* (**t**–**a1**). **t–w.** Asci (**w.** four-spored); **x–a1.** Ascospores. All vital in water. a–d, f, h, i, o-q WU 39964. e, g, j–n, r, s WU 39960 (epitype). t–a1 WU 39963. Scale bars: a, b, g 500 µm; c–e 400 µm; f 200 µm, h–a1 20 µm.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and collector, Westendorp & Wallays, Herb. Crypt. Belg. no. 714 (BR 5020097352610, lectotype of *Hypoxylon kickxii* here designated; MBT379569). FRANCE. Dept. Alpes-de-Haute-Provence (04), Gorge du Verdon near Rougon, on corticated twig of *Platanus orientalis*, 1 August 2008, *leg.* H. Voglmayr (WU 39961, culture D83 = CBS 124481); France, Dept. Côte d'Or (21), Mirebeau-sur-Bèze, Terrain de sports, on corticated branches of *Platanus* ×*hispanica*, 6 May 2015, *leg.* A. Gardiennet AG15025 (WU 39962, culture D108); GREECE. Crete, SE Rethymno, Kaloniktis, 7 June 2015, *leg.* H. Voglmayr & W. Jaklitsch (no specimen preserved). ***Hapalocystis berkeleyi*:** Austria, Wien, Währing, Türkenschanzpark, on corticated branches of *Platanus* ×*hispanica*, 11 November 2017, *leg.* H. Voglmayr (WU 39963).

N o t e s . – Within *Hapalocystis*, *H. kickxii* is well characterised by usually four-spored asci and five- to six-celled ascospores which become olive to dark brown at maturity; for a key to species and discussion on the genus *Hapalocystis* see Jaklitsch & Voglmayr (2004). Despite its distinctive features, it was reduced to a variety by Wehmeyer (1941, as *Prosthecium berkeleyi* var. *kickxii*), based on depauperate herbarium material which he considered to be abnormally developed. This was subsequently also followed by Barr (1978) who classified it as *Hapalocystis berkeleyi* var. *kickxii*. However, *H. berkeleyi* differs markedly by usually eight-spored asci and three-celled ascospores (Fig. 4t–a1). In addition, *H. berkeleyi* has distinctly smaller ascospores (28–34 × 11–16 µm vs. 42–68(91) × 14–25(33) µm in *H. kickxii*; measured without gel sheath; values in brackets in *H. kickxii* refer to a significantly larger ascospore from a monosporic ascus). Also the gelatinous appendages are of different size and shape (5–12 × 7–11 µm and blunt rectangular with broadly rounded ends in *H. berkeleyi*; 18–37 × 5–9 µm and long-tubular with tapering, narrowly rounded to subacute ends in *H. kickxii*). The presence, shape and size of ascospore appendages has been shown to be of high diagnostic value for species delimitation in Diaporthales (e.g. Voglmayr & Jaklitsch 2008, 2014; Voglmayr et al. 2012, 2017) but can often be only well-seen in fresh material. Phylogenetic analyses (Fig. 5) confirm that *H. kickxii* is clearly distinct from *H. berkeleyi* at species level. Besides the typical four-spored asci, few two- or one-spored asci (Fig. 4m, n) can occasionally be observed, with distinctly larger ascospores in the latter. Similarly, in *H. berkeleyi* four-spored asci with slightly larger ascospores are rarely present (Fig. 4w). However, apart from slightly to distinctly larger sizes, ascospores of these asci with reduced spore numbers are typical for the respective species.

Ecologically, *H. berkeleyi* and *H. kickxii* share the same hosts and can co-occur on the same branches, but *H. berkeleyi* has been more commonly recorded from *Platanus* ×*hispanica* and *H. kickxii* from *Platanus orientalis*. Additional *Hapalocystis* species are

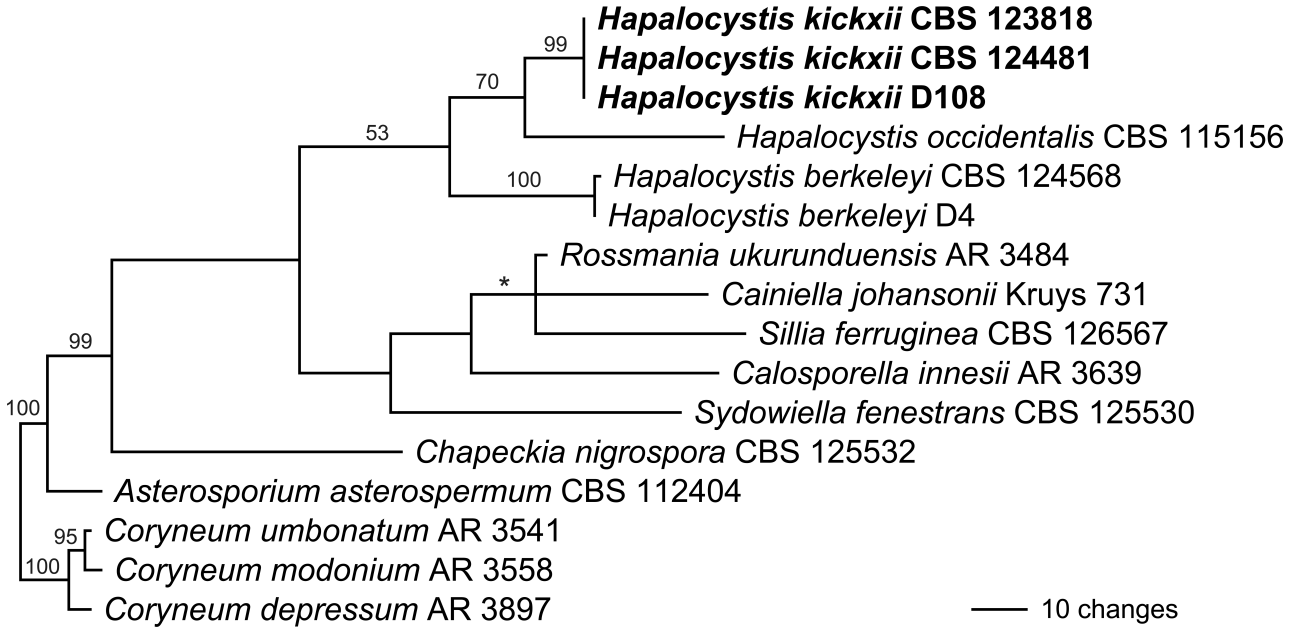

Fig. 5. Phylogram of one of two best MP trees 471 steps long revealed by PAUP from an analysis of the ITS-LSU rDNA matrix of Sydowiellaceae, with *Coryneum* (Coryneaceae) and *Asterosporium asterospermum* (Asterosporiaceae) selected as outgroup, showing the status of *Hapalocystis kickxii* (bold) as distinct species, * denoting node collapsed in the strict consensus of both MP trees. MP bootstrap support above 50 % is given above the branches.

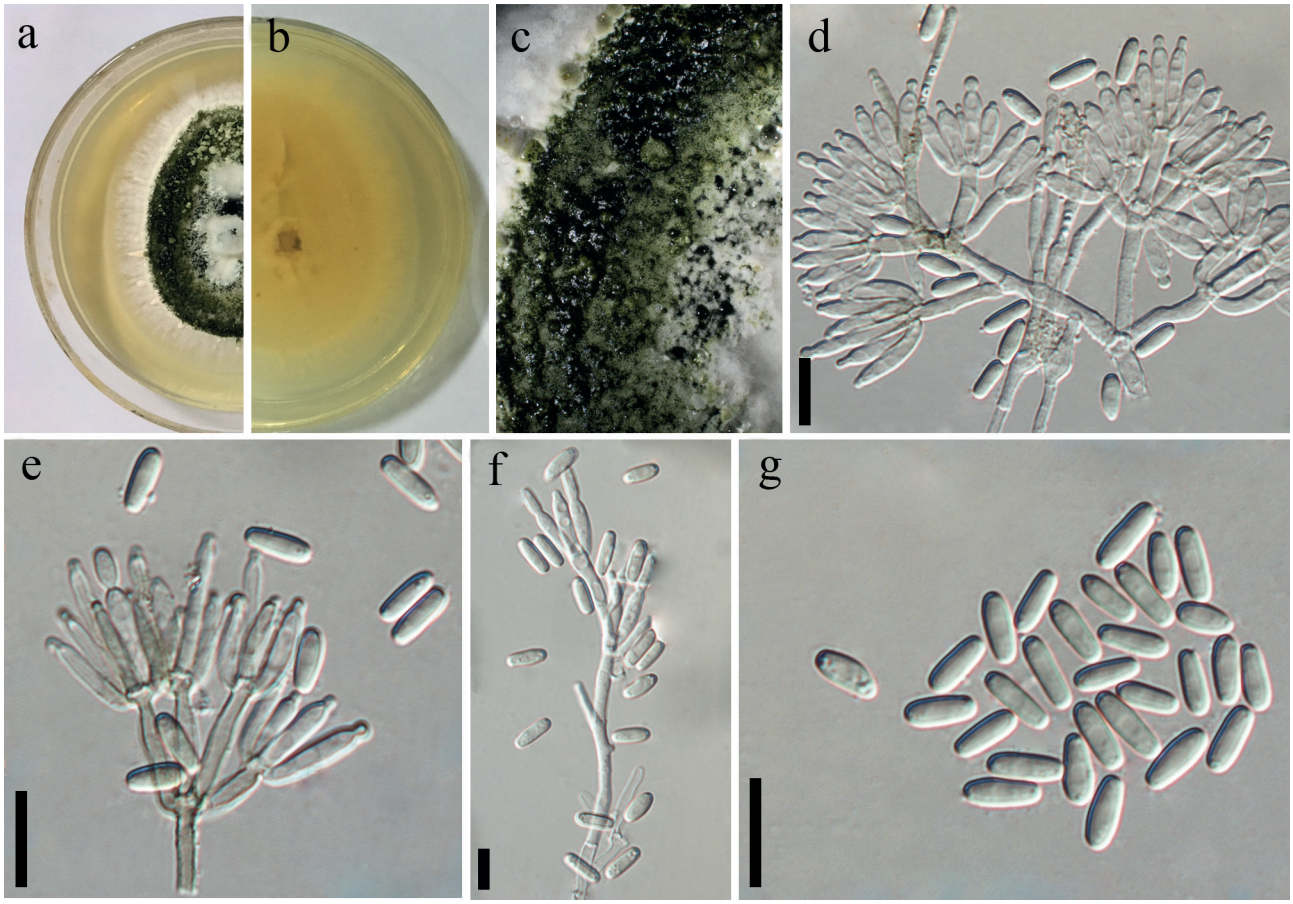

Fig. 6. *Paramyrothecium guiyangense* (HGUP 2016-8001, HGUP 2016-8002 and HGUP 2016-8007) **a**, **b**. Colonies were grown on PDA (**a**, from above; **b**, from below). **c**. Mycelium. **d**–**f**. Conidiophores and conidiogenous cells with conidia. **g**. Conidia. Scale bars 10 µm.

found on *Platanus* in North America (Barr 1978, Jaklitsch & Voglmayr 2004), but except for *H. occidentalis* no sequence data are yet available.

The type collection was distributed as Westendorp & Wallays, Herb. Crypt. Belg. no. 714, and specimen BR 5020097352610 is here selected as lectotype. As the type collection is depauperate (Wehmeyer 1941; B. Declercq, unpubl. notes) and in order to stabilise the name, a recent well-developed specimen, for which a culture and sequence data are available, is here selected as lectotype.

Author: H. Voglmayr

Paramyrothecium guiyangense Y. Chen, Yong Wang bis & Y.L. Jiang, **sp. nov.** – Fig. 6
MycoBank no.: MB 819908

Description. – Sexual morph undetermined; Asexual morph: conidiomata sporodochial, superficial, cupulate, outline oval, 20–160 µm diam., with setose fringe surrounding a slimy mass of olivaceous green conidia. Setae arising from sporodochia, thin-walled, hyaline, 1–3-septate, smooth, straight to flexuous, becoming sinuous above the apical septum, 60–120 µm long, 1–3 µm wide, tapering to an acutely rounded apex. – Conidiophores hyaline, aseptate, smooth, 10–60 × 1–3 µm, growing from the basal stroma, stipe and branched in a whorl of 1–4 conidiogenous cells arising apically. – Conidiogenous cells hyaline, phialidic, subcylindrical, collarettes with conspicuous periclinal thickening, smooth, straight to slightly curved, 8–18 × 1.6–2.7 µm. – Conidia aseptate, hyaline, smooth, cylindrical to subcylindrical, 6.6–9.0 × 2–3 µm (n = 30, $\bar{x}$ = 8 × 2.5 µm), rounded at both ends.

Colonies scattered on PDA with abundant white to pale luteous aerial mycelium. Sporodochia with slimy olivaceous green conidial masses formed on the surface of the medium. Cultures pale luteous in reverse.

