WESTERDIJK FUNGAL BIO DIVERSITY INSTITUTE

Scopulariopsis and scopulariopsis-like species from indoor environments

J.H.C. Woudenberg*, M. Meijer, J. Houbraken, and R.A. Samson

Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands

**Correspondence*: J.H.C. Woudenberg, j.woudenberg@westerdijkinstitute.nl

Abstract: Scopulariopsis-like species are often reported from the indoor environment, as well as from clinical samples. The lack of type isolates and thorough phylogenetic studies in the *Microascaceae* hampered the correct identification of these isolates. Based on recent phylogenetic studies, which resulted in multiple name changes, the aim is to molecularly identify the *Scopulariopsis* and scopulariopsis-like species which occur in the indoor environment and give an overview of the current species in these genera and their habitats. Strains from the CBS culture collection were supplemented with almost 80 indoor strains of which the internal transcribed spacer 1 and 2 and intervening 5.8S nrDNA (ITS), beta-tubulin (*tub2*) and translation elongation factor 1-alpha (*tef1*) gene regions were sequenced for phylogenetic inference. The multi-gene phylogenies recognise 33 *Microascus* species and 12 *Scopulariopsis* species and showed that the recently established genus *Fuscoannellis*, typified by *Scopulariopsis carbonaria*, should be synonymized with the genus *Yunnania*. Seven new *Microascus* species, four new *Scopulariopsis* species, and one new *Yunnania* species, are described, and a new name in *Microascus* and two new name combinations (one in *Microascus*, and one in *Yunnania*) are proposed. In the indoor environment 14 *Microascus* species and three *Scopulariopsis* species were found. *Scopulariopsis brevicaulis* (22 indoor isolates) and *Microascus melanosporus* (19 indoor isolates) are the most common indoor species, in number of isolates, followed by *M. paisii* (8 indoor isolates) and *S. candida* (7 indoor isolates). A genus phylogeny based on the ITS, *tef1* and the large subunit 28S nrDNA (LSU) of the type or representative isolates of all here recognised species is provided depicting all species habitats. No correlation between phylogenetic relationship and habitat preference could be observed. Ten species which are found indoor are also found in relation with human-derived samples. A table showing recent name changes and a key to common species of *Scopulariopsis* and scopulariopsis-like genera found indoors is included.

Key words: *Fuscoannellis*, indoor fungi, *Microascaceae*, *Microascus*, *Yunnania*.

Taxonomic novelties: New combination: *Microascus melanosporus* (Udagawa) Woudenb. & Samson, *Yunnania carbonaria* (F.J. Morton & G. Sm.) Woudenb., Houbraken & Samson; **New name:** *Microascus atrogriseus* Woudenb. & Samson; **New species:** ***Microascus*** *appendiculatus* Woudenb. & Samson, *M. cleistocarpus* Woudenb., X. Wei Wang & Samson, *M. fusisporus* Woudenb. & Samson, *M. hollandicus* Woudenb. & Samson, *M. micronesiensis* Woudenb., Seifert & Samson, *M. pseudopaisii* Woudenb. & Samson, *M. trautmannii* Woudenb. & Samson, ***Scopulariopsis*** *africana* Woudenb. & Samson, *S. albida* Woudenb. & Samson, *S. caseicola* Woudenb. & Samson, *S. sexualis* Woudenb. & Samson, ***Yunnania*** *smithii* Woudenb., Houbraken & Samson.

Available online 18 March 2017; http://dx.doi.org/10.1016/j.simyco.2017.03.001.

INTRODUCTION

People spend up to 90 % of their time indoors (Höppe & Martinac 1998). Fungi present in these indoor environments can produce toxins or carry allergens which cause health hazards. Therefore it is important to know which fungal species are present indoors. Several reports are made on the presence of *Microascaceae* in the indoor environment. The species *Scopulariopsis brevicaulis*, *S. candida*, *S. fusca* (= *S. asperula*), *S. brumptii* (= *Microascus paisii*) and *S. sphaerospora* (= *M. paisii*) are often mentioned as indoor fungi (Samson *et al.* 2010). However, in most of the indoor reports of scopulariopsis-like isolates, morphological examination has not been confirmed with molecular studies. Also the absence of thorough phylogenetic studies in these genera made it difficult to accurately identify the indoor *Microascaceae*. The first phylogenetic study of scopulariopsis-like species was based on the large subunit 28S nrDNA (LSU, Issakainen *et al.* 2003). Here the potential relationship between asexual and sexually reproducing species was assessed, with a focus on clinically occurring species. The main microascoid clade, which contained all *Microascus* and *Scopulariopsis* species studied, was divided into seven clades. Further taxonomic study is suggested to redefine or split the genus *Microascus*. A study of clinical isolates in Poland confirmed that the LSU sequence alone is insufficient for species delimitation in *Scopulariopsis* (Jagielski *et al.* 2013). A taxonomic study of cheese fungi used the beta-tubulin (*tub2*) and translation elongation factor 1-alpha (*tef1*) gene regions next to LSU to identify their *Scopulariopsis* species (Ropars *et al.* 2012). The internal transcribed spacer 1 and 2 and intervening 5.8S nrDNA (ITS) gave problems with amplification, and displayed a high variability, which made it not useful for phylogenetic study of their isolates. Translation elongation factor 1-alpha showed to be the most phylogenetically informative genomic region and was proposed for identifying *Scopulariopsis* species. A subsequent phylogenetic study on clinical *Microascus* and *Scopulariopsis* species made a combined phylogeny of the LSU and *tef1* gene region (Sandoval-Denis *et al.* 2013). They concluded that this combined analysis is useful for the identification of the most common clinically relevant *Scopulariopsis* species. However, further phylogenetic studies testing more genetic markers and reference strains are suggested, since nine phylogenetic clades in their combined phylogenies could not be properly named. This follow-up study with the aim to clarify the taxonomy and phylogeny of *Microascus*, *Scopulariopsis* and allied genera was published recently (Sandoval-Denis *et al.* 2016). On a large set of clinical and environmental isolates, including ex-type strains of multiple species, a phylogenetic

Peer review under responsibility of Westerdijk Fungal Biodiversity Institute.

Studies in Mycology

study was conducted based on the ITS, LSU, *tef1* and *tub2* gene regions, in combination with morphological and physiological analyses. In this polyphasic approach study the genera *Microascus* and *Scopulariopsis* are separated, the genus *Pithoascus* reinstated, and the new genus *Pseudoscopulariopsis* proposed. Seven new *Microascus* species and one new *Scopulariopsis* species are described, nine new name combinations are introduced, and several species are neotypified (Sandoval-Denis *et al.* 2016). A second taxonomic study on a set of clinical and environmental scopulariopsis-like fungi followed soon (Jagielski *et al.* 2016). Here another three new *Microascus* species, one new *Scopulariopsis* species and one new *Pithoascus* species are described, *S. albo-flavescens* is reinstated, *M. trigonosporus* var. *terreus* recombined in *M. terreus*, and the new genus *Fuscoannellis* proposed.

Although these two recent phylogenetic studies (Jagielski *et al.* 2016, Sandoval-Denis *et al.* 2016) make molecular identification of scopulariopsis-like isolates upon species level possible, the involved name changes can cause a lot of confusion. Commonly mentioned species from the indoor environment, like *S. brumptii* (now *M. paisii*), *S. fusca* (now *S. asperula*) and *S. sphaerospora* (now *M. paisii*), are renamed. The aim of this project is to molecularly identify the scopulariopsis-like taxa, which occur in the indoor environment. Simultaneously, a phylogenetic overview of these genera is constructed, and the species habitats are studied. All available *Microascus* and *Scopulariopsis* isolates from the Westerdijk Fungal Biodiversity Institute culture collection (CBS collection) and working collection of the Applied and Industrial Mycology department (DTO collection) are included in the study. Species phylogenetic inferences were conducted on sequence data of parts of the ITS, *tub2* and *tef1* gene regions, and a genus phylogenetic inference on the LSU, ITS and *tef1* gene regions. Phylogenetic clades which contain indoor isolates are highlighted as indoor species. New species are described, and an overview of the current species and their habitats in the genera *Microascus*, *Scopulariopsis* and *Yunnania* is provided. Furthermore, a table showing recent name changes and a key to common species of *Scopulariopsis* and scopulariopsis-like genera found in the indoor environment is provided.

MATERIALS AND METHODS

Isolates

In total 248 isolates were included in this study, comprising of 152 *Microascus* isolates, 88 *Scopulariopsis* isolates, four *Yunnania* isolates, and four out-group isolates. The isolates were obtained from the culture collection of the Westerdijk Fungal Biodiversity Institute (former CBS-KNAW Fungal Biodiversity Centre), Utrecht, the Netherlands and the working collection of the Applied and Industrial Mycology department (DTO) housed at the Westerdijk Institute (Table 1). Isolates from the culture collection of the Westerdijk Institute (CBS collection) have a world-wide distribution and are isolated from a diverse range of substrates. Isolates from the working collection of DTO are mostly isolated from indoor environments or food, and include swab and air samples mainly from Europe, and house dust samples collected world-wide (Amend *et al.* 2010). Freeze-dried strains from the CBS culture collection were revived in 2 mL malt/peptone (50 % / 50 %) and subsequently transferred to oatmeal agar (OA) (Samson *et al.* 2010). Strains stored in the liquid nitrogen (CBS collection) or the DTO collection were transferred to OA directly from the −185 °C or −80 °C storage, respectively. They were cultured for 14 d at 25 °C in the dark. From eight isolates only their DNA sequences from GenBank were obtained (Table 1, isolates without a DTO number).

DNA isolation, PCR and sequencing

DNA extraction was performed using the Ultraclean® Microbial DNA Isolation Kit (MoBio laboratories, Carlsbad, CA, USA), according to the manufacturer's instructions. The LSU, ITS, *tub2* and *tef1* gene regions were amplified and sequenced with respectively the primers LR0R (Rehner & Samuels 1994)/LR5 (Vilgalys & Hester 1990), V9G (De Hoog & Gerrits van den Ende 1998)/LS266 (Masclaux *et al.* 1995), Bt2a/Bt2b (Glass & Donaldson 1995) and EF1-983F/EF1-2218R (Rehner & Buckley 2005). The PCRs were performed in an Applied Biosystems® 2720 Thermal Cycler (Thermo Fisher Scientific, Bleiswijk, the Netherlands) in a total volume of 12.5 µl. The PCR mixture consisted of 1 µl genomic DNA, 1 × NH_4 reaction buffer (Bioline, Luckenwalde, Germany), 0.2 µM of each primer, 5 % dimethyl sulfoxide (DMSO), 20 µM (*tub2*) or 40 µM (LSU/ITS/*tef1*) of each dNTP, 1 mM (ITS) or 1.6 mM (*tef1*) or 2 mM (LSU/*tub2*) $MgCl_2$, and 0.25 U *Taq* DNA polymerase (Bioline). The PCR conditions for LSU, ITS and *tub2* consisted of an initial denaturation step of 5 min at 94 °C followed by 35 cycles of 30 s at 94 °C, 30 s at 47 °C (LSU) or 55 °C (ITS) or 59 °C (*tub2*) and 1 min at 72 °C, and a final elongation step of 7 min at 72 °C. For *tef1* a touchdown PCR protocol of 9 cycles of 30 s at 94 °C, 30 s at 66 °C (−1 °C every cycle) and 90 s at 72 °C, followed by 30 cycles of 30 s at 94 °C, 30 s at 56 °C and 90 s at 72 °C and a final elongation step of 7 min at 72 °C was used. The PCR products were sequenced in both directions using the BigDye Terminator v. 3.1 Cycle Sequencing Kit (Thermo Fisher Scientific) and analysed with an ABI Prism 3730xl DNA Analyser (Thermo Fisher Scientific) according to the manufacturer's instructions. Consensus sequences were computed from forward and reverse sequences using the Bionumerics v. 4.61 software package (Applied Maths, St-Marthens-Latem, Belgium). Several sequences obtained in this study had one or multiple nucleotide differences and length differences with already published sequenced of the same isolates. All new sequences and sequences which were longer in length or had nucleotide differences with already published sequenced were submitted to GenBank (Table 1).

Phylogenetic analyses

Multiple sequence alignments of the separate LSU, ITS, *tub2* and *tef1* sequences were generated with MAFFT v. 7.271 (http://mafft.cbrc.jp/alignment/server/index.html) using the L-INS-i method. With Findmodel (http://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html) the best nucleotide substitution models were determined. On both the single gene-sequence alignments and the combined gene-sequence alignment Bayesian analyses were performed with MrBayes v. 3.1.2 (Huelsenbeck & Ronquist 2001, Ronquist & Huelsenbeck 2003). The Markov Chain Monte Carlo (MCMC) analysis used four chains and started from a random tree topology. The sample

Table 1. Isolates used in this study and their GenBank accession numbers. Bold accession numbers were generated in other studies.

Name	Old name[1]	Strain numbers[2]	Host/Substrate	Country	GenBank accession number			
					ITS	*tub2*	*tef1*	LSU
Cephalotrichum asperulum		**CBS 582.71^{IT}, DTO 104-B7, ATCC 26885**	Soil	Argentina	KX923818		KX924043	KX924027
C. stemonitis		**CBS 103.19^{NT}, DTO 170-B3, MUCL 6960**	Seed	Netherlands	KX923819		**LN850953**	**LN850952**
Microascus alveolaris	*M. trigonosporus*	CBS 268.49, DTO 342-D8	*Avena sativa*, grain	USA	KX923823	KX924257	KX924047	
	M. trigonosporus	CBS 269.49, DTO 342-C2	*Glycine soja*, seed	USA	KX923824	KX924258	KX924048	
	M. trigonosporus	CBS 270.49, DTO 345-F7	*Hordeum vulgare*, seed	USA	KX923825	KX924259	KX924049	
	M. trigonosporus	CBS 271.49, DTO 342-D9	*Hordeum vulgare*, seed	USA	KX923826	KX924260	KX924050	
	M. trigonosporus	CBS 272.49, DTO 342-C3	*Avena sativa*, leaf	USA	KX923827	KX924261	KX924051	
	M. trigonosporus	CBS 150.64, DTO 342-E2	*Allium cepa*, seed	USA	KX923828	KX924262	KX924052	
	M. trigonosporus	CBS 494.70, DTO 342-C8	Marine sediment	Norway	**LN850757**	**LN850855**	**LN850903**	
		CBS 139501^{T}, DTO 351-E2, FMR 12252, UTHSC 07-3491	Human, BAL fluid	USA	KX923829	KX924263	KX924053	KX924029
		DTO 223-A7	Indoor	Uruguay	KX923830	KX924264	KX924054	
M. appendiculatus sp. nov.	*M. senegalensis*	**CBS 594.78^{T}, DTO 354-C3**	Human, skin	Algeria	**LN850781**	**LN850878**	KX924055	**LN850830**
M. atrogriseus nom. nov.	*Masonia grisea*	**CBS 295.52^{T}, DTO 103-H6, IFO 6795, IMI 049908, MUCL 9003**	Culture contaminant	UK	**LM652433**	KX924265	KX924056	KX924030
		CBS 897.68, DTO 356-C3, ATCC 16279, IFO 31245, MUCL 8993	Wheat field soil	Germany	**LM652436**	**LM652649**	**LM652571**	
	S. chartarum	CBS 410.76, DTO 345-B1	Burnt soil	Netherlands	KX923831	KX924266	KX924057	
		DTO 139-D7	Indoor	Germany	KX923832	KX924267	KX924058	
		DTO 191-C2	Indoor horse arena	Netherlands	KX923833	KX924268	KX924059	
M. brunneosporus		**CBS 138276^{T}, DTO 351-D8, UTHSC 06-4312, FMR 12343**	Human, BAL fluid	USA	KX923834	KX924269	**HG380420**	**HG380497**
M. chartarus	*Masonia chartarum*	**CBS 294.52^{T}, IMI 049909, MUCL 9001**	Wall paper	UK	**LM652393**	**LM652607**	**HG380386**	**HG380463**
M. chinensis		**CBS 139628^{T}, BMU 01837**	Human, nail	China	**LN850760**	**LN850858**	**LN850906**	**LN850809**
M. cinereus	*M. griseus^{T}*	CBS 365.65, DTO 104-A3, DTO 104-A4, ATCC 16204, HACC 1252, IMI 113680	Soil	India	**LM652399**	KX924270	KX924060	
		CBS 664.71, DTO 104-B8	Human, lung	USA	KX923835	**LN850860**	KX924061	
		CBS 324.72, DTO 342-G2	Clay	Namibia	KX923836	KX924271	KX924062	
		CBS 138709^{NT}, DTO 351-E1, UTHSC 10-2805, FMR 12217	Human, BAL fluid	USA	KX923837	KX924272	KX924063	KX924031
M. cirrosus		**CBS 217.31^{T}, DTO 103-G1**	*Prunus* sp., leaf	Italy	KX923838	KX924273	KX924064	KX924032
		CBS 277.34, DTO 345-A7, MUCL 9050, MUCL 9055	*Vitis vinifera*, root	Italy	KX923839	KX924274	**LM652556**	
	M. longirostris	CBS 267.49, DTO 170-B9, IFO 7029	*Sciurus vulgaris*, skin	Netherlands	KX923840	KX924275	KX924065	
		CBS 240.58, DTO 342-E1, IMI 086913	Compost soil	Germany	KX923841	KX924276	KX924066	
		CBS 301.61, DTO 345-A8, IMI 086914, NRRL 1689, MUCL 9054	Unknown	UK	KX923842	KX924277	KX924067	
		CBS 302.61, DTO 345-D1	Unknown	Canada	KX923843	KX924278	KX924068	
		CBS 424.62, DTO 345-A9	Polyvinylchloride	Netherlands	KX923844	KX924279	KX924069	
		CBS 541.74, DTO 342-I8	Rodent dung	USA	KX923845	KX924280	KX924070	
		CBS 157.92, DTO 342-G6, FRR 4174	*Arachis hypogaea*, nut	Indonesia	KX923846	KX924281	KX924071	
		CBS 115860, DTO 345-D4, FMR 8575	Air	Spain	KX923847	KX924282	KX924072	
		CBS 116405, DTO 345-D6	Antique tapestries	Poland	**LN850763**	**LN850861**	**LN850909**	
		DTO 342-D4, RGR 84.0007	*Helianthus annuus*, oilseed	USA	KX923848	KX924283	KX924073	
		DTO 342-D5, RGR 84.0033	Unknown	Unknown	KX923849	KX924284	KX924074	
		DTO 342-D7, RGR 84.0051	Unknown	Unknown	KX923850	KX924285	KX924075	