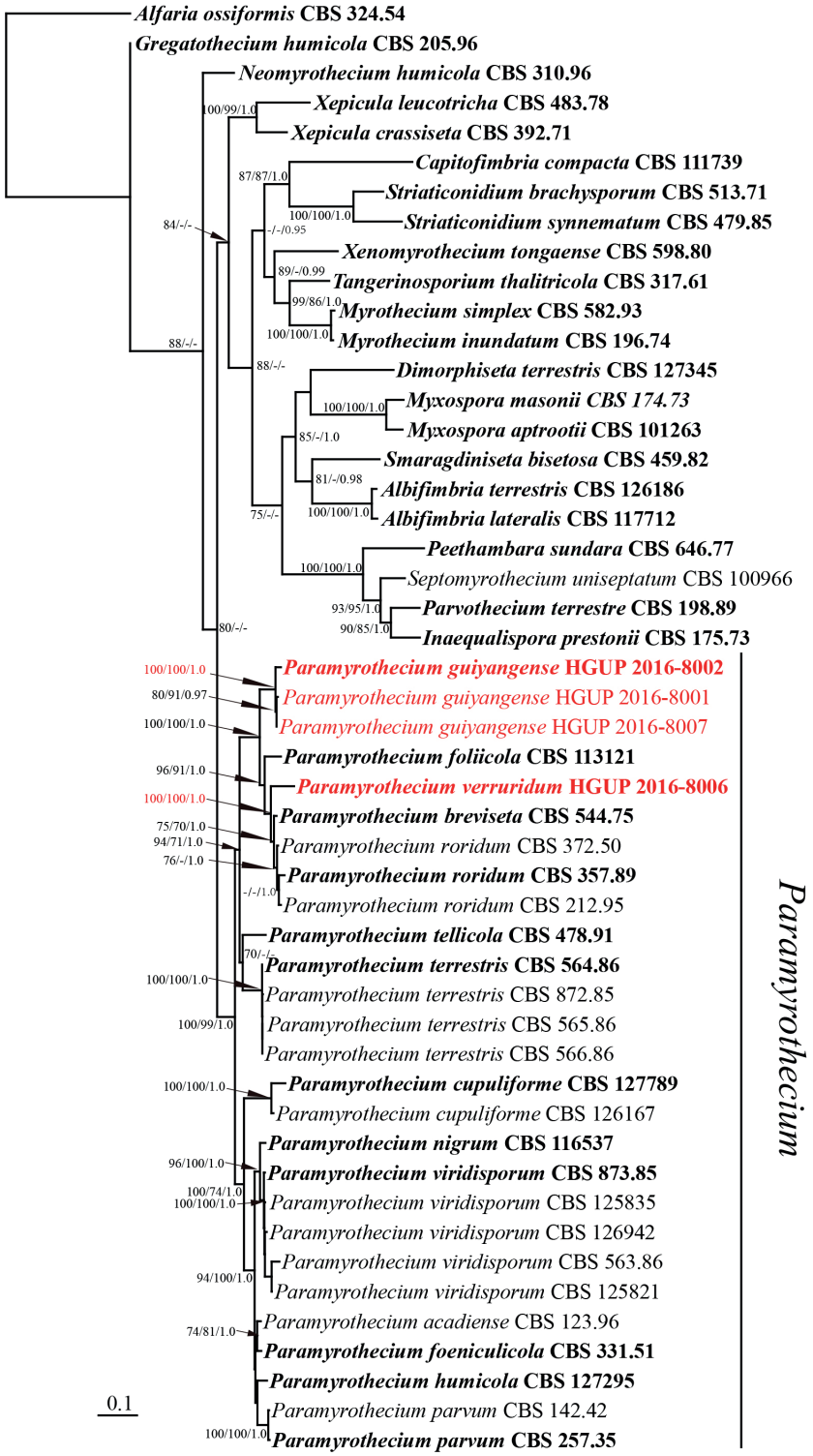

Fig. 7. A *Paramyrothecium* consensus tree generated using sequence data of the *cmdA*, ITS, LSU, *rpb*2, *tef*1 and *tub*2 genes, with *Alfaria ossiformis* as an outgroup (CBS 324.54). Maximum likelihood, Maximum parsimony, and Bayesian approaches were used, but only the maximum likelihood tree is shown. Values of maximum likelihood and maximum parsimony bootstrap ≥ 70 % (MLBS/MPBS) with the third values of posterior probabilities (BI PP ≥ 0.95) are presented above or below the branches, respectively. Ex-type and ex-epitype strains are shown in bold, black text. Those strains used in this study and their support values are shown in red.

Etymology. – *guiyangense*, referring to the collection locality.

Habitat and distribution. – Agricultural soil, China.

Holotypus. – CHINA. Guizhou Province, Guiyang City, Huaxi District, Yangguang park, from soil, 10 August 2016, *leg.* Y. Chen [holotype, GUCC 201608S01; sequences: KY196193 (*cmdA*), KY126418 (ITS), KY196209 (LSU), KY123426 (*tef*1), KY196201 (*tub*2)].

Further material examined. – CHINA. ibid. (HGUP 2016-8001, HGUP 2016-8002, HGUP 2016-8007, holotype, GUCC 201608S01); living culture, HGUP 2016-8002. Sequences accession numbers: HGUP 2016-8001 KY196192 (*cmdA*), KY126417 (ITS), KY196208 (LSU), KY126425 (*tef*1), KY196200 (*tub*2). HGUP 2016-8007 KY196198 (*cmdA*), KY126423 (ITS), KY196214 (LSU), KY126430 (*tef*1) and KY196206 (*tub*2).

Notes. – *Paramyrothecium* sp. (HGUP 2016-8001, HGUP 2016-8002, HGUP 2016-8007) clustered into a highly supported cluster (100%/100%/1.0) with *P. foliicola*, *P. breviseta*, *P. roridum* and *P. verruridum*. However, three strains could be clearly distinguished from these, forming an independent branch (Fig. 7). Morphologically, three strains had shorter conidiogenous cell (8–18 µm) and longer conidia (8 × 2.5 µm) among species in the branch. Based on their phylogeny and morphology, three of these strains were identified as belonging to the new species *P. guiyangense*.

Paramyrothecium species are saprobe, weakly pathogenic fungi, able to grow in air, sands, soil and on plants, worldwide (Lombard et al. 2016). Lombard et al. (2016) performed a phylogenetic analysis of *Myrothecium*-like species using the *cmdA*, ITS, *rpb*2, and *tub*2 genes and identified twelve *Myrothecium*-like species (two *Myrothecium* species [*M. acadiense* (CBS 123.96), Seifert et al. (2003), *M. roridum* (CBS 357.89), Tulloch (1972)]; ten *Myrothecium*-like species [*M. breviseta* (CBS 544.75), *M. cupuliforme* (CBS 127789), *M. foeniculicola* (CBS 331.51), *M. foliicola* (CBS 113121), *M. humicola* (CBS 127295), *M. nigrum* (CBS 116537), *M. parvum* (CBS 257.35), *M. tellicola* (CBS 478.91), *M. terrestris* (CBS 564.86), and *M. viridisporum* (CBS 873.85)]) that formed a conspicuous independent clade with strong bootstrap values. Combined with the special long cylindrical-shaped conidia, Lombard et al. (2016) proposed the genus *Paramyrothecium* within the family Stachybotryaceae and *Paramyrothecium roridum* (Tode) L. Lombard & Crous was suggested as type species for *Paramyrothecium*, whose characteristics include: Sporodochia cupulate, surficial, covered by a slimy mass of olivaceous green to dark green conidia; setose, 1–4 septate, thin-walled, hyaline, straight or sinuous; conidiophores branched, smooth, hyaline, macronematous; conidiogenous cells phialidic, hyaline or darker at the apex, surface smooth or lightly guttulate, cylindrical or subcylindrical special collarettes; conidia cylindrical or ellipsoidal, straight or curve, smooth and tinting hyaline or pale green.

Paramyrothecium verruridum Y. Chen & Yong Wang bis, Y.L. Jiang, **sp. nov.** – Fig. 8
MycoBank no.: MB 819909.

Description. – Sexual morph, undetermined; asexual morph, conidiomata sporodochial, superficial, cupulate, outline oval or irregular, 20–36 µm diam., white setose fringe surrounding a mass of slimy conidia, olivaceous green to dark green. Setae growing from sporodochia, thin-walled, hyaline, 1–3-septate, smooth, straight or flexuous becoming sinuous at the apical septum, 40–120 µm long, 2–3 µm wide, tapering to a sharply rounded apex. – Conidiophores hyaline, aseptate, smooth, 20–40 × 1.5–2.5 µm, growing from the basal stroma, one whorl of 2–8 conidiogenous cells growing apically. – Conidiogenous cells phialidic, cylindrical to subcylindrical, hyaline, smooth, straight to slightly curved, 12–20 × 1.7–2.7 µm, conspicuous collaretes and periclinal thickenings. – Conidia aseptate, hyaline, smooth, cylindrical to ellipsoidal, 6.8–7.8 × 2.0–2.7 µm (n = 30, $\bar{x}$ = 7.2 × 2.4 µm), with a slightly curved sides, rounded at both ends.

Colonies generated abundant white to pale grey aerial mycelium on PDA. Sporodochia formed on the surface of the medium covered with plenty of slimy olivaceous green conidia. Cultures pale luteous in reverse.

Etymology. – The name reflects the morphology of conidia and its resemblance to *P. roridum*.

Habitat and distribution. – Agricultural soil, China.

Holotype. – CHINA. Guizhou Province, Guiyang City, Huaxi District, Yangguang county, agricultural garden, from soil, 10 August 2016, *leg.* Y. Chen (Holotype, GUCC 201608S01; sequences: KY196197 (*cmdA*), KY126422 (ITS), KY196213 (LSU), KY126429 (*tef*1), KY196205 (*tub*2). (living culture HGUP 2016-8006).

Notes. – *Paramyrothecium* sp. HGUP 2016-8006 was placed amongst *P. breviseta*, *P. foliicola*, *P. guiyancola* and *P. roridum* with strong bootstrap support (100%(MLBS)/100%(MPBS)/1.0(BI PP)). However, by phylogenetic analyses (Fig 7), its morphological characters are distinctive, with 2–8 conidiogenous cells arisen at ends of conidiophores. Taking the above special characters into account, we considered identifying *Paramyrothecium* sp.

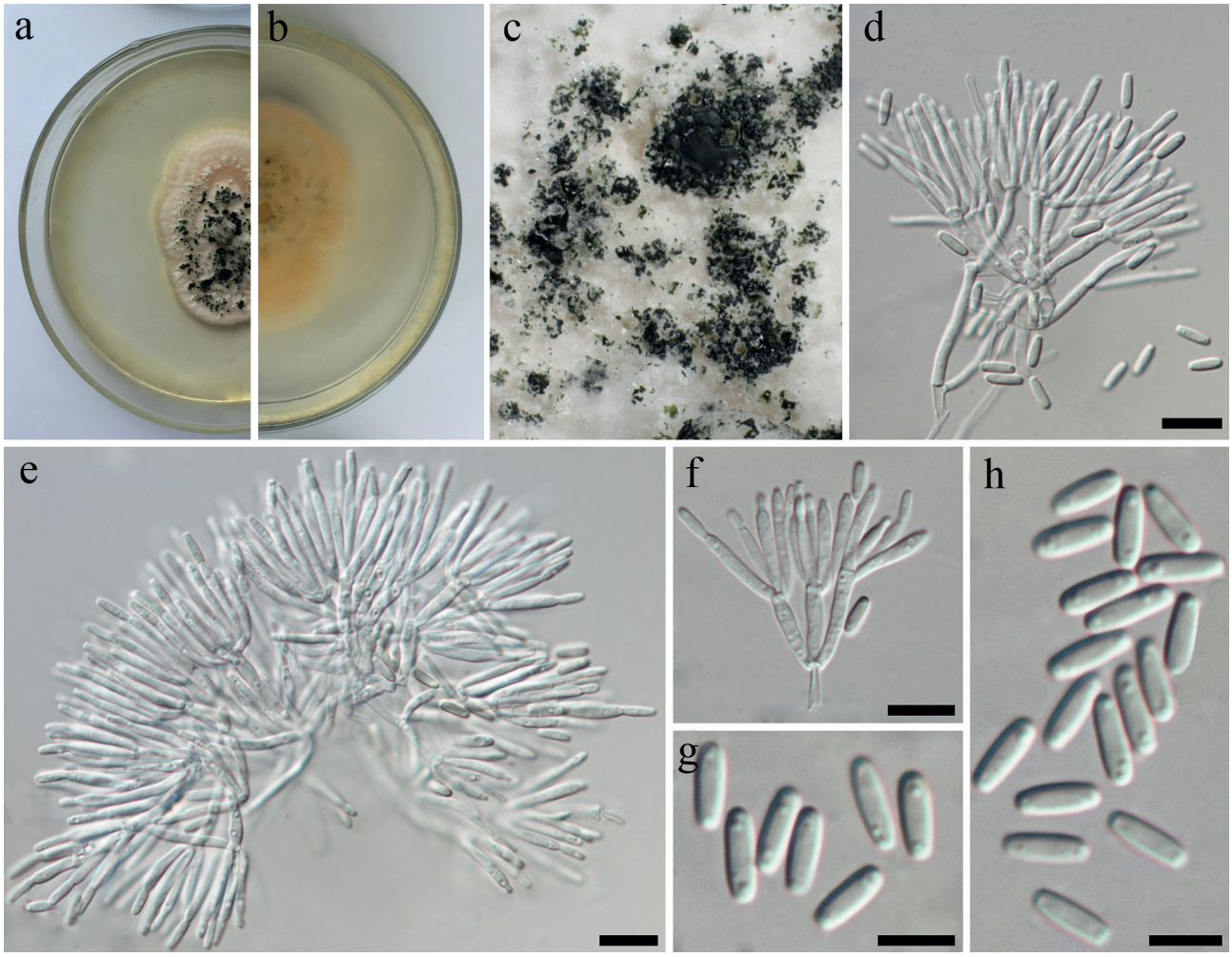

Fig. 8. *Paramyrothecium verruridum* (HGUP 2016-8006). **a**, **b**. Colonies grown on PDA (**a**, from above; **b**, from below). **c**. Mycelium and conidiomata. **d**–**f**. Conidiophores and conidiogenous cells with conidia. Scale bars = 10 µm. **g**, **h.** Conidia. Scale bars 5 µm.

HGUP 2016-8006 as a new species *Paramyrothecium verruridum*.

We discriminated *Paramyrothecium* from among 16 *Myrothecium*-like genera, mostly based on morphological characteristics. Thus, this genus has a special shape and can be recognised easily. We also attempted to use a dichotomous key to classify *Paramyrothecium*. However, we found that some of the species could not be discriminated by morphology (*P. foeniculicola vs. P. parvum*; *P. tellicola vs. P. terrestris*; *P. cupuliforme vs. P. humicola*; *P. verruridum vs. P. guiyangense;* and *P. roridum vs. P. nigrum*) so, it is the better way that a combined phylogeny for the taxonomy of *Paramyrothecium* species is used presently (Fig. 7).

The following is a list of main morphologic characteristics of each *Myrothecium*-like genus: 1) *Albifimbria* – Conidia ellipsoidal to fusiform to limoniform to subglobose, sometimes bearing a funnel-shaped mucoid apical appendage and straight to its circinate setae (Lombard et al. 2016); 2) *Capitofimbria* – Olivaceous brown conidia conspicuously verrucose at both ends and shortage of a white setose fringe (Lombard et al. 2016); 3) *Dimorphiseta* – Formed fusiform, with a funnel-shaped mucoid apical appendage and two types of setae (Type I, flexuous to circinate, verrucose, tapering to an obtuse apex; Type II, tapering to a sharp apex) (Lombard et al. 2016); 4) *Gregatothecium* – Special character of the slimy olivaceous green conidial masses grown on the conidiophores and sporodochia (Lombard et al. 2016); 5) *Inaequalispora* – Conidia fusiform to ellipsoidal to asymmetrically ellipsoidal with a slightly curved acute apex and a narrow truncate

base with a funnel-shaped mucoid apical appendage and setae tapering to an obtuse apex that becomes lightly verrucose (Lombard et al. 2016); 6) *Myrothecium* – Conidia ellipsoidal to obovoid, < 5 µm in length (Tulloch 1972); 7) *Myxospora* – Forming many fusiform conidia, bearing an apical hilum without funnel-shaped mucoid appendages and synnematal conidiomata (Lombard et al. 2016); 8) *Neomyrothecium* –Similar to *Paramyrothecium* except that the pulvinate sporodochia lack a white setose fringe (Lombard et al. 2016); 9) *Parvothecium* – Conidiogenous cells verrucose and conidia asymmetrically ellipsoidal, with slightly curved acute apex and a narrow truncate base (Lombard et al. 2016); 10) *Peethambara* – Special fusiform conidia morphology with two triangle-shaped marks at its opposite ends and conidiophores gregarious (Subramanian & Bhat 1978a, b, Seifert 1985, Rossman et al. 1999); 11) *Smaragdiniseta* – Two types of setae (Type I, compacted, verrucose, emerald green; Type II, originating from the marginal hyphae, lightly verrucose, tapering to an obtuse apex, soon growing beyond the length of Type I) (Lombard et al. 2016); 12) *Striaticonidium* – Synnemata, conidiogenous cells conspicuously curved and conidia black (Lombard et al. 2016); 13) *Tangerinosporium* – Generating distinctively orange conidial masses on its conidiophores (Lombard et al. 2016); 14) *Xenomyrothecium* – with oblong-ellipsoidal conidia and lacking setae formed from stroma (Lombard et al. 2016); 15.) *Xepicula* – Forming an appendage-bearing conidium (Nag Raj 1993).

To our knowledge, these are the first *Paramyrothecium* species described from China. A more precise taxonomic system of *Myrothecium*-like was provided by Lombard et al. (2016). Furthermore, the placement of *Paramyrothecium* is distinctive based on its morphology and phylogenetic analysis in the confusion fungi. Thus, *Myrothecium* (Tulloch 1972) should be separated into multiple genera to overcome the chaos of having multiple fungal taxonomies (Nag Raj 1993, 1995; Lombard et al. 2016).

Authors: Y. Chen, C. Norphanphoun, J.-Y. Yu, S.-P. Wu, Y. Wang, Y.-M. Wu & Y.-L. Jiang

Pluteus romellii* var. *luteoalbus Ševčíková & Borovička, **var. nov.** – Figs. 9–11
MycoBank no.: MB 821253, EMBL-Bank: LT 838190

Diagnosis. – Differs from *Pluteus romellii* var. *romellii* by a yellow pileus and a whitish stipe.

Description. – Pileus 14–16 mm broad, convex to plano-convex with indistinct umbo, very slightly rugulose at centre, slightly hygrophanous, glabrous, striate and shortly lacerate at margin, yellow (S00 C00 Y60–S00 C00 Y70), paler towards margin (S00 C00 Y50), distinctly darker at umbo (S10 Y99 M00–Y99 M00–10 C00). – Lamellae free, moderately distant, ± ventricose, whitish to pale yellow (Y10 M00 C00–Y20 M00 C00), later pinkish with concolourous, slightly pubescent edge. – Stipe 60 × 1–2 mm, cylindrical, slightly broadened at base, smooth, finely longitudinally fibrillose, whitish. – Context whitish at a cap, whitish to pale yellow at a stipe part. – Smell and taste indistinct.

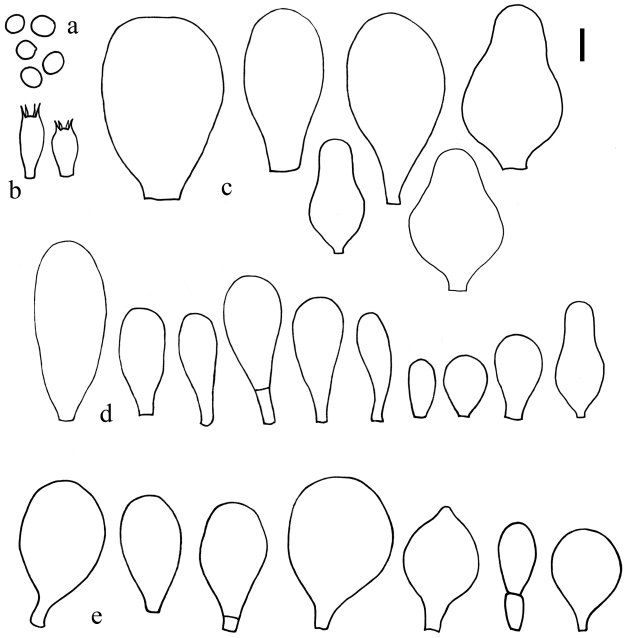

Fig. 9. *Pluteus romellii* var. *luteoalbus*, holotype: **a.** Basidiospores. **b.** Basidia., **c.** Pleurocystidia, **d.** Cheilocystidia. **e.** Pileipellis elements. Scale bar 10 µm.

Basidiospores 60/3/2 (5.5)6.0–7.5(8) × 5–6.5(7) µm, avl × avw = 6.6 × 5.5 µm, Q = 1–1.35(1.4), avQ = 1.20, broadly ellipsoid, subglobose or globose. – Basidia 15–29(35) × 6–9(10) µm, tetrasterigmate, cylindrical, clavate to subfusiform, colourless. – Pleurocystidia scattered to moderately abundant, (38)45–65(80) × 21–45(55) µm, broadly clavate, broadly cylindrical, broadly utriform to utriform, sometimes with pedicel up to 10(12) µm, rarely ventricose or vesiculose-fusiform, thin-walled, colourless. Lamellar edges sterile, cheilocystidia (18)25–62(72) × 9–31(47) µm, cylindrical, narrowly to broadly clavate, utriform, rarely broadly utriform or broadly cylindrical, thin-walled, colourless. – Pileipellis a euhymeniderm, consists of ventricose, spheropedunculate

Figs. 10–11. *Pluteus romellii* var. *luteoalbus*, holotype, basidiocarp, scale bar 1 cm.

and broadly clavate elements (20)33–49(60) × (11)15–29(45) µm, with yellow intracellular pigment. – Stipitipellis a cutis of 4–10 (16) µm wide cylindrical colourless hyphae, caulocystidia absent. Clamp connections absent in all tissues.

Etymology. – The epithet *luteoalbus* refers to yellow pileus and white stipe.

Habitat and distribution. – On fallen mossy stem of undetermined deciduous tree. So far known from only one site in thermophilic *Querceto-Carpinetum*, South Moravia, Czech Republic.

Holotypus. – CZECH REPUBLIC. Brno-venkov district, Kanice, Zadní Hády Nature reserve, *Querceto-Carpinetum*, on mossy fallen stem of undetermined deciduous tree. 23 July 2016, *leg.* P. Ševčík et H. Ševčíková (BRNM 788199).

Material examined (besides holotype). – ***Pluteus chrysophlebius*** (orig. *P. chrysophaeus*): CZECH REPUBLIC. Chynín, Chynínské buky, dead trunk of *Fagus*, 22 September 1983, *leg.* J. Baier, *det.* Herink (BRNM 289486); Čučice, Oslava a Chvojnice, near Oslava river, deciduous woods, 25 October 2016, *leg. et det.* J. Běťák (BRNM 781487); Dolní Věstonice, Děvičky, *Acereto-Fraxinetum*, 13 July 1955, *leg.* K. Kříž, *det.* H. Ševčíková (BRNM 332458); stump of *Fraxinus excelsior*, 31 August 1955, *leg.* K. Kříž, *det.* H. Ševčíková (BRNM 332459); Horní Lomná, Mionší, deciduous woods, 30 August 1962, *leg.* Novotný, *det.* H. Ševčíková (BRNM 332444); Kuřim, Šiberná, *Querceto-Potentilletum albae*, trunk of *Quercus*, 32 July 1961, *leg.* F. Šmarda, *det.* H. Ševčíková (BRNM 332424); *Quercetum*, 23 October 1954, *leg.* et *det.* F. Šmarda 332388); Kuřim, Zlobice, *Querceto-Potintilletum albae*, *Quercus*-stump, May 1950, *leg.* F. Šmarda, *det.* H. Ševčíková (BRNM 332422); *Ulmus*-stump, 22 May 1960, *leg.* F. Šmarda, *det.* H. Ševčíková (BRNM 332429); Lanžhot, Ranšpurk, dead trunk of *Ulmus*, 22 June 1967, *leg.* Lazebníček, *det.* H. Ševčíková (BRNM 332447); decaying deciduous trunk, 26 June 1992, *leg. et det.* A. Vágner (BRNM 571060); fallen deciduous trunk, 10 October 1992, *leg. et det.* A. Vágner (BRNM 571059); dead deciduous trunk, two trees, 24 May 2013, *leg. et det.* H. Ševčíková (BRNM 747556, 747557); fallen deciduous trunk, 10 October 2013, *leg. et det.* H. Ševčíková (BRNM 751770); deciduous decaying trunk, 11 April 2014, *leg. et det.* J. Běťák (BRNM 761727); Omice, 15 June 1952, *leg.* F. Valkoun, *det.* H. Ševčíková (BRNM 332419); Velká nad Veličkou, Zahrady pod Hájem, dead woods of *Carpinus*, 27 July 2005, *leg. et det.* V. Antonín (BRNM 695505); SLOVAKIA. Lehota nad Rimavicou, Dúbrava, *Querceto-Carpinetum*, deciduous wood, 7 December 2015, *leg.* J. Hraško, *det.* H. Ševčíková (BRNM 772178); Snina, Stambočská úboč, fallen trunk of *Carpinus*, 3 June 2015, *leg.* J. Pavlík, *det.* H. Ševčíková (BRNM 781079); HUNGARY. Bátorliget, Fényi erdö, alluvial forest, fallen stem of *Quercus robur*, 25 October 2006, *leg. et det.* V. Antonín (BRNM 705010); (*Pluteus chrysophlebius* - *P. luteovirens* s. s.): CZECH REPUBLIC. Adamov, Josefovské údolí, Býčí skála, decaying trunk of *Carpinus*, *leg. et det.* A. Vágner (BRNM 603145); 17 May 1995, decaying trunk of *Fagus*, 19 June 2002, *leg. et det.* A. Vágner (BRNM 670848); fallen trunk of *Fagus*, 15 September 2011, *leg.* H. Ševčíková et V. Antonín, *det.* V. Antonín (BRNM 737386); Josefovské údolí, Slovenská stráň, decaying trunk of *Carpinus*, 17 September 1986, *leg. et det.* A. Vágner (BRNM 457767); decaying trunk of *Fagus*, 18 July 1990, *leg. et det.* V. Antonín (BRNM 523408); Horní Lomná, Mionší, decaying trunk of *Fagus*, 29 September 1992, *leg. et det.* V. Antonín (BRNM 571062); decaying trunk of *Fagus*, 16 June 2007, *leg.* L. Hagara, *det.* V. Antonín (BRNM 706722); Ivaň, Dolní Mušov, floodplain forest, decaying deciduous trunk, 29 June 2001, *leg. et det.* A. Vágner (BRNM 665359); Kladeruby nad Oslavou, Vlčí kopec, fallen *Fagus*, 28 September 1994, *leg. et det.* A. Vágner (BRNM 603007); Lanžhot, Ranšpurk, trunk of *Ulmus*, 5 October 1988, *leg. et det.* V. Antonín (BRNM 461736); dead trunk of *Ulmus*, 28 May 1993, *leg. et det.* V. Antonín (BRNM 576439); deciduous branch, 27 July 1993, *leg. et det.* V. Antonín (BRNM 576522); decaying deciduous trunk, two places, 24 May 1995, *leg. et det.* A. Vágner (BRNM 603178, 603179); Mladeč, NPR Vrapač, fallen deciduous trunk, 1 July 1999, *leg. et det.* A. Vágner (BRNM 648444); Nové Mlýny, Křivé jezero, floodplain forrest, fallen deciduous trunk, 16 June 2005, *leg. et det.* V. Antonín (BRNM 695486); Pivonice u Pohorské Vsi, Žofínský prales, dead trunk of *Fagus*, 17 September 2015, *leg. et det.* H. Ševčíková (BRNM 772294); fallen mosses trunk of *Fagus*, 17 September 2015, *leg.* V. Kunca, *det.* H. Ševčíková (BRNM 772060); Útěchov u Brna, Coufavá, decaying trunk of *Fagus*, 14 July 1984, *leg. et det.* A. Vágner (BRNM 457772); 30 September 1984, *leg. et det.* A. Vágner (BRNM 457765); 14 June 1986, *leg. et det.* A. Vágner