(*continued on next page*)

Table 1. (Continued).

Name	Old name[1]	Strain numbers[2]	Host/Substrate	Country	GenBank accession number			
					ITS	*tub2*	*tef1*	LSU
M. cleistocarpus sp. nov.		**CBS 134638^{T}, DTO 342-D2, CGMCC 3.15222**	Discarded cloth	China	KX923851	KX924286	KX924076	KX924033
M. croci	*S. croci*	**CBS 158.44^{T}, DTO 103-H3, IMI 078261, MUCL 9002**	*Crocus* sp.	Netherlands	KX923852	KX924287	KX924077	**LM652508**
	Masoniella tertia^{T}	CBS 296.61, DTO 103-I6, IMI 109550, MUCL 9005	Air	Brazil	KX923853	KX924288	KX924078	
	S. chartarum	CBS 522.69, DTO 342-C7	Forest soil	Canada	KX923854	KX924289	KX924079	
		DTO 220-I5	Indoor	Indonesia	KX923855	KX924290	KX924080	
		DTO 252-D8	Indoor	Germany	KX923856	KX924291	KX924081	
		DTO 305-B3	Indoor	Mexico	KX923857	KX924292	KX924082	
		DTO 305-B5	Indoor	Mexico	KX923858	KX924293	KX924083	
M. expansus		**CBS 138127^{T}, DTO 351-D6, UTHSC 06-4472, FMR 12266**	Human, sputum	USA	KX923859	KX924294	KX924084	**HG380492**
M. fusisporus sp. nov.	*M. paisii*	**CBS 896.68^{T}, DTO 356-C2, ATCC 16278, IFO 31244, MUCL 8989**	Wheat-field soil	Germany	**LM652432**	**LM652645**	**HG380372**	**LN850825**
M. gracilis	*M. cinereus*	CBS 126.14, DTO 347-C4, IMI 086916	Unknown	Unknown	KX923860	KX924295	KX924085	
	M. cinereus	CBS 195.61, DTO 345-C8, IMI 075542, MUCL 9048	Soil	UK	**LM652416**	**LM652629**	**HG380391**	
		CBS 300.61, DTO 345-C9, MUCL 9049	*Zea mays*, stored seed	USA	**LM652417**	KX924296	**LM652563**	
		CBS 369.70^{T}, DTO 104-B3, IFO 7561	Wheat flour	Japan	KX923861	KX924297	KX924086	**HG380467**
		CBS 794.91, DTO 345-D2	Rice flour	Australia	KX923862	KX924298	KX924087	
		CBS 156.92, DTO 345-D3	*Arachis hypogaea*, nut	Thailand	KX923863	KX924299	KX924088	
	M. cinereus	CBS 116059, DTO 345-D5	Polyethylene with starch	Poland	KX923864	**LN850863**	KX924089	
		CBS 120886, DTO 342-D1	*Prunus persica*	South Africa	KX923865	KX924300	KX924090	
		DTO 220-I4	Indoor	Indonesia	KX923866	KX924301	KX924091	
	M. cinereus	DTO 342-D6, RGR 84.0038	Unknown	Unknown	KX923867	KX924302	KX924092	
	M. cinereus	DTO 342-G8, RGR 84.0040	Unknown	Unknown	KX923868	KX924303	KX924093	
M. hollandicus sp. nov.		**CBS 141582^{T}, DTO 191-C3**	Indoor horse arena	Netherlands	KX923869	KX924304	KX924094	KX924034
M. hyalinus		**CBS 766.70^{T}, DTO 170-F2**	Cow dung	USA	KX923870	KX924305	**LM652564**	**LM652513**
		CBS 134639, DTO 342-I9	Goat dung	China	KX923871	KX924306	KX924095	
M. intricatus		**CBS 138128^{T}, DTO 351-D7, UTHSC 07-156, FMR 12264**	Human BAL fluid	USA	KX923872	KX924307	**HG380419**	**HG380496**
		DTO 223-A6	Indoor	Micronesia	KX923873	KX924308	KX924096	
M. longicollis		CBS 752.97, DTO 338-G8	*Anacardium occidentale*, nut	Brazil	KX923874	KX924309	KX924097	KX924035
M. longirostris		**CBS 196.61^{NT}, IMI 086908, MUCL 9058, NRRL 1717**	Wasp's nest	USA	**LM652421**	**LM652634**	**LM652566**	**LM652515**
		CBS 415.64, IFO 7554	Soil	Japan	**LM652422**	**LM652635**	**LM652567**	
M. macrosporus		CBS 662.71, DTO 170-F6, NRRL A-8018	Soil	USA	**LM652423**	**LM652636**	**LM652568**	**LM652517**
	M. cirrosus	CBS 540.74, DTO 347-D1	Soil	USA	KX923875	KX924310	KX924098	
M. melanosporus comb. nov.	*S. melanospora*	**CBS 272.60^{T}, DTO 103-I1, IFO 6441, IMI 078257, LCP 59.1590, MUCL 9040, NHL 6045**	*Oryza sativa*, milled	USA	KX923876	KX924311	**LM652572**	KX924036
		CBS 854.68, DTO 220-H7	Compost soil	Germany	KX923877	KX924312	KX924099	
	S. fusca	CBS 102829, DTO 342-E7	Cheese warehouse	Netherlands	KX923878	KX924313	KX924100	
		CBS 116060, DTO 136-G8	Antique tapestries	Poland	**LN850775**	**LN850872**	KX924101	
		DTO 043-A1	Unknown	Unknown	KX923879	KX924314	KX924102	
		DTO 043-A2	Unknown	Unknown	KX923880	KX924315	KX924103	
		DTO 049-E4	Archive	Netherlands	KX923881	KX924316	KX924104	
		DTO 049-E5	Archive	Netherlands	KX923882	KX924317	KX924105	
		DTO 049-F2	Office	Netherlands	KX923883	KX924318	KX924106	
		DTO 053-H2	Between concrete Floor and carpet	Netherlands	KX923884	KX924319	KX924107	
		DTO 067-G7	Bakery	Netherlands	KX923885	KX924320	KX924108	
		DTO 138-B6	Indoor	Germany	KX923886	KX924321	KX924109	

Table 1. (Continued).

Name	Old name[1]	Strain numbers[2]	Host/Substrate	Country	GenBank accession number			
					ITS	*tub2*	*tef1*	LSU
		DTO 220-H9	Indoor	South Africa	KX923887	KX924322	KX924110	
		DTO 220-I1	Indoor	South Africa	KX923888	KX924323	KX924111	
		DTO 220-I2	Indoor	South Africa	KX923889	KX924324	KX924112	
		DTO 220-I3	Indoor	South Africa	KX923890	KX924325	KX924113	
		DTO 223-A9	Indoor	Germany	KX923891	KX924326	KX924114	
		DTO 240-A9	Archive	Netherlands	KX923892	KX924327	KX924115	
		DTO 240-B1	Archive	Netherlands	KX923893	KX924328	KX924116	
		DTO 240-B3	Archive	Netherlands	KX923894	KX924329	KX924117	
		DTO 240-B4	Archive	Netherlands	KX923895	KX924330	KX924118	
		DTO 252-D7	Indoor	Germany	KX923896	KX924331	KX924119	
		DTO 255-A5	Airsampling	Germany	KX923897	KX924332	KX924120	
		DTO 255-A6	Airsampling	Germany	KX923898	KX924333	KX924121	
		DTO 255-A7	Airsampling	Germany	KX923899	KX924334	KX924122	
		DTO 255-B1	Plaster	Germany	KX923900	KX924335	KX924123	
		DTO 255-B3	Polystyrene	Germany	KX923901	KX924336	KX924124	
		DTO 255-B5	Oriented strand board	Germany	KX923902	KX924337	KX924125	
		DTO 255-B6	Wood	Germany	KX923903	KX924338	KX924126	
		DTO 255-C3	Unknown	Germany	KX923904	KX924339	KX924127	
M. micronesiensis sp. nov.		**CBS 141523^{T}, DTO 220-I9**	Indoor	Micronesia	KX923905	KX924340	KX924128	KX924037
		DTO 223-A5	Indoor	Micronesia	KX923906	KX924341	KX924129	
M. murinus		CBS 621.70, DTO 347-C8	Composted municipal waste	Germany	KX923907	**LN850868**	KX924130	
		CBS 830.70^{T}, DTO 104-B5, DTO 170-F5, IMI 161540	Composted municipal waste	Germany	KX923908	KX924342	KX924131	**HG380481**
		CBS 864.71, DTO 347-C9	Municipal waste	Germany	KX923909	**LN850867**	KX924132	
M. onychoides		**CBS 139629^{T}, BMU 03911**	Human, nail	China	**LN850774**	**LN850871**	**LN850920**	**LN850823**
M. paisii	*Torula paisii*	**CBS 213.27^{T}, DTO 103-F9, IMI 036480, MUCL 7915, VKM F-424**	Human	Italy	**LM652434**	KX924343	KX924133	**LM652518**
	S. sphaerospora^{T}	CBS 402.34, DTO 103-G8, MUCL 9045	Unknown	Austria	**LM652437**	KX924344	**LM652651**	
	S. brumptii^{T} (?)	CBS 333.35, DTO 220-H5	Small-pox vaccine	France	KX923910	KX924345	KX924134	
		CBS 345.58, DTO 220-H6	Human, skin and hair	Germany	**LN850777**	**LN850874**	**LN850923**	
		DTO 073-F1	Moist wall of archive	Netherlands	KX923911	KX924346	KX924135	
		DTO 109-G6	Indoor	Denmark	KX923912	KX924347	KX924136	
		DTO 220-I6	Indoor	New Zealand	KX923913	KX924348	KX924137	
		DTO 220-I7	Indoor	New Zealand	KX923914	KX924349	KX924138	
		DTO 252-D9	Indoor	Germany	KX923915	KX924350	KX924139	
		DTO 255-A8	Airsampling	Germany	KX923916	KX924351	KX924140	
		DTO 255-A9	Airsampling	Germany	KX923917	KX924352	KX924141	
		DTO 255-B2	Plaster	Germany	KX923918	KX924353	KX924142	
		DTO 255-B4	Oriented strand board	Germany	KX923919	KX924354	KX924143	
		DTO 255-B7	Plaster	Germany	KX923920	KX924355	KX924144	
		DTO 255-B8	Polystyrene	Germany	KX923921	KX924356	KX924145	
		DTO 255-B9	Airsampling	Germany	KX923922	KX924357	KX924146	
M. pseudolongirostris	*M. cirrosus*	**CBS 462.97^{T}, DTO 351-D5**	Human, nail	Netherlands	**LN850782**	**LN850879**	KX924147	**LN850831**
M. pseudopaisii sp. nov.		**CBS 141581^{T}, DTO 116-A3**	Air, basement	Netherlands	KX923923	KX924358	KX924148	KX924038
		DTO 116-A4	Air, basement	Netherlands	KX923924	KX924359	KX924149	
M. pyramidus		**CBS 212.65^{T}, DTO 104-A1, DTO 104-A2, ATCC 36763, IMI 109887**	Desert soil	USA	KX923925	KX924360	KX924150	**HG380435**
		CBS 668.71, DTO 342-E4	Pocket mouse, hair	USA	KX923926	**LN850876**	**LN850925**	
	M. trigonosporus	CBS 663.71, DTO 342-G1	Soil	USA	KX923927	KX924361	KX924151	
M. restrictus		**CBS 138277^{T}, DTO 347-B4, UTHSC 09-2704, FMR 12227**	Human, left hallux	USA	KX923928	KX924362	KX924152	**HG380494**
M. senegalensis		**CBS 277.74^{T}, DTO 351-E4**	Mangrove soil	Senegal	KX923929	KX924363	KX924153	**LM652523**
		CBS 760.84, DTO 347-D2	*Helianthus annuus*, seed	USA	KX923930	KX924364	KX924154	
		CBS 761.84, DTO 342-G5	*Helianthus annuus*, seed	USA	KX923931	KX924365	KX924155	
		CBS 775.84, DTO 342-C9	*Helianthus annuus*, seed	Germany	KX923932	KX924366	KX924156	
		DTO 342-F1, RGR 84.0112	Unknown	Unknown	KX923933	KX924367	KX924157	
		DTO 342-G9, RGR 84.0113	Unknown	Unknown	KX923934	KX924368	KX924158	

(*continued on next page*)

Table 1. (Continued).

Name	Old name[1]	Strain numbers[2]	Host/Substrate	Country	GenBank accession number			
					ITS	*tub2*	*tef1*	LSU
		DTO 342-H1, RGR 84.0158	Unknown	Unknown	KX923935	KX924369	KX924159	
		DTO 342-H2, RGR 84.0159	Unknown	Unknown	KX923936	KX924370	KX924160	
		DTO 342-H4, RGR 85.0058	unknown	Unknown	KX923937	KX924371	KX924161	
M. terreus		**CBS 601.67^{T}, DTO 104-A8, ATCC 22360, NRRL A-18283, VKM F-1144**	Soil	Ukraine	**LN850783**	**LN850880**	**LN850928**	**LN850832**
	M. trigonosporus	CBS 665.71, DTO 342-E3	Soil	USA	KX923938	KX924372	KX924162	
	M. trigonosporus	CBS 807.73, DTO 342-E5	Saline desert soil	Kuwait	KX923939	KX924373	KX924163	
		CBS 138275, UTHSC 07-1823, FMR 12342	Human, sputum	USA	**LM652384**	**LM652600**	**HG380412**	
	M. trigonosporus	DTO 342-D3, RGR 84.0004, ATCC 62716	*Helianthus annuus*, confectionary seed	USA	KX923940	KX924374	KX924164	
	M. trigonosporus	DTO 343-A1, RGR 84.0003	*Helianthus annuus*, seed	USA	KX923941	KX924375	KX924165	
M. trautmannii sp. nov.		**CBS 141583^{T}, DTO 255-C1**	oriented strand board	Germany	KX923942	KX924376	KX924166	KX924039
M. trigonosporus		**CBS 218.31^{T}, DTO 103-G2, HACC 178, IMI 113702**	Unknown	Puerto Rico	KX923943	KX924377	**HG380359**	**HG380436**
		CBS 198.61, DTO 342-C5, IMI 086911, NRRL 1570	Unknown	Unknown	KX923944	KX924378	KX924167	
		CBS 199.61, DTO 342-C6, IFO 7027, IMI 086912, MUCL 9061, NHL 2265	*Oryza sativa*, milled	Burma	**LM652444**	KX924379	**HG380361**	
		CBS 366.65, DTO 342-F9, ATCC 16203, HACC 178	Unknown	India	KX923945	KX924380	KX924168	
		CBS 158.92, DTO 342-E6, FRR 4046	*Arachis hypogaea*, nut	Thailand	KX923946	KX924381	KX924169	
		DTO 220-I8	Indoor	Micronesia	KX923947	KX924382	KX924170	
		DTO 223-A1	Indoor	Micronesia	KX923948	KX924383	KX924171	
		DTO 223-A2	Indoor	Micronesia	KX923949	KX924384	KX924172	
M. verrucosus		**CBS 138278^{T}, DTO 351-D9, UTHSC 10-2601, FMR 12219**	Human, BAL fluid	USA	KX923950	**LM652658**	**HG380416**	**HG380493**
	S. sphaerospora	CBS 210.61, DTO 347-B3, IMI 086939	Unknown	Unknown	KX923951	KX924385	KX924173	
Pithoascus stoveri		**CBS 176.71^{T}, DTO 104-B6, ATCC 11173**	*Beta vulgaris*, root seedling	USA	KX923952	KX924386	KX924174	**LM652532**
Pseudoscopulariopsis schumacheri		**CBS 435.86^{NT}, DTO 170-H5**	Soil	Spain	KX923953	KX924387	KX924175	**LM652534**
Scopulariopsis africana sp. nov.	*M. manginii*	**CBS 118736^{T}, DTO 336-D1**	Mud, salt pan	South Africa	KX923954	KX924388	KX924176	KX924040
S. albida sp. nov.	*S. flava*	**CBS 119.43^{T}, DTO 334-G7**	Soil	Netherlands	**LN850800**	**LN850897**	**LM652592**	**LN850849**
	S. acremonium	CBS 415.51, DTO 334-H2	Unknown	Germany	KX923955	KX924389	KX924177	
S. alboflavescens	*S. koningii*	CBS 152.22, DTO 347-C5, IMI 086928, MUCL 9044	Unknown	France	**LN850785**	**LN850882**	KX924178	
		CBS 399.34^{T}, DTO 103-G6, UAMH 934	Human, skin	Austria	KX923956	**JQ434537**	KX924179	**LM652539**
	S. koningii	CBS 208.61, DTO 170-C6, IMI 086926, FMR 3654	Elephant	Unknown	**LN850786**	**LN850883**	**LN850931**	
		DTO 104-C7	Unknown	Unknown	KX923957	KX924390	KX924180	
S. asperula	*S. arnoldii*^{T}	CBS 204.27, DTO 334-F5, MUCL 9009, UAMH 923	Unknown	France	KX923958	KX924391	KX924181	
	S. fusca^{T}	CBS 401.34, DTO 103-G7, IFO 8181, IMI 086934, MUCL 9032, UAMH 930	Rabbit carcass	Austria	**LM652463**	KX924392	KX924182	
		CBS 105.35, DTO 334-F8, IMI 086925	Unknown	Unknown	KX923959	KX924393	KX924183	
	Torula bestae^{T}	CBS 289.38, DTO 103-H1, IMI 086927, MUCL 9012, UAMH 924	Human	Italy	KX923960	KX924394	KX924184	**LM652538**
	S. fusca	CBS 351.49, DTO 342-C4, MUCL 9033	*Sciurus vulgaris*, dead	Unknown	KX923961	KX924395	KX924185	
		CBS 390.52, DTO 334-H4, IMI 086924, LCP 224, MUCL 9043	*Calliphora vomitoria*, proboscis	France	KX923962	KX924396	KX924186	