(BRNM 457759); Vilémovice, near Macocha, stump of *Fraxinus excelsior*, 20 September 1983, *leg.* D. Vágnerová, *det*. A. Vágner (BRNM 457758); Vranov, Jelení skok, decaying trunk of *Fagus*, 21 June 1986, *leg. et det*. A. Vágner (BRNM 457768); SLOVAKIA. Badín, Badínský prales, decaying trunk of *Fagus*, 22 August 1995, *leg. et det*. V. Antonín (BRNM 603576); (*Pluteus chrysophlebius – P. galeroides s.s.*): CZECH REPUBLIC. Lanžhot, Ranšpurk, fallen trunk of *Ulmus*, 19 September 1996, *leg.* V. Antonín, *det*. H. Ševčíková (BRNM 612145); ***P. cinereofuscus***: CZECH REPUBLIC. Mladá Boleslav, slope, mixed forest of *Tilia*, *Corylus*, *Ulmus*, *Carpinus*, *Quercus*, 13 July 2013, *leg.* S. Tutka, *det*. H. Ševčíková BRNM 751705; Habrůvka, Habrůvecká bučina, fallen trunk of *Fagus*, 6 September 2013, *leg. et det*. H. Ševčíková (BRNM 751723); ***P.* cf. *insidiosus***: CZECH REPUBLIC. Kulatý dub between Březina and Ochoz u Brna, fallen *Quercus*, 25 August 2016, *leg. et det*. H. Ševčíková (BRNM 781263); ***P. fenzlii***: HUNGARY. Vas, Hosszúpereszteg, on heap of sawdust, 7 October 1990, *leg.* P. Serediuk, *det*. J. Borovička (BP 88763 originally as *P. variabilicolor*); ***P. leoninus***: CZECH REPUBLIC. Brno, Baba, near U boudy, mixed forest, heap of branches of *Tilia*, *Quercus*, *Corylus*, 4 September 2014, *leg.* J. Hrabáková et H. Ševčíková (BRNM 766775); ibid, another heap of branches, 4 September 2014, *leg.* J. Hrabáková et H. Ševčíková (BRNM 788272); ***Pluteus romellii* var. *romellii***: CZECH REPUBLIC. Bílovice nad Svitavou, Anenské údolí, near path, mulch, 2 June 2015, *leg. et det*. M. Tomšovský (BRNM 771934); Brno, Líšeň, brushwood with *Populus tremulae* under Hády, deciduous branch, 6 June 2013, *leg.* F. Fejta, *det*. H. Ševčíková (BRNM 747550); Brno, Hády, deciduous forest near quarry, decayed deciduous trunk, 21 September 2013, M. Fejta, *det*. H. Ševčíková (BRNM 751776); Brno, between Hády and U Brněnky, on soil near deciduous twigs, 5 September 2013, *leg. et det*. H. Ševčíková BRNM (751889); Brno, Hádecká planinka, *Querceto-Carpinetum*, decayed deciduous woods, 13 May 2010, *leg. et det*. V. Antonín (BRNM 724855); decayed trunk of *Quercus petraea*, 11 August 2010, *leg. et det*. A. Vágner (BRNM 733091); Brno, Kohoutovický potok valley, decayed deciduous woods, 11 October 2001, *leg. et det*. Z. Bieberová (BRNM 728377); Brno, Bystrc, Rakovec valley, decayed woods of *Carpinus betulus*, 7 September 2012, *leg. et det*. V. Antonín et H. Ševčíková (BRNM 745972); Habrůvka, Habrůvecká bučina, near decayed trunk of *Fagus*, 8 October 2014, *leg. et det*. V. Antonín et H. Ševčíková (BRNM 767027); Hodonín, Doubrava, mixed forest on sandy soil, 20 June 1984, *leg. et det*. V. Antonín et A. Vágner (BRNM 305513); Kanice, U Brněnky, *Querceto-Carpinetum*, deciduous trunk, 5 September 2013, *leg. et det*. H. Ševčíková (BRNM 751731); Kosmonosy, obora, *Carpinus betulus*, 26 August 2013, *leg. et det*. S. Tutka (BRNM 761736); Lanžhot, Cahnov, trunk of *Quercus*, 11 April 2014, *leg. et det*. H. Ševčíková (BRNM 761731); Louka u Ostrohu, Háj u Louky, *Querceto-Carpinetum*; on soil, 2 June 2013, *leg. et det*. R. Maňák (BRNM 766577); Machnín, Hamrštejn u Liberce, deciduous forest, on soil, 25 August 2013, *leg.* S. Tutka, *det*. H. Ševčíková (BRNM 761735), ibid, under *Fagus*, (BRNM 767004); Mokrá, Mokerský les, *Querceto-Carpinetum*, decaying deciduous woods, 10 April 2001, *leg. et det*. A. Vágner (BRNM 665216); near quarry, on soil, 20 September 2013, *leg. et det*. H. Ševčíková (BRNM 751772); ibid, on soil, 19 November 2014, *leg. et det*. H. Ševčíková (BRNM 762111); Mokrá u Brna, Sivický les, on soil under *Picea abies*, *Quercus*, *Rubus*, 14 June 2006, *leg. et det*. A. Vágner (BRNM 699773); decaying deciduous branch, 17 August 2006, *leg. et det*. A. Vágner (BRNM 705298); Nevojice, Malhotky, decaying trunk of *Quercus*, 26 September 1997, *leg. et det*. Z. Bieberová (BRNM 728340); Ochoz u Brna, Údolí Říčky, under *Carpinus betulus*, 11 November 2001, *leg. et det*. A. Vágner (BRNM 667875); ibid, Zadní Hády, *Querceto-Carpinetum*, on soil, 31 May 1981, *leg. et det*. A. Vágner (BRNM 457750); ibid, decaying trunk *Quercus*, 22 June 2016, *leg. et det*. H. Ševčíková (BRNM 781181); ibid, Lysá hora, Údolí Říčky, decaying branch of *Corylus avellana*, 15 May 2014, *leg. et det*. H. Ševčíková (BRNM 761858); Prodašice, branch of *Populus tremula*, 7 September 2014, *leg. et det*. S. Tutka (BRNM 771985); Veselí nad Moravou, Hutník, mulch of *Populus nigra*, 1 November 2012, *leg. et det*. R. Maňák (BRNM 761840); Vápenný Podol, quarry, twig of *Quercus*, 1 June 2014, *leg. et det*. R. Doležal (BRNM 767024); SLOVAKIA. Ružomberok-Černová, Černovské lúky (Zrazy), pasture with grove of *Corylus* and *Crataegus*, fallen deciduous trunk, 3 April 2014, *leg. et det*. H. Ševčíková (BRNM 761711); ibid, deciduous twig (BRNM 761712); ROMANIA. Baile Tusnad, Muntii Harghita, in rupe "Stinca Soimilor" ad occidentem ab oppido Baile Tusnad versus, *Fagus* wood, 2 July 1986, *leg. et det*. V. Antonín (BRNM 398129); ***P. variabilicolor***: REPUBLIC OF KOREA. Taean Peninsula, Deoksung, Sudeoksa Monastery, mixed forest, dead trunk of *Castanea*, 7 August 2014, *leg.* V. Antonín, *det*. H. Ševčíková (BRNM 788273); SLOVAKIA. Snina, Hrb, heap of sawdust, 10 May 2010, *leg.* J. Pavlík, *det*. H. Ševčíková (BRNM 788274).

N o t e s . – According to our analysis, *P. romellii* (including the new variety) is a sister species to *P. aurantiorugosus* which was also demonstrated in the molecular study by Justo & al. (2011). As indicated by tree topology (Fig. 12), *P. romellii* shows some sequence divergence. The sequence of *P. romellii* var. *luteoalbus* completely matches the sequence FJ774073, belonging to a collection of *P. romellii* from Russia.

Pluteus romellii var. *luteoalbus* is characterized by a yellow pileus, a whitish stipe, a pileipellis in the form of a euhymeniderm and broadly clavate, broadly cylindrical, broadly utriform to utriform pleurocystidia. Cheilocystidia are narrowly to broadly clavate, utriform to cylindrical. Phylogenetically and microscopically, *P. romellii* var. *luteoalbus* is identical to *P. romellii* var. *romellii*. Macroscopically, the yellow pileus and whitish stipe are significant for differentiating of this new variety because *P. romellii* var. *romellii* has a brown pileus and a yellow stipe. *Pluteus romellii* f. *albidus* (Britzelm.) Ferisin is an albinotic form of *P. romellii*, it has a white pileus and stipe, and a whitish context. *Pluteus romellii* is commonly found on soil, woodchips or decayed wood. *Pluteus romellii* f. *albidus* is known to grow on fallen stem of a deciduous tree. *Pluteus romellii* var. *luteoalbus* was found on decayed deciduous tree, but its growth on soil or on woodchips cannot be excluded.

Pluteus chrysophlebius (Berk. & M.A. Curtis) Sacc. is macroscopically very similar to *P. romellii* var. *luteoalbus*. In European literature, species with a yellow pileus and a pileipellis composed of

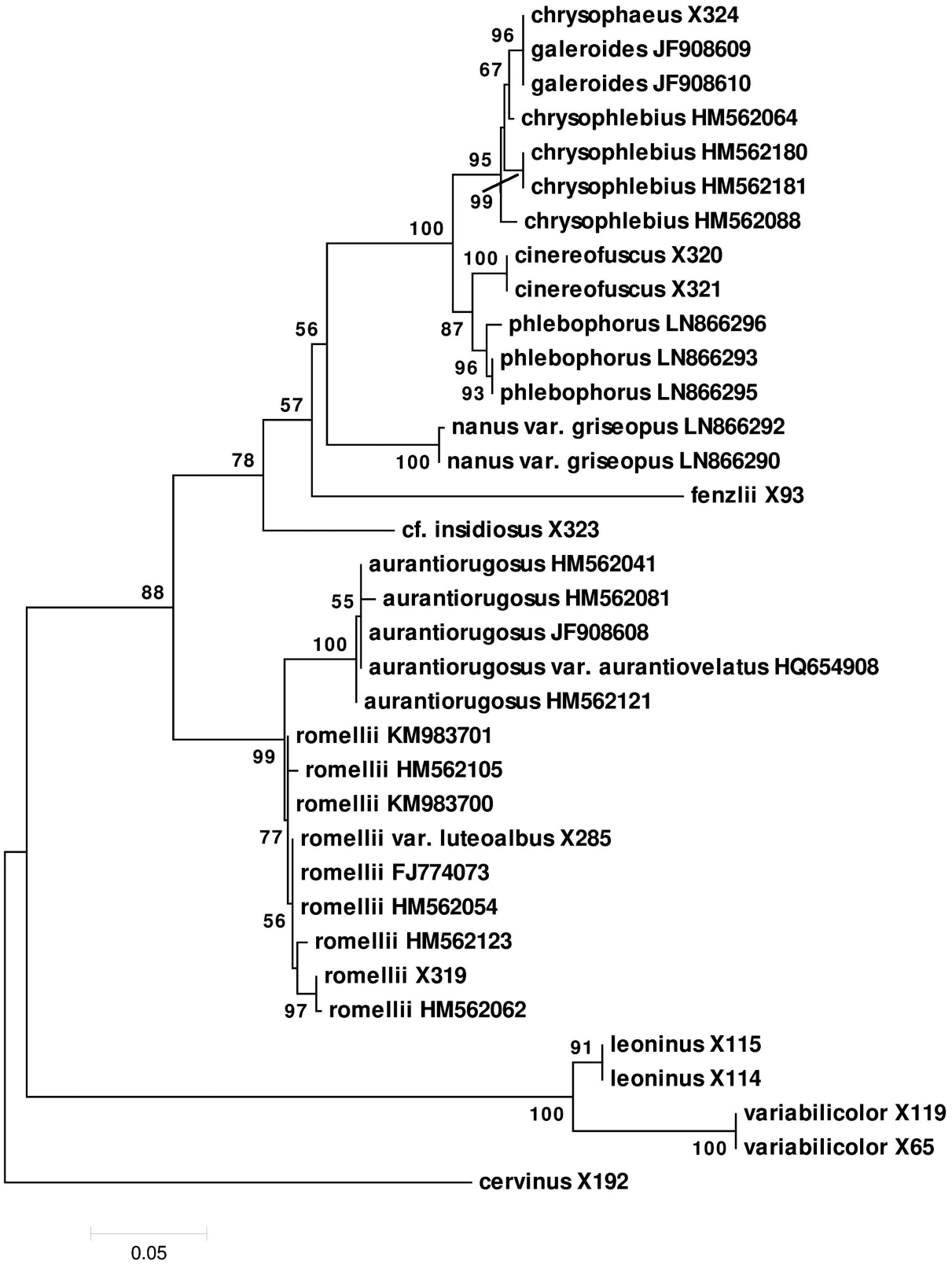

Fig. 12. Phylogenetic placement of *Pluteus romellii* var. *luteoalbus* within closely related *Pluteus* species inferred from a maximum likelihood analysis of the ITS rDNA molecular data using MEGA7.

spheropedunculate elements is known as *P. chrysophaeus* (Schaeff.) Quél., but Justo & al. (2011: 469) selected a lectotype for this species having the brown-pileus. Orton (1986) distinguished three taxa within the *P. chrysophaeus*: *P. luteovirens* Rea, *P. galeroides* P.D. Orton, and *P. xanthophaeus* P.D. Orton. *Pluteus luteovirens*, with a lemon-yellow pileus (when it has not greenish-yellow tinge) and a whitish stipe and flesh, is macroscopically the most similar to *P. romellii* var. *luteoalbus*. However, Vellinga & Schreurs (1985) synonymized these three taxa under *P. chrysophaeus*. Additionally, Justo & al. (2011) recently pointed out the similarity of the American *P. chrysophlebius* (Berk. & M.A. Curtis) Sacc. and the European *P. chrysophaeus* sensu Vellinga & Schreurs; for the final solution further studies are therefore necessary. With regard to our new variety of *P. romellii*, taxa of *P. chrysophlebius* complex have mostly lageniform to fusiform or broadly fusiform pleurocystidia. Broadly clavate, broadly cylindrical to (broadly) utriform pleurocystidia of *P. romellii* thus represent a significant microscopical difference.

The phylogenetically closest species to *P. romellii* is *P. aurantiorugosus* (Trog) Sacc. Macroscopically, colours of the pileus have red or orange tinges and the stipe sometimes has yellow or orange tinges. Microscopically, pleurocystidia of *P. aurantiorugosus* are mostly vesiculose-fusiform to clavate-fusiform.

Further species with yellow pilei are *P. leoninus* (Schaeff.) P. Kumm., *P. fenzlii* (Schulzer) Corriol & P.-A. Moreau, and *P. variabilicolor* Babos. However, pileipellis of these taxa is not composed of spheropedunculate elements and also differ by the cystidia shape. Moreover, *Pluteus fenzlii* is macroscopically different by having annulus on stipe and *P. variabilicolor* by dark floccules on stipe.

Authors: H. Ševčíková, T. Konvalinková & J. Borovička

Sclerostagonospora elegiae Marinc., M.J. Wingf. & Crous, **sp. nov.** – Figs. 13F, 15A–C, 16A
MycoBank no.: MB 823475

Description. – Conidiomata *in planta* pycnidial, scattered or gregarious, subepidermal, remaining immersed, with the tip of the ostiolar papilla reaching the surface, in vertical section subglobose to globose, 190–240 × 170–215 µm; peridium pseudoparenchymatous, consisting of a few layers of brown, moderately thick-walled, compressed cells (less compressed towards the apex), 8–11 µm thick, inside lined with a layer of hyaline fertile cells. – Conidiogenous cells blastic, hyaline, discrete, doliiform, 4–6 × 2.5–3 µm. – Conidia brown, fusiform to cylindrical, the apex pointed to rounded, the base truncated, (12.5)14–15(17) × (4)5(6) µm, smooth, 3-septate.

Etymology. – Named after the host genus, *Elegia*.

Culture characteristics. – Colonies on 2 % malt extract agar (MEA) at 20 °C showing optimum growth reaching 37.7 mm in 13 days in the dark, mycelium cottony with raised elevation, showing circular growth with smooth to undulate margin, above greenish grey becoming paler towards the edge, reverse olivaceous, no growth at 30 °C and 35 °C, on oatmeal agar (OA) at 20 °C showing optimum growth reaching 53 mm, above greenish grey to iron grey, reverse greenish black, on potato dextrose agar (PDA) at 20 °C showing optimum growth reaching 44 mm, mycelium cottony with velvety inner circle, above smoky grey with iron grey, reverse olivaceous mouse grey with paler edge, sterile on MEA, OA, PDA, and CLA (carnation leaf agar).

Material examined. – SOUTH AFRICA. Western Cape province, Kirstenbosch National Botanical Garden, culm litter of *Elegia equisetacea*, 3 December 2001, *leg.* S. Marincowitz, SL937, holotype, PREM 58934, living culture ex-holotype CBS 118142 = CMW 18281.

Notes. – *Sclerostagonospora* is characterized by pycnidial conidiomata, holoblastic conidiogenous cells, and pigmented conidia. Conidial morphology of known species is diverse, from elongated to short, smooth to verruculose or striated, lightly pigmented to dark pigmented, and 1- to multi-septation (Fig.13).

Sclerostagonospora Höhn. was treated as a synonym of *Stagonospora* until Sutton (1980) separated them based on the pigmented conidia of the former. At the same time he relocated some of *nomen rejiciendum Hendersonia* into the genus. A total of 12 species are currently registered in MycoBank under *Sclerostagonospora*, of which six are relocated from *Hendersonia*, namely, *S. sabaleos*, *S. donacis*, *S. heraclei*, *S. opuntiae*, *S. salsolae*, and *S. sessilis* (Höhnel 1917, Gallego et al. 1986a, b, Huhndorf 1992, Schwarczinger et al. 2000). So far only three species, *S. ericae*, *S. cycadis* and *S. phragmiticola,* are provided with DNA sequence data and living cultures (Crous et al. 2011, 2015, 2016; Quaedvlieg et al. 2013).

Two sexual morphs *Leptosphaeria leucadendri* (*Pleosporales*) and *Montagnula opuntiae* (*Pleosporales*) are linked to *Sclerostagonospora* (Crous & Palm 1999, Huhndorf 1992). A recent study based on sequences of partial 28S rRNA and *rpb*2 genes

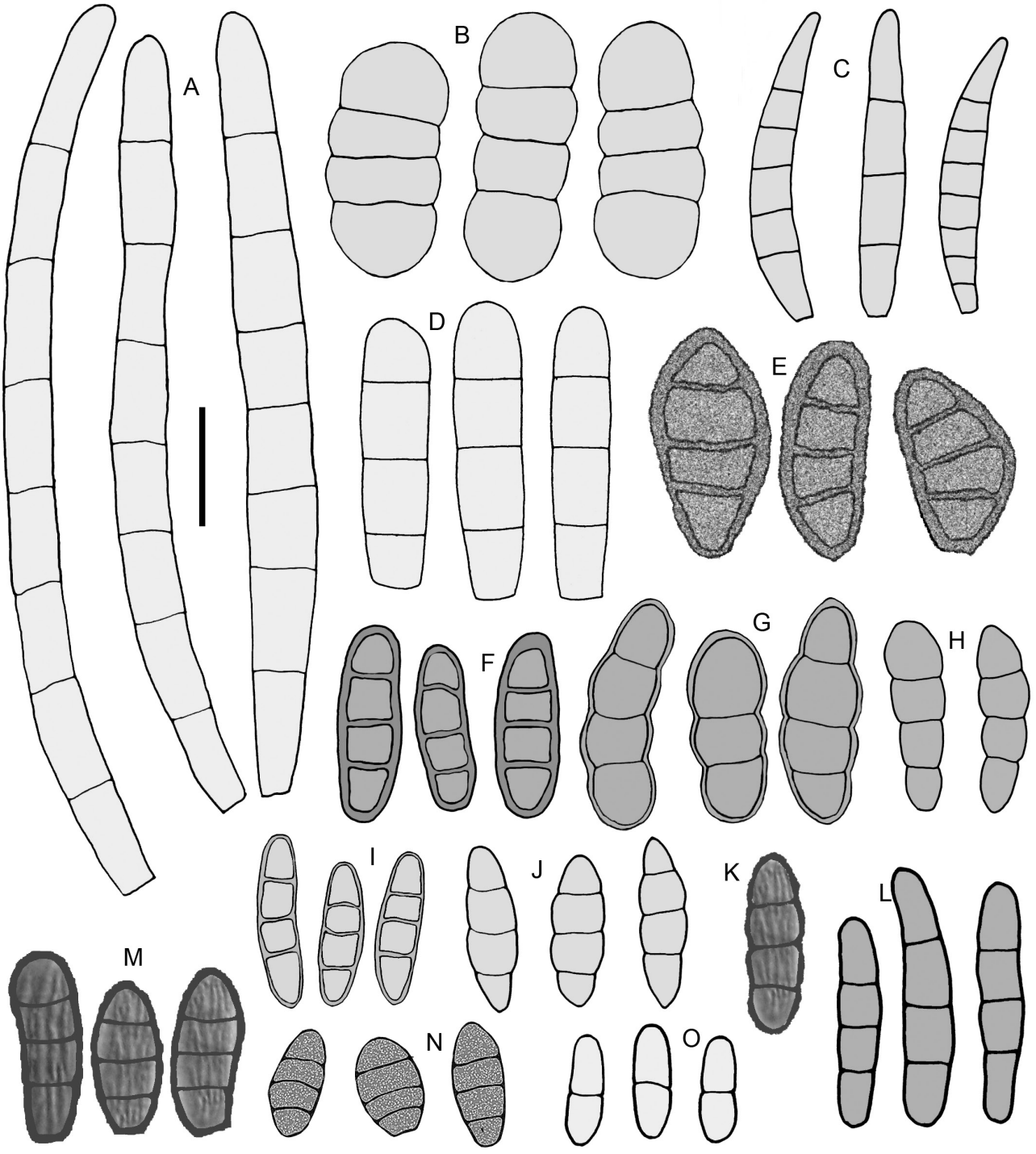

Fig. 13. Line drawings of the conidia of *Sclerostagonospora* spp. from previous photos and line drawings. **A.** *S. leucadendri* (Crous & Palm 1999). **B.** *S. salsolae* (Schwarczinger et al. 2000). **C.** *S. centaureae* (Sameva & Vanev 1998). **D.** *S. heraclei* (Sutton 1980). **E.** *S. pinguis* (this study). **F.** *S. elegiae* (this study). **G.** *S. sessilis* (Gallego et al. 1986a). **H.** *S. sabaleos* (Gallego et al. 1986b). **I.** *S. fusiformis* (this study). **J.** *S. donacis* (Gallego et al. 1986a). **K.** *S. opuntiae* (Huhndorf 1992). **L.** *S. phragmiticola* (Quaedvlieq et al. 2013). **M.** *S. sulcata* (this study). **N.** *S. cycadis* (Crous et al. 2011, 2015). **O.** *S. ericae* (Crous et al. 2016). Scale bar 10 µm.

showed that a *Sclerostagonospora*, *S. phragmiticola*, resides within the *Phaeosphaeriaceae* (*Pleosporales*), suggesting a sexual morph of the genus is phaeosphaeria-like (Quaedvlieg et al. 2013). However, the lack of living culture or DNA sequence data of the type species, *S. heraclei*, makes the concept of the genus and its status in the family unsettled (Crous et al. 2016).

Several fungi were isolated from the culm litter of Restionaceae (Poales) in South Africa, of which morphological features resemble those of *Sclerostagonospora*. Phylogenetic analysis based on ITS sequence data, with recently introduced species and those in GenBank, confirmed these isolates are the members of *Sclerostagonospora* (Fig. 14). Based on both morphological and molecular studies, four species have been identified and proposed as new species in this study.

Sclerostagonospora elegiae can be distinguished morphologically by its smooth and brown conidia (Figs. 13F, 15C). Phylogenetic analysis (Fig. 14) using ITS sequence data indicated that CBS 118142 clusters distinctly from the other known species. This isolate differs from its closest phylogenetic neighbour *S. pinguis* (CBS 118146) by 23 bp in ITS.

Sclerostagonospora fusiformis Marinc., M.J. Wingf. & Crous, **sp. nov.** – Figs. 13I, 15D–F, 16B
MycoBank no.: MB 823476

Description. – Conidiomata *in planta* pycnidial, scattered, superficial with the base firmly attached to the substrate, in vertical section subglobose with an ostiolar pore, 110–130 × 115–135 µm; peridium pseudoparenchymatous, 19–20 µm thick throughout the conidioma except for the basal re-

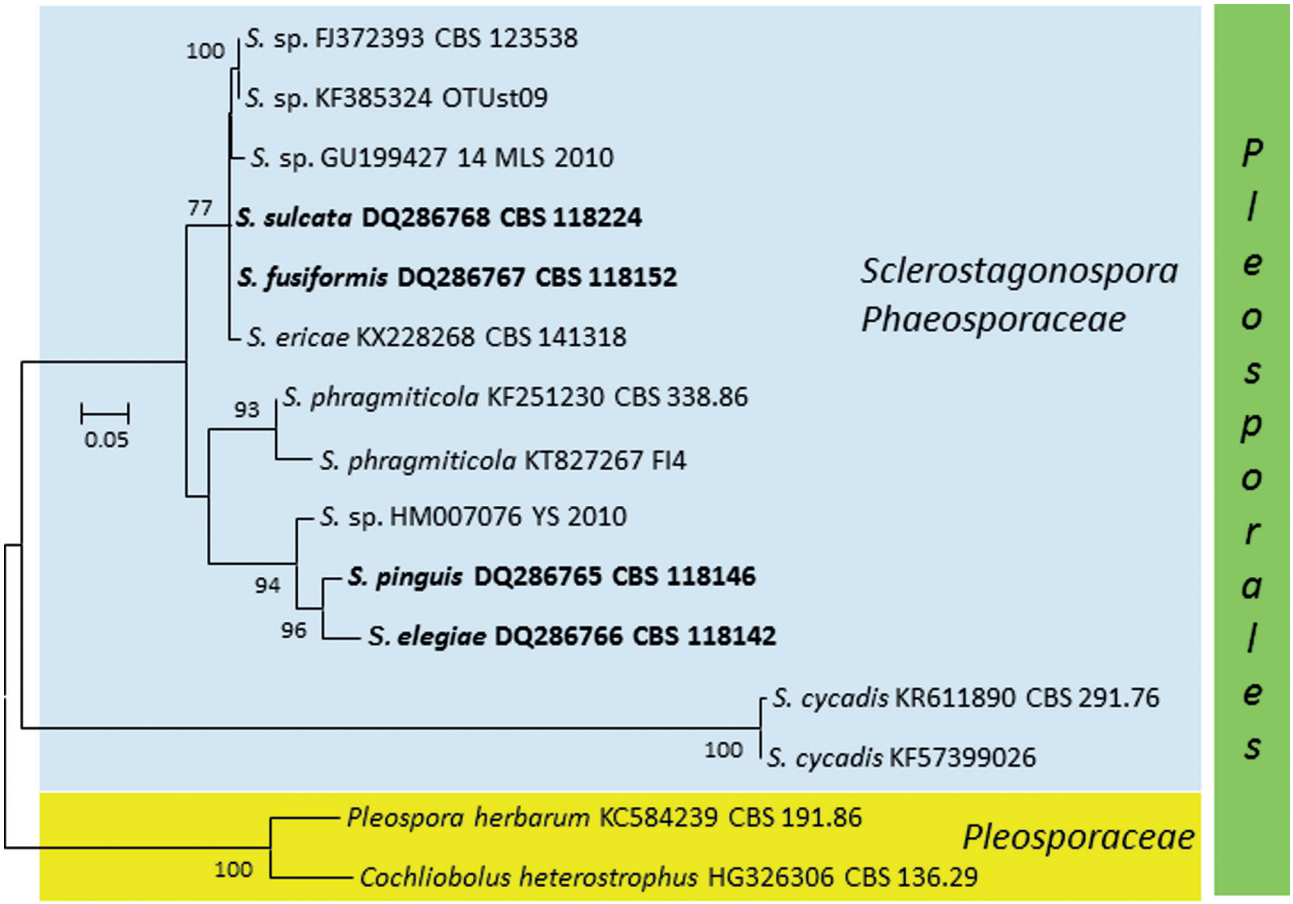

Fig. 14. Phylogram obtained from Maximum likelihood (ML) analyses of ITS region using RA×ML V8.2.4 on the CIPRES Science Gateway v3.3 (Stamatakis 2014). Novel sequences are printed in bold type. ML bootstrap support values (1000 replicates) above 70 % are indicated at the nodes. Scale bar = total nucleotide difference between taxa. The tree was rooted to *Phaeosphaeria herbarum* and *Cochliobolus heterostrophus*.

gion attached to the substrate 10–15 µm thick, consisting of a few layers of pale brown, moderately thick-walled cells outlined with a few layers of brown, thick-walled cells, the base lack outer layer, the innermost layer consisted of a hyaline, fertile cells. – Conidiogenous cells blastic, hyaline, discrete, ampulliform, 3–4.5 × 3–5 µm. – Conidia yellow to pale brown, fusiform, straight or slightly curved, the apex pointed to rounded, the base truncated, (11)13(15) × (3)3.5–4 µm, 1–3-septate, smooth.

Etymology. – Name refers to the fusiform shape of conidia.

Culture characteristics. – Colonies on 2 % MEA at 25 °C showing optimum growth reaching 15 mm in 13 days in the dark, mycelium velvety, with slightly raised elevation, showing circular growth with smooth margin, aerial mycelium dense, above hazel, reverse olivaceous, no growth at 30 °C and 35 °C, on OA at 25 °C showing optimum growth reaching 23.5 mm, above and reverse greenish grey, on PDA at 25 °C showing optimum growth reaching 19.3 mm, above and reverse saffron, sterile on MEA, OA, and PDA, fertile on CLA.

Material examined. – SOUTH AFRICA. Western Cape province, Kirstenbosch National Botanical Garden, culm litter of *Thamnochortus spicigerus*, 3 December 2001, *leg*. S. Marincowitz, SL917, holotype, PREM 58933, living culture ex-holotype CBS 118152 = CMW 18025.

Notes. – *Sclerostagonospora fusiformis* has smooth, pale brown and fusiform conidia which distinguishes it from the known species (Figs. 13I, 15F). Due to the lack of specimens a limited number of fruiting structures in host tissue were measured.

Phylogenetic analysis (Fig. 14) using ITS sequence data indicated that CBS 118152 clusters distinctly from the other known species. This isolate differs from its closest phylogenetic neighbour *S. ericae* (CBS 141318) by 6 bp in ITS.

Sclerostagonospora pinguis Marinc., M.J. Wingf. & Crous, **sp. nov.** – Figs. 13E, 15G–I, 16C
MycoBank no.: MB 823477

Description. – Conidiomata *in planta* pycnidial, scattered or gregarious, subepidermal, remaining immersed with the tip of the ostiolar papilla reaching the surface or becoming superficial by eroding of the host tissue, in vertical section subglobose, 85–145 × 95–240 µm; peridium pseudoparenchymatous, uneven in thickness, around the ostiole 15–22 µm thick, consisting of several layers of brown, thick-walled cells, lateral tissue 12–16 µm thick, consisting of a few layers of brown, moderately thick-walled, compressed cells, at the base 5–10 µm thick, a few layers of hyaline to pale brown, moderately thick-walled, highly compressed cells, lined with a layer of hyaline, fertile cells inside. – Conidiogenous cells blastic, hyaline, discrete, ampulliform, 3.5–10 × 2–4 µm. – Conidia subhyaline to pale brown at young, becoming dark brown when mature, fusiform to ellipsoidal, often asymmetrical, the apex pointed, the base truncated, (16)18.5–19(21.5) × (6)8–9 µm (avg. 18.9 × 9 µm), 3-septate, verruculose, thick-walled.

Etymology. – Name refers to a plump feature of conidia.