Table 1. (Continued).

Name	Old name[1]	Strain numbers[2]	Host/Substrate	Country	GenBank accession number			
					ITS	*tub2*	*tef1*	LSU
	S. fusca	CBS 334.53, DTO 334-H5	Human, nail	Netherlands	**LN850788**	**LN850885**	KX924187	
		CBS 298.67, DTO 334-I4	*Triticum aestivum*	Turkey	**LN850789**	**LN850886**	**LN850934**	
		CBS 853.68, DTO 334-I5	Compost soil	Germany	KX923963	**JQ434558**	KX924188	
		CBS 872.68, DTO 334-I6, ATCC 16281	Wheat field soil	Germany	KX923964	KX924397	KX924189	
		CBS 668.74, DTO 335-A5	Soil	Egypt	KX923965	KX924398	KX924190	
		CBS 373.76, DTO 170-G6	Unknown	Netherlands	KX923966	KX924399	KX924191	
		CBS 114063, DTO 038-B3, DTO 335-B3	Wood sample	Germany	KX923967	KX924400	KX924192	
		CBS 117767, DTO 038-B6	Wood sample	Germany	KX923968	**LN850884**	KX924193	
	S. fusca	CBS 138116, DTO 335-D1	Alkaline soil	Russia	KX923969	KX924401	KX924194	
S. brevicaulis		CBS 120.20, DTO 334-F4, MUCL 9021	Unknown	Unknown	KX923970	KX924402	KX924195	
		CBS 273.30, DTO 334-F6, VKM F-175	Unknown	Unknown	KX923971	KX924403	KX924196	
	S. flava	CBS 334.35, DTO 334-G1	*Arge berberidis*, pupa	Czech Republic	**LN850790**	**LN850887**	**LN850935**	
	S. flava	CBS 335.35, DTO 334-G2, IMI 086922, MUCL 9035	*Pteronus pini*, pupa	Netherlands	**LM652477**	KX924404	KX924197	
		CBS 340.39, DTO 336-C4	Bone	South Africa	KX923972	KX924405	KX924198	
		CBS 341.39, DTO 334-G4	Unknown	Unknown	KX923973	KX924406	KX924199	
		CBS 147.41, DTO 334-G5	Human, nail	Netherlands	KX923974	KX924407	KX924200	
		CBS 467.48, DTO 103-H4, ATCC 7903, IMI 040026, IMI 061534, NRRL 1096	Unknown	Unknown	KX923975	KX924408	KX924201	
		CBS 398.54, DTO 170-C3, IMI 086919	Human, toe nail	UK	KX923976	KX924409	KX924202	
		CBS 112377, DTO 011-H5, DTO 038-A8	Indoor	Germany	KX923977	KX924410	KX924203	
		CBS 115540, DTO 335-B4	Air biofilter	Mexico	KX923978	KX924411	KX924204	
		CBS 116112, DTO 335-B5	Tattoo-paint	Czech Republic	KX923979	KX924412	KX924205	
		CBS 117277, DTO 001-F7, DTO 012-E7	Hat-rack in museum	Netherlands	KX923980	KX924413	KX924206	
		CBS 118469, DTO 338-H1	Tattoo-paint	UK	KX923981	KX924414	KX924207	
		CBS 118470, DTO 336-C8	Tattoo-paint	UK	KX923982	KX924415	KX924208	
		CBS 118471, DTO 335-B6	Tattoo-paint	UK	KX923983	KX924416	KX924209	
		CBS 118472, DTO 335-B7	Tattoo-paint	UK	KX923984	KX924417	KX924210	
		CBS 118473, DTO 338-H2	Tattoo-paint	UK	KX923985	KX924418	KX924211	
		CBS 118474, DTO 336-C9	Tattoo-paint	UK	KX923986	KX924419	KX924212	
		CBS 118993, DTO 335-B8	Unknown	France	KX923987	KX924420	KX924213	
		CBS 119549, DTO 335-B9	Human, skin biopsy	USA	KX923988	KX924421	KX924214	
		CBS 119550, DTO 335-C1	Human, blood culture	USA	KX923989	KX924422	KX924215	
	M. brevicaulis[T]	CBS 127812, DTO 138-E6, DTO 138-E7, UAMH 7770, MUCL 40726	Indoor air	Canada	**LM652465**	KX924423	**HG380363**	**HG380440**
		CBS 127825, DTO 138-E8, DTO 138-E9, UAMH 7880	Indoor air	Canada	KX923990	KX924424	KX924216	
		CBS 137631, DTO 335-C8	Alkaline soil	Russia	KX923991	KX924425	KX924217	
		CBS 137632, DTO 335-C9	Alkaline soil	Russia	KX923992	KX924426	KX924218	
		DTO 012-C7	Indoor air	Germany	KX923993	KX924427	KX924219	
		DTO 012-D9	Wall paper	Unknown	KX923994	KX924428	KX924220	
		DTO 012-F6	Plaster	Germany	KX923995	KX924429	KX924221	
		DTO 106-B6	Indoor, giraffes stay	Netherlands	KX923996	KX924430	KX924222	
		DTO 109-H4	Indoor	Denmark	KX923997	KX924431	KX924223	
		DTO 145-C7	Indoor	Germany	KX923998	KX924432	KX924224	
		DTO 168-A4	Indoor air, poultry house	Poland	KX923999	KX924433	KX924225	
		DTO 168-A5	Indoor air, poultry house	Poland	KX924000	KX924434	KX924226	
		DTO 168-A6	Indoor air, poultry house	Poland	KX924001	KX924435	KX924227	
		DTO 195-A1	Indoor, swab sample bakery	Netherlands	KX924002	KX924436	KX924228	
		DTO 197-F3	Indoor air sample	Netherlands	KX924003	KX924437	KX924229	
		DTO 240-A8	Archive	Netherlands	KX924004	KX924438	KX924230	
		DTO 305-A2	Indoor	South Africa	KX924005	KX924439	KX924231	
		DTO 305-A3	Indoor	USA	KX924006	KX924440	KX924232	
		DTO 305-A4	Indoor	USA	KX924007	KX924441	KX924233	
		DTO 305-A5	Indoor	USA	KX924008	KX924442	KX924234	
		DTO 305-A8	Indoor	USA	KX924009	KX924443	KX924235	

(*continued on next page*)

Table 1. (Continued).