Culture characteristics. – Colonies on 2 % MEA at 20 °C showing optimum growth reaching 44 mm in 13 days in the dark, mycelium cottony with slightly raised elevation, showing circular growth with smooth margin, above greenish grey becoming paler towards the edge, often with white patches, reverse olivaceous, no growth at 30 °C and 35 °C, on OA at 20 °C showing optimum growth reaching 52 mm, colony features similar to that on MEA, on PDA at 20 °C showing optimum growth reaching 41.8 mm, above pale purplish grey, reverse greenish black with paler margin, sterile on all MEA, OA, PDA, and CLA.

Material examined. – SOUTH AFRICA. Western Cape province, Jonkershoek Nature Reserve, culm litter of *Cannomois virgata*, 15 June 2001, *leg*. S. Marincowitz, SL744, holotype, PREM 58931, living culture ex-holotype CBS 118146 = CMW 17948; culm litter of *Ischyrolepis* cf. *gaudichaudiana*, 31 July 2001, *leg*. S. Marincowitz, SL881, PREM 58932.

Notes. – *Sclerostagonospora pinguis* is distinguished by its brown, verruculose, and thick-walled conidia (Figs. 13E, 15I).

Phylogenetic analysis (Fig. 14) using ITS sequence data indicated that CBS 118146 clusters distinctly from the other known species. This isolate differs from its closest phylogenetic neighbour *S. elegiae* (CBS 118142) by 23 bp in ITS.

Sclerostagonospora sulcata Marinc., M.J. Wingf. & Crous, **sp. nov.** – Figs. 13M, 15J–L, 16D
MycoBank no.: MB 823478

Description. – Conidiomata *in planta* pycnidial, scattered or gregarious, subepidermal, remaining immersed with the tip of the ostiolar papilla or pore reaching the surface, in vertical section globose to ovoid, occasionally loculated, 60–100 × 50–90 µm; peridium pseudoparenchymatous, uneven in thickness, around the ostiole 5.5–10 µm thick, consisting of a few layers of dark brown, thick-walled cells, lateral and basal tissue 8–9 µm thick, consisting of a few layers of hyaline to slightly pigmented, moderately thick-walled cells, the inner-

most layer composed of a layer of hyaline, fertile cells. – Conidiogenous cells blastic, hyaline, discrete, cylindrical to doliiform, 3–10 × 2.5–4 µm. – Conidia brown, cylindrical, straight or slightly curved, the apex rounded, tapering to the truncate base with minute marginal frills, (13)14–15(17) × (4)5–6(7) µm, 3-septate, slightly constricted at each septum, vertically furrowed, thick-walled.

Etymology. – Name refers to a furrowed surface of conidia.

Culture characteristics. – Colonies on 2 % MEA at 25 °C showing optimum growth reaching 17.2 mm in 13 days in the dark, mycelium velvety, showing circular growth with smooth to undulate edge, aerial mycelium dense, above honey to dark brown with white edge, reverse sepia, no growth at 35 °C, on OA at 20 °C showing optimum growth reaching 50.8 mm, mycelium woolly, flat, aerial mycelium medium sparse, above smoky grey to grey olivaceous, reverse sepia, on PDA at 20 °C showing optimum growth reaching 45.8 mm, above saffron with ochreous patches, reverse sepia with paler edge, slight pigmentation on medium on MEA and on PDA at 25 °C, sterile on MEA, OA, PDA, and CLA.

Material examined. – SOUTH AFRICA. Western Cape province, Kirstenbosch National Botanical Garden, culm litter of *Ischyrolepis subverticellata*, 3 December 2001, *leg.* S. Marincowitz, SL1101, holotype, PREM 58935, living culture ex-holotype, CBS 118224 = CMW 18063.

Notes. – *Sclerostagonospora sulcata* has furrowed ornamentation in conidia, which reminds of *S. opuntiae*, however differs in its truncated base with minute marginal frill (Figs. 13M, 15L). This fungus shows better growth on OA and PDA (45–50 mm) than on MEA (17 mm).

Phylogenetic analysis (Fig. 14) data indicated that CBS 118224 is identical with *S. fusiformis* (CBS 118152) in ITS sequence. However, CBS 118224 is introduced as a new species based on morphological features. CBS 118224 has brown, cylindrical and sulcate conidia, whereas *S. fusiformis* has pale brown, fusiform and smooth conidia.

The same isolates representing four new *Sclerostagonospora* spp. in this study were also examined by Crous et al. (2012). They sequenced the ITS and LSU regions of the isolates and the sequence data were identical to the ones produced in this study, except for *S. sulcata* (CBS 118224) of which sequences showed some discrepancy in both gene regions. The reason of this discrepancy needs a further investigation.

Authors: S. Marincowitz, F. Jami, M.J. Wingfield & P.W. Crous

Interesting taxonomical notes, host and geographical records

Cortinarius scaurocaninus Chevassut & Rob. Henry, Doc. Mycol. 12 (no. 47): 25 (1982). – Fig. 17

Synonyms. – *Cortinarius glaucopus* var. *olivaceus* f. *ingratus* Moënne-Locc., *Cortinarius olidovolvatus* Bon &Trescol s. auct.

Material examined. – AUSTRIA. Styria, Bad Gleichenberg, Kurpark, near *Quercus* (*Fagus, Carpinus*), 22 October 1994, *leg.* W. & S. Klofac, WU 13419, Genbank no. MG489871. The investigated collection was characterized by a strongly innately fibrillose pileus, absence of blue-violet colours, a stipe base with a marginate bulb, abundant veil at the bulb margin, dark brown reaction of potassium hydroxyde on pileus surface and stipe base and Lugol negative with NH_3.

Notes. – In the course of the **A**ustrian **B**arcode **O**f **L**ife project, ABOL (https://www.abol.ac.at/en/), specimens of the genus *Cortinarius* were sequenced. It turned out that the ITS sequence of a collection, morphologically determined as *C. glaucopus* var. *acyaneus*, because of lack of blueish colours, matched 100 % with the *C. scaurocaninus* sequence KF732641 (Limatainen et al. 2014). *Cortinarius scaurocaninus* was described from the Mediterranean area and is a member of the complicated *C. glaucopus* alliance. It is characterized by ample veil on young basidiomata, very prominently innately fibrillose pileus surface, only very young bluish lamellae and bluish hues on the stipe and in the stipe context, and brown reaction of potassium hydroxyde on pileus surface (Schmidt-Stohn et al. 2016). Ecologically, it forms ectomycorrhizae with *Quercus* species. It occurs in warm-toned, Central European and Mediterranean deciduous forests over limestone and silicate, mostly near *Quercus* and *Carpinus,* once also near *Fagus*. So far collections are known from Germany, France, Italy, Spain and Hungary (Schmidt-Stohn et al. 2016). This is the first record of this species for Austria.

Author: I. Krisai-Greilhuber

Humicola grisea Traaen, Nytt Mag. Natur. 52: 34 (1914). – Fig. 18

Description. – Vegetative hyphae septate, branched, straight to flexuous, hyaline to light olivaceous brown, smooth to verruculose, thin-walled, 1.5–4.5 µm wide, often with thick, dark septa. Conidiogenous cells mono- to polyblastic, scattered or forming more or less dense clusters, arising laterally at right angles from undifferentiated hyphae, but sometimes terminal or intercalary, mostly subcylindrical to clavate, light olivaceous to dark olivaceous brown, smooth to verruculose, thin-

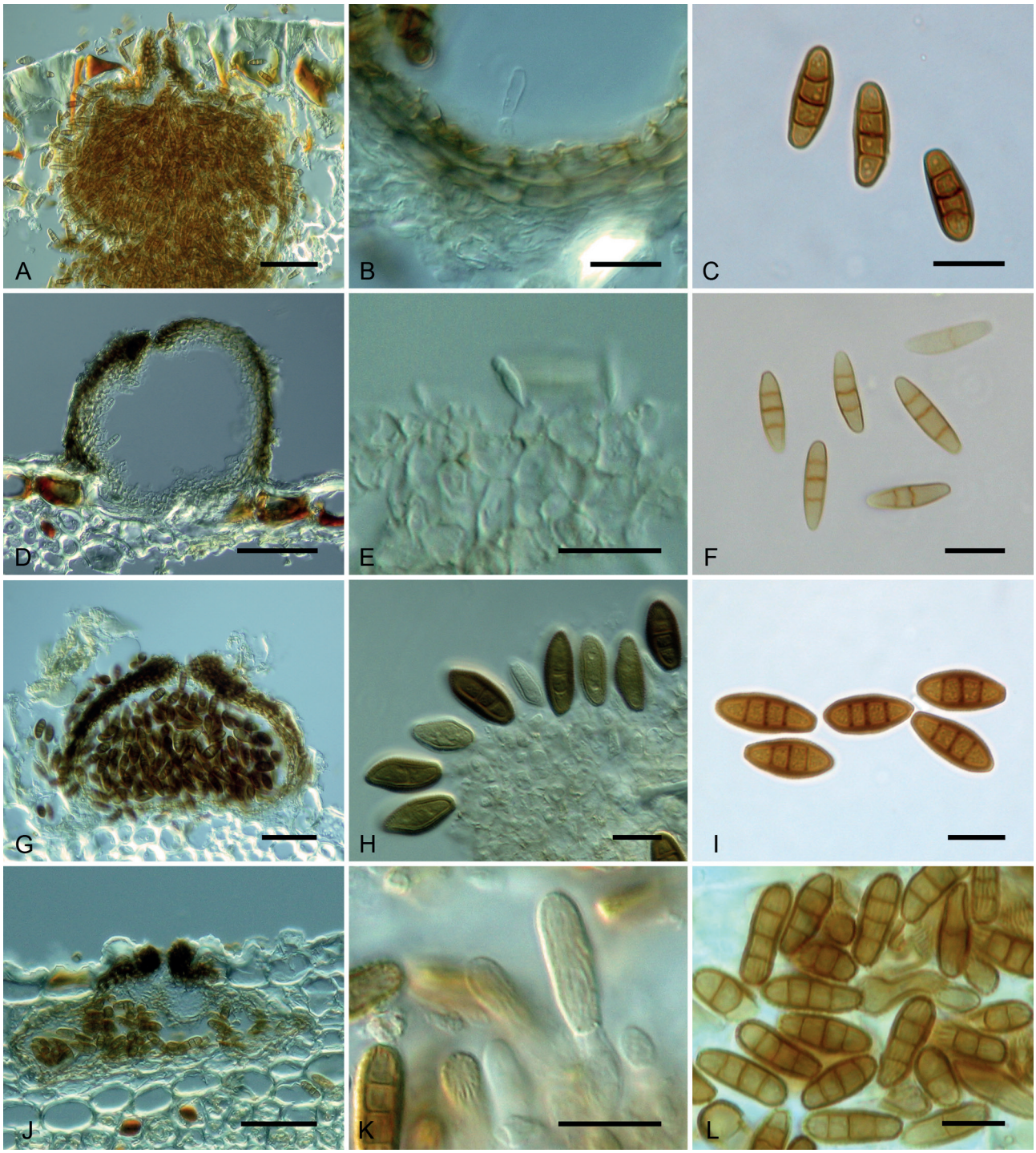

Fig. 15. Microscopic images of *Sclerostagonospora* species from restios. **A–C.** *S. elegiae*, **D–F.** *S. fusiformis*, **G–I.** *S. pinguis*, **J–L.** *S. sulcata*. **A, D, G. J.** Vertical section of conidioma, **B, E, H, K.** Conidiogenous cells, **C, F, I, L.** Conidia (in bright field). Scale bars: A, D, G, J 50 µm; B, C, E, F, H, I, K, L 10 µm.

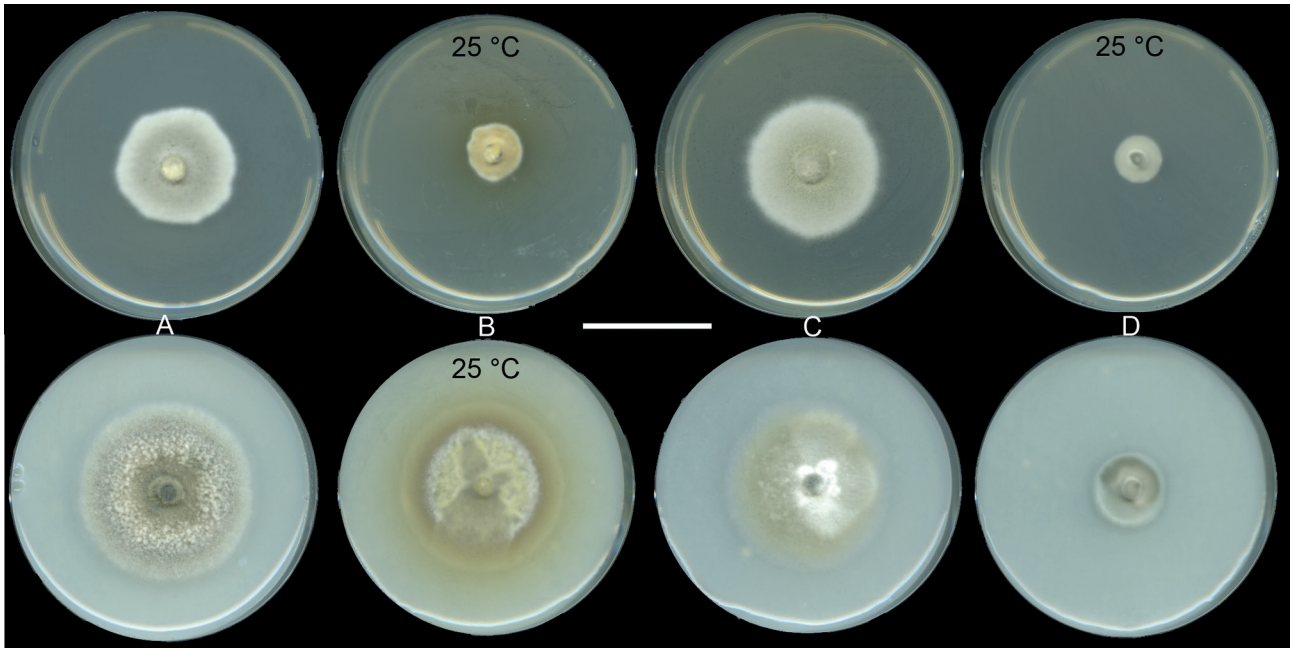

Fig. 16. Cultures with optimum growth on 2 % MEA (upper) and on OA (lower) in the dark in 13 days at 20 °C except for the ones indicated as 25 °C. **A.** *S. elegiae*, **B.** *S. fusiformis*, **C.** *S. pinguis*, **D.** *S. sulcata*. Scale bar 20 mm.