Name	Old name[1]	Strain numbers[2]	Host/Substrate	Country	GenBank accession number			
					ITS	*tub2*	*tef1*	LSU
S. candida	*Nephrospora manginii*^{T}	CBS 170.27, DTO 347-C6, IMI 086931, UAMH 9135	Unknown	France	**LM652488**	**LM652694**	**LM652594**	
	M. manginii	CBS 205.27, DTO 347-C7, MUCL 9026	Unknown	France	**LM652483**	KX924444	KX924236	
	S. acremonium	CBS 305.31, DTO 336-C3	Unknown	USA	KX924010	KX924445	KX924237	
	M. manginii	CBS 353.36, DTO 334-G3	Indoor air, hospital	unknown	KX924011	KX924446	KX924238	
	S. acremonium	CBS 389.52, DTO 334-H3	Unknown	Italy	KX924012	KX924447	KX924239	
	M. manginii	CBS 254.69, DTO 335-A1	Greenhouse soil	Netherlands	KX924013	KX924448	KX924240	
	M. manginii	CBS 132.78, DTO 342-G3	Human, dentine	France	KX924014	**LN850898**	KX924241	
		DTO 032-A6	Indoor air, house	Netherlands	KX924015	KX924449	KX924242	
		DTO 138-B7	Indoor air	Germany	KX924016	KX924450	KX924243	
		DTO 139-D8	Indoor	Germany	KX924017	KX924451	KX924244	
		DTO 139-E7	Indoor	Germany	KX924018	KX924452	KX924245	
		DTO 139-E8	Indoor	Germany	KX924019	KX924453	KX924246	
		UAMH 9004^{ET}, MUCL 40743	Indoor air	Canada	**LM652484**	**LM652690**	**HG380381**	**HG380458**
S. caseicola sp. nov.	*S. acremonium*	**CBS 480.62^{T}, DTO 342-F8**	Cheese-coating	Netherlands	KX924020	KX924454	KX924247	KX924041
S. cordiae	*M. manginii*	CBS 816.73, DTO 335-A4	Soil	Australia	KX924021	KX924455	KX924248	
		CBS 138129^{T}, DTO 335-D2, UTHSC 09-866, FMR 12338	Human, finger	USA	KX924022	KX924456	KX924249	**HG380499**
S. flava		**CBS 207.61^{NT}, DTO 170-C5, IMI 086921, MUCL 9031**	Cheese	UK	KX924023	KX924457	**HG380387**	**HG380464**
	S. brevicaulis	CBS 108960, DTO 335-B2	Cheese	Denmark	**LN850804**	**LN850901**	**LN850949**	
S. macurae	*M. manginii*	**CBS 506.66^{T}, DTO 334-I3, ATCC 16685**	Chicken litter	Canada	**LN850805**	**LN850902**	KX924250	**LN850854**
S. sexualis sp. nov.	*M. manginii*	**CBS 250.64^{T}, DTO 338-G3, IFO 7555, NHL 2278, UAMH 1923**	*Oryza sativa*, milled	Burma	KX924024	KX924458	KX924251	KX924042
	M. manginii	CBS 667.71, DTO 335-A3, NRRL A-8022	Bat dung	USA	KX924025	KX924459	KX924252	
	M. manginii	CBS 332.78, DTO 342-G4	*Brassica oleracea*, seed	India	KX924026	KX924460	KX924253	
S. soppii		**UAMH 9169^{T}**	*Populus tremuloides*, wood	Canada	**LM652495**	**LM652698**	**LM652595**	**LM652552**
Yunnania carbonaria	*S. carbonaria*	**CBS 205.61^{T}, DTO 103-I3, IFO 8116, IMI 086941, MUCL 9027, NRRL 1860**	Soil	Panama	KX923820	KX924254	KX924044	**HG380462**
	S. brumptii	CBS 121662, DTO 220-H8	Dead hardwood branch	USA	KX923821	KX924255	KX924045	
Y. penicillata		**CBS 130296^{T}, DTO 139-F4**	Molded pork sample	China	**JN831361**	KY659807	KY659808	KY659809
Y. smithii sp. nov.	*S. carbonaria*	**CBS 855.68^{T}, DTO 354-C2**	Garden soil	Germany	KX923822	KX924256	KX924046	KX924028

[1] The ^{T} indicates the ex-type isolate of the synonymised species.

[2] ATCC: American Type Culture Collection, Manassas, VA, USA; BMU: Beijing Medical University (Peking University), Beijing China; CBS: Culture Collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: China General Microbiological Culture Collection Center, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China; DTO: Working Collection of the Applied and Industrial Mycology Group of the Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands; FMR: Facultat de Medicina i Ciències de la Salut, Reus, Spain; FRR: Division of Food Research, Food Research Laboratory, CSIRO, North Ryde, Australia; HACC: Research Laboratory, Hindustan Antibiotics Ltd., Pimpri, Pune, India; IFO: Institute for Fermentation Culture Collection, Osaka, Japan; IMI: Culture Collection of CABI Europe-UK, Egham, UK; LCP: Laboratory of Cryptogamy, National Museum of Natural History, Paris, France; MUCL: (Agro)Industrial Fungi and Yeast Collection of the Belgian Co-ordinated Collections of Micro-organisms (BCCM), Louvain-la Neuve, Belgium; NHL: National Institute of Hygienic Sciences, Tokyo, Japan; NRRL: ARS Culture Collection, U.S. Department of Agriculture, Peoria, IL, USA; RGR: Personal Collection of Rodney G. Roberts; UAMH: University of Toronto, UAMH Centre for Global Microfungal Biodiversity, Toronto, Canada; UTHSC: Fungus Testing Laboratory, Department of Pathology, University of Texas Health Science Center, San Antonio, TX, USA; VKM: All-Russian Collection of Microorganisms, Moscow, Russia. Ex-epitype, -isotype, -type, and -neotype isolates are indicated with ^{ET}, ^{IT}, ^{T} and ^{NT}, respectively, and printed in bold.

frequency was set at 1 000 and the temperature value of the heated chain was set at 0.1. The run stopped when the average standard deviation of split frequencies reached below 0.01. Burn-in was set to 25 % after which the likelihood values were stationary. Tracer v. 1.5.0 (Rambaut & Drummond 2009) was used to confirm the convergence of chains. Maximum-likelihood analyses including 500 bootstrap replicates using RAxML v. 7.2.6 (Stamatakis & Alachiotis 2010) were additionally run on both the single gene-sequence alignments and the combined gene-sequence alignment. The resulting trees were printed with TreeView v. 1.6.6 (Page 1996) and, together with the alignments, deposited into TreeBASE (http://www.treebase.org).

In order to get optimal sequence alignments, the dataset was divided in three different phylogenies. Based on the ITS, *tub2* and *tef1* sequences a separate species phylogeny for *Microascus* (157 isolates) and for *Scopulariopsis* (89 isolates) was constructed. Following these species phylogenies a genus phylogeny including one isolate per recognised species (when present the ex-type isolate) was constructed based on the LSU, ITS and *tef1* sequences (52 isolates). The *tub2* sequences were omitted in the genus phylogeny because of alignment difficulties. Based on former phylogenetic studies (Jagielski *et al.* 2016, Sandoval-Denis *et al.* 2016) *Pithoascus stoveri* (CBS 176.71) was used as out-group in the *Microascus* phylogeny, *Pseudoscopulariopsis schumacheri* (CBS 435.86) in the *Scopulariopsis* phylogeny, and *Cephalotrichum stemonitis* (CBS 103.19) in the genus phylogeny.

Habitat study

All studied *Microascus*, *Scopulariopsis* and *Yunnania* isolates are assigned to one of nine different habitats (animal, dung, food, human, indoor, insect, plant, soil, others) based on their origin of isolation. Subsequently, these habitats are plotted behind the species name, to which the isolate belongs, in the genus phylogeny tree. The habitats from isolates studied by others (Ropars *et al.* 2012, Jagielski *et al.* 2016, Sandoval-Denis *et al.* 2016) are also included. Finally, a table showing which *Microascus*, *Scopulariopsis* and *Yunnania* species are present in which habitat is constructed.

Morphology

Cultures were incubated on oatmeal agar (OA), malt extract agar (MEA) and dichloran 18 % glycerol agar (DG18) plates (recipes Samson *et al.* 2010) at 25 °C in the dark. After 14 d the colony diameters were measured and the colony characters noted. Colony colours were rated according to Rayner (1970). Measurements and descriptions of microscopic structures were made from cultures grown on synthetic nutrient agar (SNA, Samson *et al.* 2010) at 25 °C in the dark for 14 d or longer to ensure ascomata development. Slide preparations of the asexual morph structures were made with the sellotape technique (Schubert *et al.* 2007) or mounted in 85 % lactic acid, like the sexual morph structures. Photographs of characteristic structures were made with a Zeiss Axio Imager A2 microscope equipped with a Nikon DS-Ri2 high-definition colour camera head using differential interference contrast (DIC) optics and the Nikon software NIS-elements D v. 4.50. Furthermore, growth at 36 °C and 40 °C in the dark on OA was tested.

RESULTS

Microascus phylogeny

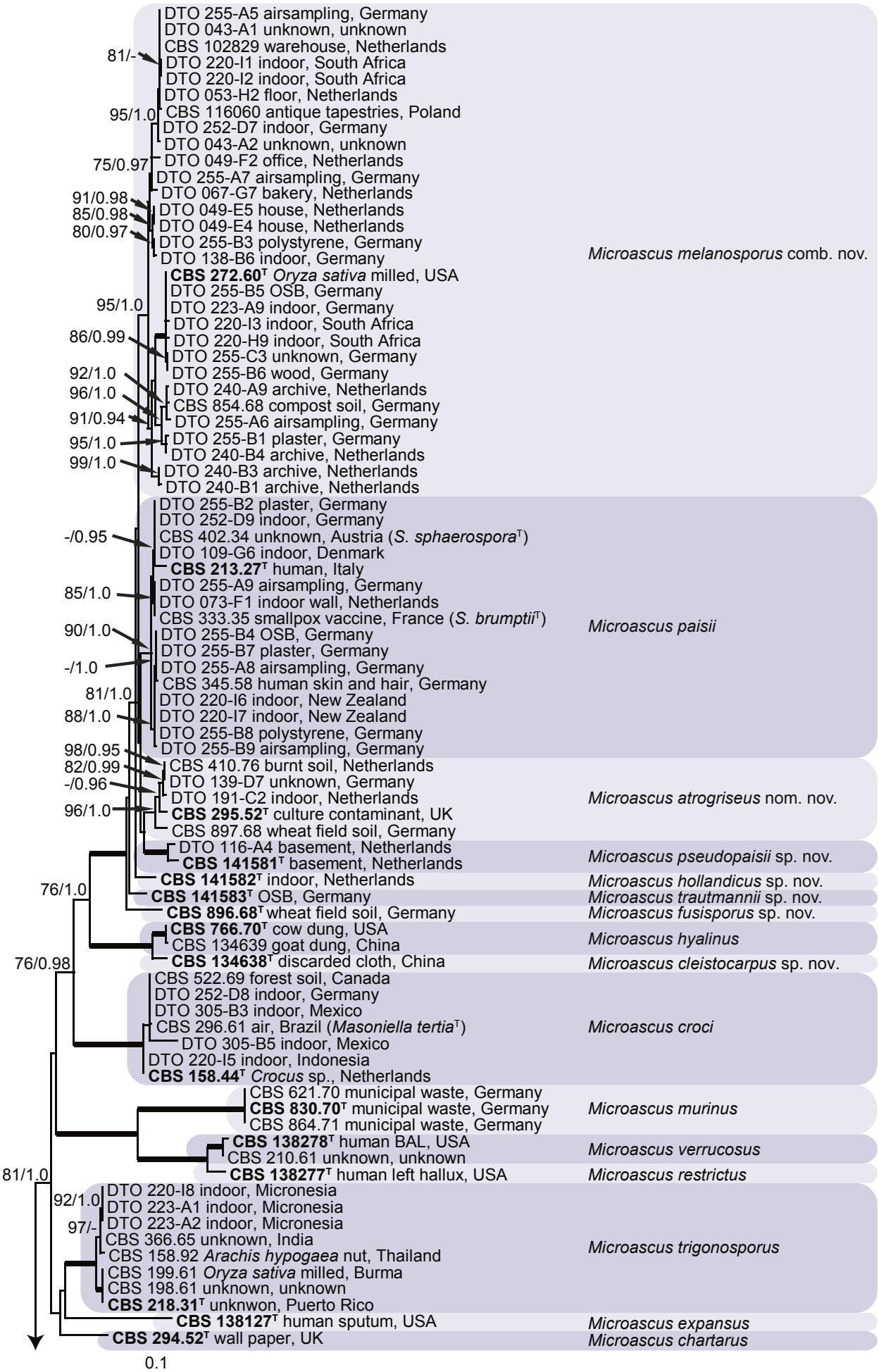
For the phylogeny 157 isolates were selected to represent the genus *Microascus* (Table 1) including the outgroup-isolate *Pithoascus stoveri* (CBS 176.71). The aligned sequences of the ITS (474 characters), *tub2* (529 characters), and *tef1* (898 characters) gene regions had a total length of 1 901 characters, with respectively 147, 253, and 221 unique site patterns. The GTR model with a gamma-distributed rate variation was suggested as model for the ITS and *tef1* alignments and the HKY model with a gamma-distributed rate variation for the *tub2* alignment. After discarding the burn-in phase trees, the multi-gene Bayesian analysis resulted in 4 172 trees from two runs from which the majority rule consensus tree and posterior probabilities were calculated. The multi-gene phylogeny divided the isolates in 33 *Microascus* species (clades, Fig. 1), and three *Yunnania* species (clades, Fig. 1). As a result of this study, seven new *Microascus* species (*M. appendiculatus*, *M. cleistocarpus*, *M. fusisporus*, *M. hollandicus*, *M. micronesiensis*, *M. pseudopaisii*, and *M. trautmannii*), one new *Yunnania* species (*Y. smithii*), one new name (*M. atrogriseus*) and two new name combinations (*M. melanosporus*, and *Y. carbonaria*) are proposed. The recently established genus *Fuscoannellis* is synonymised under *Yunnania*. All descriptions are provided below in the taxonomy section. For the genus *Microascus*, only the *tef1* phylogeny can distinguish all identified species. This is in congruence with Ropars *et al.* (2012) and Jagielski *et al.* (2016). With *tub2*, the species *M. restrictus* and *M. verrucosus* cannot be separated, they can molecularly only clearly be distinguished based on their *tef1* sequence (ITS 2 nt difference, *tub2* 1 nt difference, *tef1* 20 nt difference). The ITS single gene phylogeny is least distinctive. Besides *M. restrictus* and *M. verrucosus*, *M. alveolaris* and *M. terreus*, *M. intricatus* and *M. onychoides*, *M. paisii* and *M. melanosporus* and the three *Yunnania* species cannot be separated based on their ITS sequences. Furthermore, the four isolates of *M. cinereus* are split into two clades based on their ITS sequence alone (data not shown, all single gene phylogenies are submitted to TreeBase).

Scopulariopsis phylogeny

For the phylogeny 89 isolates were selected to represent the genus *Scopulariopsis* (Table 1) including the outgroup-isolate *Pseudoscopulariopsis schumacheri* (CBS 435.86). The aligned sequences of the ITS (441 characters), *tub2* (502 characters), and *tef1* (887 characters) gene regions had a total length of 1 830 characters, with respectively 58, 143, and 109 unique site patterns. The TrN model with a gamma-distributed rate variation was suggested as model for the ITS alignment, the GTR model with a gamma-distributed rate variation as model for the *tef1* alignment and the HKY model with a gamma-distributed rate variation for the *tub2* alignment. After discarding the burn-in phase trees, the multi-gene Bayesian analysis resulted in 2 214 trees from both runs from which the majority rule consensus tree and posterior probabilities were calculated. The multi-gene phylogeny divided the isolates in 12 species (clades, Fig. 2) of which four are proposed as new; *S. africana*, *S. albida*, *S. caseicola* and *S. sexualis*. Their descriptions are provided below in the taxonomy section. Both with only the *tub2* or *tef1* sequence all 12 species can be identified, although the *S. candida* isolates do not form a monophyletic clade. Based on ITS alone, only five species can be identified, *S. alboflavescens*, *S. brevicaulis*, *S. flava*, *S. macurae* and *S. soppii* (data not shown, all single gene phylogenies are submitted to TreeBase).