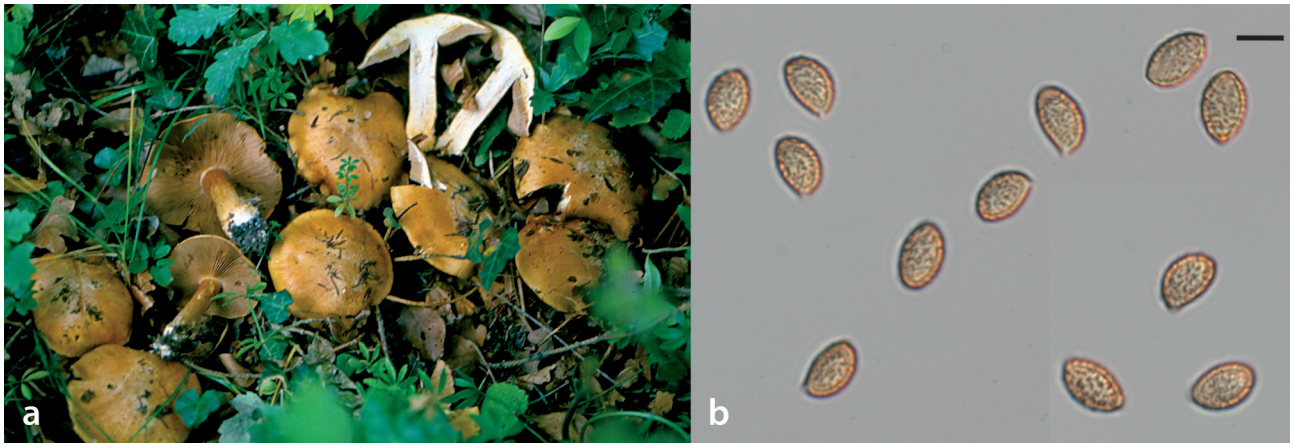

Fig. 17. *Cortinarius scaurocaninus*, WU 13419. **a.** Basidiomata, phot. W. Klofac. **b.** Spores, scale bar 5 µm.

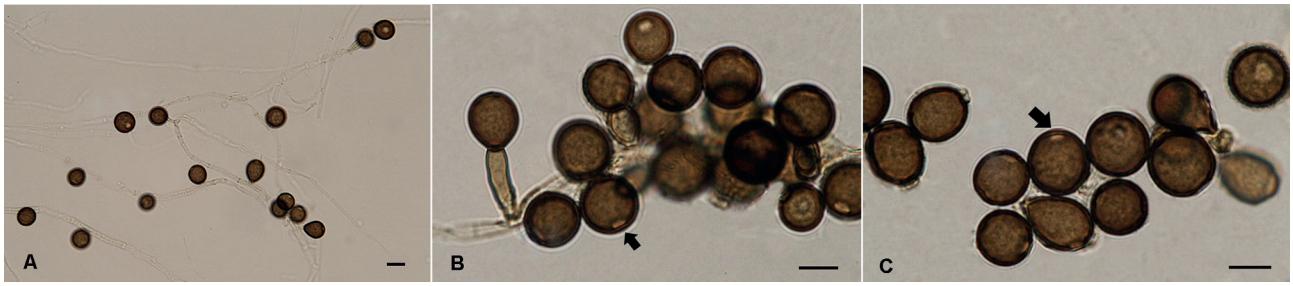

Fig. 18. *Humicola grisea* (CCCT 17.02). **A, B.** Fertile hyphae, conidiogenous cells and conidia. **C.** Conidia. Scale bars 10 µm. The arrows in B and C show conidial germ pores.

to thick-walled, 1–18 × 2–7 µm. Conidia almost always solitary, very rarely forming chains of 2–3, dry, globose to dacryoid, aseptate, pale olivaceous brown to dark brown, smooth to inconspicuously verruculose, 9–14(17.5) × 8–13.5(15.5) µm, with 1(2) conspicuous germ pore(s) 2–4 µm wide.

Culture characteristics. – Colonies after 7 d at 25 °C attaining 41 mm. diam. on MEA and 37 mm. on PDA. On MEA velvety, dark grey to black at the centre, with abundant drops of a colourless exudate, light grey to whitish towards the periphery, with a slightly lobulated margin; reverse black with a light grey margin. On PDA velvety to cottony, umbonate, dark grey at the centre, light brownish grey to light grey at the periphery, with a fimbriate margin; reverse black with a light brownish grey to light grey margin.

Material examined. – CHILE, Región Metropolitana, Santiago, from decaying bark of unidentified Arecaceae on soil, 27 April 2015, *leg.* H. Madrid (culture CCCT 17.02).

Notes. – During a taxonomic study of saprobic fungi in central Chile, an interesting dematiaceous hyphomycete was isolated from decaying palm bark (CCCT 17.02). The fungus produced abundant whitish mycelium on the natural substrate after 3 weeks of incubation in a moist chamber at room temperature. This strain was originally identified as "*Gilmaniella* sp." on account of its mono- to polyblastic cells giving rise to one-celled, mostly globoid, melanised conidia with conspicuous germ pores (Barron 1964, Seifert et al. 2011). Conidial dimensions were clearly different from those of the currently accepted species (Barron 1964, Moustafa 1975, Sivanesan & Sutton 1985, Moustafa & Ezz-Eldin 1989, Umali et al. 1998, Dubey et al. 2011, Goh et al. 2013) and this initially led us to suspect that it was a novel taxon.

A BLAST search, however, revealed that the ITS sequence of CCCT 17.02 (GenBank KU705826) was 100 % identical to that of an authentic, probably ex-type strain of *Humicola grisea*, CBS 119.14 (GenBank AY706334). This finding was surprising, since the presence of conidial germ pores has been considered as the main morphological feature separating the genus *Gilmaniella* from *Humicola* (Ellis 1971, Seifert et al. 2011). Other close matches to the Chilean strain were *Chaetomium vitellinum* CBS 250.85 (GenBank JX280859, 99 % identical), *C. crispatum* CBS 408.81 (GenBank JX280781, 99 % identical) and *Thielavia antarctica* CBS 123565 (GenBank KM655343, 98 % identical), indicating affinities to the Chaetomiaceae, where the type species of *Humicola*, *H. fuscoatra*, resides (Wang et al. 2016). We also attempted to generate ITS and LSU sequences from the ex-type strain of *Gilmaniella humicola*, CBS 220.65, the type species of *Gilmaniella*. Sequences were not of optimal quality, but BLAST searches with the preliminary ITS and LSU sequences suggested affinities to species traditionally placed in Lasiosphaeriaceae, with the closest matches being members of a phylogenetic group named "clade A" in Cai et al. (2006). This clade includes an assemblage of morphologically diverse species in polyphyletic sexually-typified genera such as *Apiosordaria*, *Cercophora*, *Podospora* and *Zopfiella*, as well as asexual morphs referred to as *Cladorrhinum*, humicola-like or chrysosporium-like (Guarro et al. 1991, Cai et al. 2006, Madrid et al. 2011). The definitive phylogenetic placement of *G. humicola* requires further study, and we will attempt to generate new ITS and LSU sequences for this fungus. An ITS-based tree showing the placement of *H. grisea* among other conidial and sexual members of Chaetomiaceae has been published in Nonaka et al. (2012), and we consider it unnecessary to include a similar phylogenetic analysis herein.

Micromorphological features of CCCT 17.02 were described from cultures on water agar with sterilized pine needles after 7 d at 25 °C. Colonies on this medium produced very scarce, sparse, mostly immersed mycelium, appearing practically translucent to the naked eye, except for areas with clusters of dark brown conidia. Therefore, we preferred to describe colonies on more nutritive media, i.e. MEA and PDA, where they appeared richer in texture and colour. The morphology of strain CCCT 17.02 (Fig. 18) suggests that the presence or absence of conidial germ pores is not a reliable feature to distinguish the genera *Gilmaniella* and *Humicola*. Although *H. grisea* traditionally has been considered to lack conidial germ pores (Ellis 1971, Seifert et al. 2011), these structures can be observed in microphotographs from the ex-type strain published by White & Downing (1953). Those authors, however, did not mention germ pores in their description of the fungus. The type species of *Gilmaniella*, *G. humicola*, produces a conidiogenous apparatus formed by inflated cells (Barron 1964), which has not been described in *Humicola*. This character might be more helpful in separating the genera *Gilmaniella* and *Humicola*, but a detailed study of all species available in culture is necessary to corroborate this hypothesis.

The conidial size described for *H. grisea* by Traaen (1914) and Ellis (1971), i.e. 12–17 µm diam., closely resembles that of CCCT 17.02 and so the identification of this species is supported by both morphology and DNA sequence data. A phialidic synasexual stage illustrated in Ellis (1971) was

rarely observed in culture, but it was absent in the slides used for the species description provided herein. *Humicola grisea* is a strongly cellulolytic fungus which might deserve further studies due to its potential biotechnological applications (White & Downing 1953). It has a widespread geographical distribution and has been reported from soil, wood and plant debris mainly from regions with cold winters in Europe and North America (White & Downing 1953, Ellis 1971). This taxon, however, has not been mentioned in comprehensive lists of fungal species from Chile (Mujica et al. 1980, Lazo 1996, Minter & Peredo Lopez 2006) and represents an interesting new record.

Authors: H. Madrid, A. Kolecka & T. Boekhout

there are many lichenologically unexplored parts needed to be studied in the country.

Twenty taxa of *Opegrapha*, and 57 taxa of *Rinodina* have thus far been reported from Turkey. Although more than 1650 lichen taxa have been noted from Turkey (Yazici & Aptroot 2015), only six lichen taxa have thus far been reported from the Muş region (Yazici & Aslan 2016a,b), and 31 lichen species were noted from Bitlis region (Çobanoğlu 2005, Çobanoğlu & Yavuz 2007, Vondrák et al. 2012). Within our projects "Lichen flora of Muş and Bitlis Provinces" we identified two lichens as new records for Turkey. *Opegrapha parasitica* is one of them. It is known from Europe (England, France, Germany, Greece, Ireland, Norway, Poland, Spain, now also

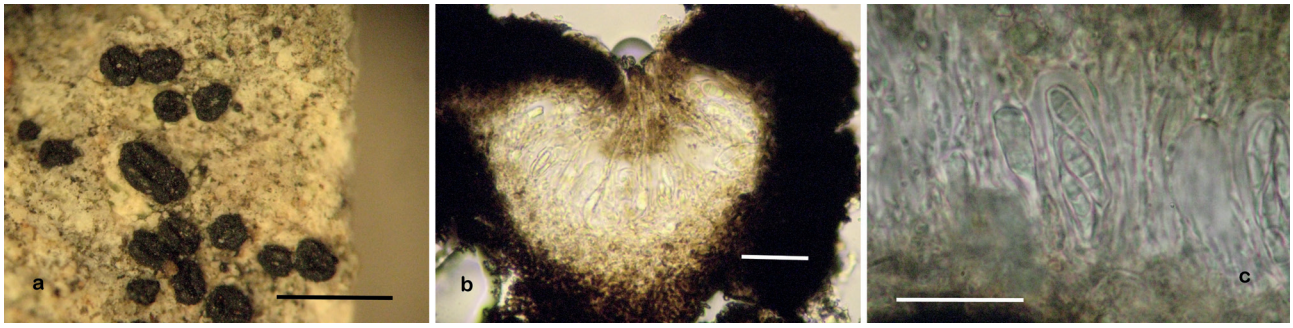

Fig. 19. *Opegrapha parasitica*. **a**. Lirellate apothecia, parasite on *Aspicilia* sp. Scale bar 1 mm. **b**.Section through apothecium with obscured hymenium, asci and ascospores. Scale bar 25 µm. **c**. Cross-section of apothecium with ascus and ascospores. Scale bar 25 µm.

Opegrapha parasitica (A. Massal.) H. Olivier, Bull. Acad. Intern. Géogr., Bot. 16: 190 (1906) – Fig. 19

Description. – Lichenicolous. – Apothecia lirellate, short or long, broad, black, with a narrow slit, partly immersed in the thallus of *Aspicilia* sp., 0.25 × 0.7 mm diam. or 0.25 × 0.25 mm diam. – Hymenium obscured. – Hypothecium colourless. – Asci clavate-cylindrical, 40–50 × 12–14 µm, 4-spored. – Ascospores 17 × 6 µm, hyaline, 4-celled, verrucose (Fig. 19a–c).

Notes. *Opegrapha parasitica* is a lichenicolous fungus, growing on crustose lichens on limestones (*Aspicilia* species, *Caloplaca cirrochroa, Verrucaria hochstetteri*) and on *Xanthoria parietina* (Hawksworth 1983, Seaward & Pentecost 2001). A detailed description is provided by Smith et al. (2009).

In recent years many noteworthy new records have been added to the lichen flora of Turkey (Aptroot & Yazıcı 2009, Aptroot et al. 2015; for further references see Yazici & Aslan 2016a,b). However, Turkey), Middle East (Syria), New Zealand, North America, and northern Africa (Hawksworth 1983, John et al. 2004, Wirth et al. 2011).

Material examined: TURKEY. Muş: Bulanık, 5 km to Arakonak village, roadside, 39° 04' 17.42" N, 42° 07' 35.93" E, 1605 m, on *Aspicilia* cf. *calcarea*, 29 May 2015, *leg. et det*. K.Yazici, A. Aslan & A. Aptroot. (KTUB–2457). Associated hosts: *Lepraria membranacea, L. incana, Solenopsora candicans*, *Rinodina* sp., *Lecanora* cf. *hageni*.

Rinodina zwackhiana (Kremp.) Körb., Syst. Lich. Germ. (Breslau): 126 (1855). – Fig. 20

Description. – Thallus crustose, ± squamulose, sometimes forming ± rosettes, 2–2.5 cm diam., appressed to the substratum, distinctly areolate, light brown, light brown-orange, lobate; lobes short, thick, hump, formed like tiles, surface with white crystals in points, with ellipsoidal tips, undivided or dichotomic, sometimes overlapping, 0.25–0.30 diam.; – soralia absent; – Apothecia aggregated, sessile or sometimes constricted at the base, 1.25–1.30 mm diam., mostly in the centre of the thallus, rare towards the lobes; thalline margin concolo-

rous with the thallus, 0.25 mm diam., entire; exciple ± pigmented; disc 1 mm diam., reddish brown or dark red, ± concave, flat at first, some large ones horizontal, saddle-shaped and rarely slightly convex later, fissured. – Hymenium ± pigmented, 120–140 µm; – epihymenium with blue-grey pigmentation. – Hypothecium hyaline, 120–190 µm, light yellow-brown; asci 8-spored, clavate, 60–90 × 20–25 µm. – Ascospores 2-celled, brown, ellipsoid with rounded lumina, pigmented septa at maturity, *Bicincta*-type, 15.45–17.20 × 9.8–11.25 µm. – Pycnidia absent. All spot tests negative.

Notes. – *Rinodina zwackhiana* is a mainly mild-temperate lichen, found on steeply inclined to slightly underhanging calcareous rocks, on walls, over disc, central disc yellowish brown, not viscid, margin smooth to slightly dentate; context thin to moderately thick at central disc, soft to firm, white, unchanging when bruised or cut. – Lamellae cream to white, adnate to adnexed, subdistant, edges entire, fleshy, centrally thick, lamellulae alternating with lamellae. – Stipe 3.5–12 × 0.3–0.5 cm (incl. pseudorhiza), yellowish brown, central, cylindrical to sub-cylindrical, base tapering, firm and woody without volva or zones. – Odour mild.

Basidiospores 13.0–18.0 × 11.5–13.5 µm, Q = 1.23 ellipsoidal to broadly ellipsoidal, rarely subglobose, hyaline, pale yellow in 5 % KOH, thin-walled, prominent apiculus 1.9–3 µm, inamyloid, non-dextrinoid. – Basidia 28.5–40.12 × 10.0–

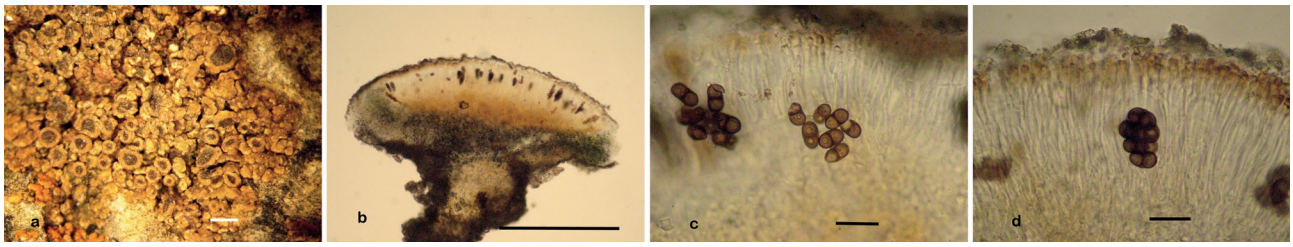

Fig. 20. *Rinodina zwackhiana*. **a**. Habitus. Scale bard 1 mm. **b**.Section through apothecium with hypothecium, hymenium and blue gray epihymenium. Scale bar 500 µm. **c**. Section through apothecium with young ascospores and paraphyses. Scale bar 25 µm. **d.** Cross-section of apothecium with ascus ascospores, paraphyses and blue-gray epihymenium. Scale bar 25 µm

and sometimes a juvenile parasite on other lichens, probably more widespread, and much overlooked. A detailed description is provided by Nash et al. (2001). It is known from Asia (China), Europe (Austria, Czech Republic, France, Germany, Italy, Poland, Romania, Slovakia, Slovenia), North Africa (Morocco), and North America (Bates et al. 2010, Nash et al. 2001, Vondrák et al. 2006, Wilfling & Mayrhofer 2002). *Rinodina zwackhiana* is new to Turkey.

Material examined. – TURKEY. Bitlis: Centre, mainroad of Siirt-Bitlis, 4 km to Bitlis, roadside, 38° 21¢ 36.89² N, 42° 03¢ 51.44² E, 1416 m, on calcareous rock, 08 August 2016, *leg. et det.* K. Yazici, A. Aslan & A. Aptroot. (KTUB–2459). Associated species: *Acarospora cervina, Aspicilia cinerea, Caloplaca saxicola, Collema tenax, Psorotichia shaereri, Verrucaria fuscella, Xanthoria elegans.*

Authors: K. Yazici, A. Aptroot & A. Aslan

Xerula strigosa Zhu L. Yang, L. Wang & G. M. Mueller, Acta Bot. Yunnanica 2009. – Figs. 21–22

Description. – Pileus 20–45 mm diam., convex to plano-convex, light brown to dark brown, fibrillose or fine scaly, umbonate, depressed broadly 13.0 µm, 4–spored, rarely 2-spored, clavate, hyaline, clamp connection not observed, hyaline to olive green granules or droplets in 5 % KOH. – Pleurocystidia 101.5–118.0 × 19.0–26.0 µm, fusiform, ventricose, hyaline to pale yellow, thick-walled, 3–5 µm, with bluntly ended apex, yellow crystals on apices. – Cheilocystida similar to pleurocystidia. – Peillipellis loosely arranged hyphae, light yellowish-brown, pileocystidia 33.5–105.0 × 23.5–33.0 µm, thick-walled, broadly clavate, hyaline.

Material examined. – PAKISTAN. Khyber Pakhtunkhwa, Himalayan Moist Temperate Forests, Khanspur (34.0167° N, 73.4167° E), at 2250 m a.s.l., solitary, on moist ground near a mixed vegetation of *Abies pindrow* (Royle ex D.Don) Royle, *Pinus wallichaina* A. B. Jacks. and *Quercus incana* Bartram, 24 August 2010, *leg.* A. Razaq (LAH 240806).

Notes. – The Pakistani specimen is in accordance with the holotype description by Wang et al. (2008). The four-spored basidia and the size and shape of the thick-walled pleurocystidia of our collection conform to the holotype but the length of spore varies slightly (Chinese 9.5–16.5 × 8.5–15.5µm vs. Pakistani 13.0–18.0 × 11.5–13.5µm). Ecologically, both collections have been observed in mixed pine

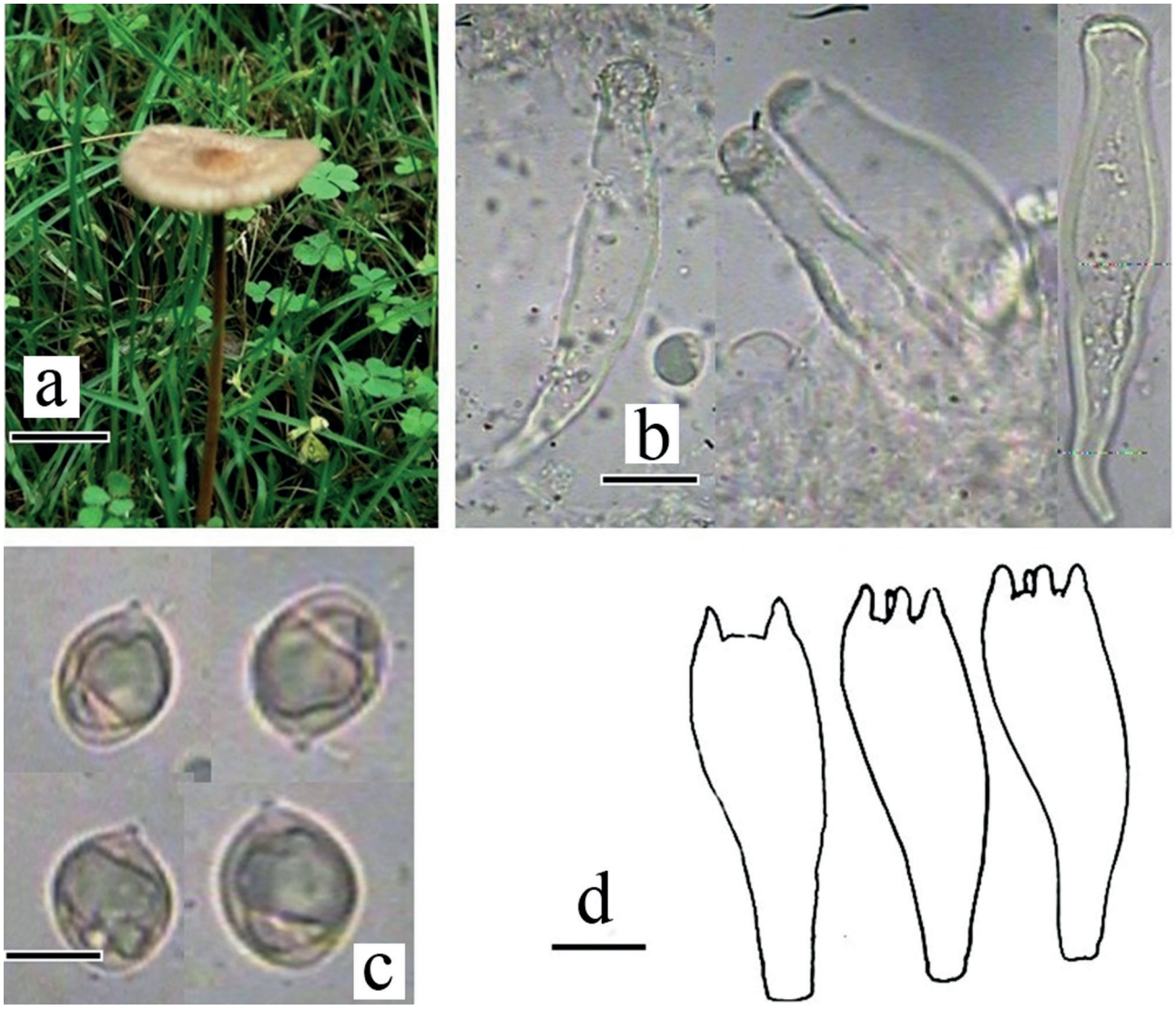

Fig. 21. *Xerula strigosa*. **a.** Basidiocarp. **b.** Pleurocystidia. **c.** Basidiospores. **d.** Basidia. Scale bars: a 1 cm; b 30 µm; c 12 µm; d 15 µm.

forests with deciduous trees like oak (Wang et al. 2008).

The internal transcribed spacers (ITS1 & ITS2) and 5.8S rDNA was sequenced of our specimen using universal primers pairs (ITS1f & ITS4) (White et al. 1990) and showed maximum nucleotide resemblance with *X. strigosa* sequences (KF530552.1, KF530553.1, KF530555.1) from China as highest nucleotide similarity matches. In phylogenetic analysis, all the sequences of *Xerula* and its allied genera recovered in three clades: clade I, *Xerula*, clade II, *Strobilurus* and *Paraxerula* (Fig. 22). Our phylogenetic analysis showed that the two latter genera are monophyletic, while the former is polyphyletic as already noted by Petersen & Hughes (2010). Pakistani specimen recovered in sub-clade I.I (Fig. 22) along with its respective *X. strigosa* sequences from China. In this subclade, two sequences are noteworthy: *X. strigosa* (KF530556.1) and *X. hispida* (AF321485.1). The placement of *X. hispida* (AF321485.1) from China among the sequences of *X. strigosa* showed that actually it is *X. strigosa* while the clustering of *X. strigosa* (KF530556.1) as a sister clade to all other sequences of *X. strigosa* indicates either that it has more intraspecific variation or is a misidentification (Fig. 22, clade I.I). *Xerula strigosa* has been described from China and is now reported first from Pakistan based on morpho-

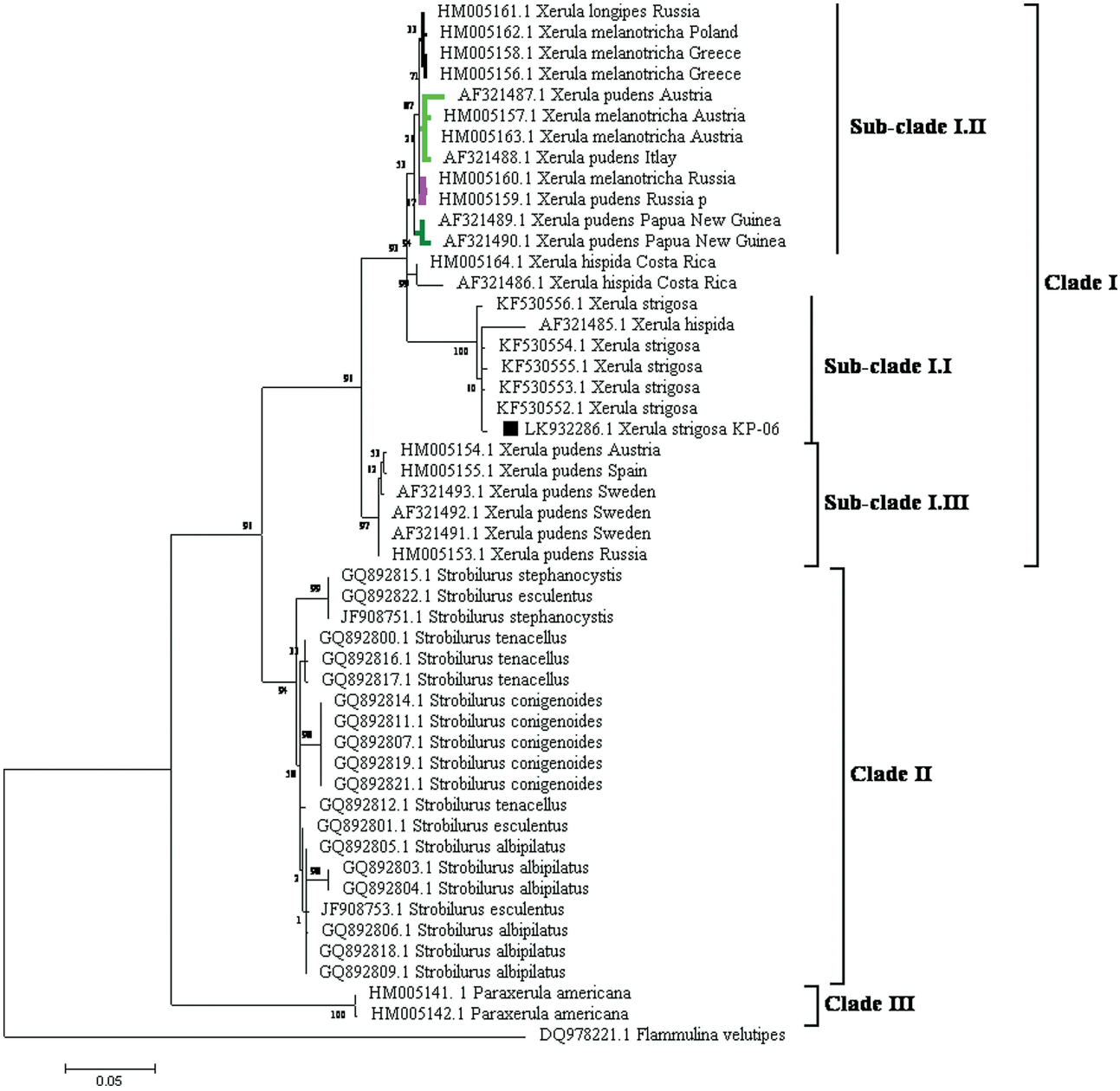

Fig. 22. Phylogenetic analysis of *Xerula strigosa* collected from Pakistan (■) based on nrITS-rDNA regions. The tree is based on maximum likelihood method using Jukes-Cantor model (Jukes & Cantor 1969). Bootstrap values have been shown on each branch. The analysis involved 50 sequences, with *Flammulina velutipes* as the outgroup.

logical and molecular characterizations. Petersen & Nagasawa (2005) also mentioned Pakistani material but without a details.

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