Genus phylogeny with habitat study

For the genus phylogeny (Fig. 3) 52 isolates were selected to represent all above recognised species in the genera *Microascus*, *Scopulariopsis* and *Yunnania* together with *Pithoascus*


DTO 255-A5 airsampling, Germany
DTO 043-A1 unknown, unknown
CBS 102829 warehouse, Netherlands
DTO 220-I1 indoor, South Africa
DTO 220-I2 indoor, South Africa
DTO 053-H2 floor, Netherlands
CBS 116060 antique tapestries, Poland
DTO 252-D7 indoor, Germany
DTO 043-A2 unknown, unknown
DTO 049-F2 office, Netherlands
DTO 255-A7 airsampling, Germany
DTO 067-G7 bakery, Netherlands
DTO 049-E5 house, Netherlands
DTO 049-E4 house, Netherlands
DTO 255-B3 polystyrene, Germany
DTO 138-B6 indoor, Germany
CBS 272.60T Oryza sativa milled, USA
DTO 255-B5 OSB, Germany
DTO 223-A9 indoor, Germany
DTO 220-I3 indoor, South Africa
DTO 220-H9 indoor, South Africa
DTO 255-C3 unknown, Germany
DTO 255-B6 wood, Germany
DTO 240-A9 archive, Netherlands
CBS 854.68 compost soil, Germany
DTO 255-A6 airsampling, Germany
DTO 255-B1 plaster, Germany
DTO 240-B4 archive, Netherlands
DTO 240-B3 archive, Netherlands
DTO 240-B1 archive, Netherlands
Microascus melanosporus comb. nov.
DTO 255-B2 plaster, Germany
DTO 252-D9 indoor, Germany
CBS 402.34 unknown, Austria (S. sphaerospora T)
DTO 109-G6 indoor, Denmark
CBS 213.27T human, Italy
DTO 255-A9 airsampling, Germany
DTO 073-F1 indoor wall, Netherlands
CBS 333.35 smallpox vaccine, France (S. brumptii T)
DTO 255-B4 OSB, Germany
DTO 255-B7 plaster, Germany
DTO 255-A8 airsampling, Germany
CBS 345.58 human skin and hair, Germany
DTO 220-I6 indoor, New Zealand
DTO 220-I7 indoor, New Zealand
DTO 255-B8 polystyrene, Germany
DTO 255-B9 airsampling, Germany
Microascus paisii
CBS 410.76 burnt soil, Netherlands
DTO 139-D7 unknown, Germany
DTO 191-C2 indoor, Netherlands
CBS 295.52T culture contaminant, UK
CBS 897.68 wheat field soil, Germany
Microascus atrogriseus nom. nov.
DTO 116-A4 basement, Netherlands
CBS 141581T basement, Netherlands
Microascus pseudopaisii sp. nov.
CBS 141582T indoor, Netherlands
Microascus hollandicus sp. nov.
CBS 141583T OSB, Germany
Microascus trautmannii sp. nov.
CBS 896.68T wheat field soil, Germany
Microascus fusisporus sp. nov.
CBS 766.70T cow dung, USA
CBS 134639 goat dung, China
Microascus hyalinus
CBS 134638T discarded cloth, China
Microascus cleistocarpus sp. nov.
CBS 522.69 forest soil, Canada
DTO 252-D8 indoor, Germany
DTO 305-B3 indoor, Mexico
CBS 296.61 air, Brazil (Masoniella tertia T)
DTO 305-B5 indoor, Mexico
DTO 220-I5 indoor, Indonesia
CBS 158.44T Crocus sp., Netherlands
Microascus croci
CBS 621.70 municipal waste, Germany
CBS 830.70T municipal waste, Germany
CBS 864.71 municipal waste, Germany
Microascus murinus
CBS 138278T human BAL, USA
CBS 210.61 unknown, unknown
Microascus verrucosus
CBS 138277T human left hallux, USA
Microascus restrictus
DTO 220-I8 indoor, Micronesia
DTO 223-A1 indoor, Micronesia
DTO 223-A2 indoor, Micronesia
CBS 366.65 unknown, India
CBS 158.92 Arachis hypogaea nut, Thailand
CBS 199.61 Oryza sativa milled, Burma
CBS 198.61 unknown, unknown
CBS 218.31T unknwon, Puerto Rico
Microascus trigonosporus
CBS 138127T human sputum, USA
Microascus expansus
CBS 294.52T wall paper, UK
Microascus chartarus
81/-
95/1.0
75/0.97
91/0.98
85/0.98
80/0.97
95/1.0
86/0.99
92/1.0
96/1.0
91/0.94
95/1.0
99/1.0
-/0.95
85/1.0
90/1.0
-/1.0
81/1.0
88/1.0
98/0.95
82/0.99
-/0.96
96/1.0
76/1.0
76/0.98
81/1.0
92/1.0
97/-
0.1

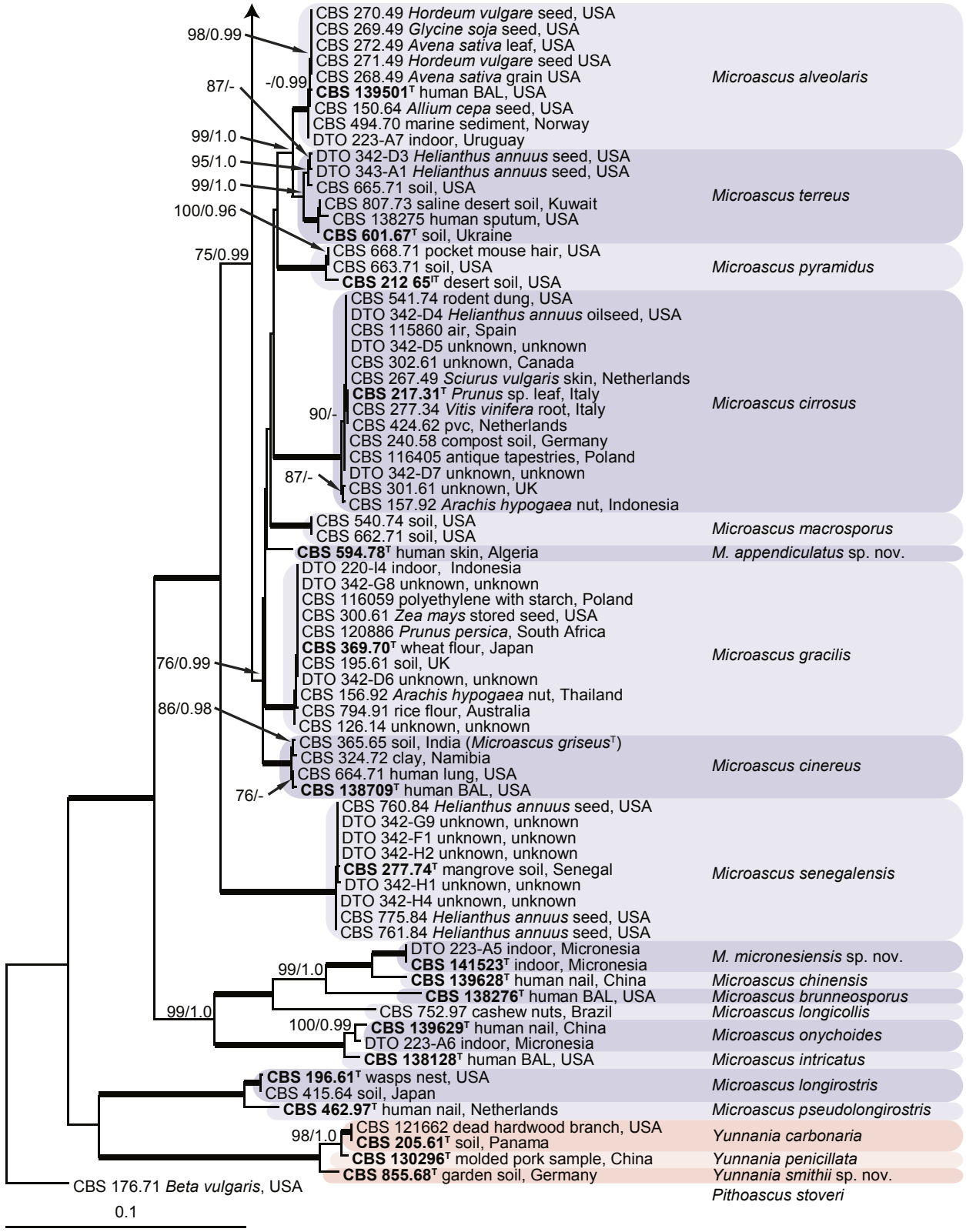


Fig. 1. (Continued).

stoveri (CBS 176.71), *Pseudoscopulariopsis schumacheri* (CBS 435.86), *Cephalotrichum asperulum* (CBS 582.71) and the outgroup isolate *Cephalotrichum stemonitis* (CBS 103.19). The phylogeny was constructed based on the LSU, ITS and *tef1* sequences. The aligned sequences of the LSU (533 characters), ITS (474 characters), and *tef1* (814 characters) gene regions had a total length of 1 821 characters, with respectively 93, 175, and 209 unique site patterns. The GTR model with a gamma-

Fig. 1. Maximum likelihood tree based on the ITS, *tub2* and *tef1* sequences of 157 isolates representing the genera *Microascus* and *Yunnania*. The RAxML bootstrap support values ≥75 % (BS) and Bayesian posterior probabilities ≥0.95 (PP) are given at the nodes. Thickened lines indicate a BS of 100 % and a PP of 1.0. Ex-type strain numbers are in **bold** face and indicated with ^{T} (or ^{NT} when ex-neotype). Species names between parentheses represent synonymised species names. The tree was rooted to *Pithoascus stoveri* (CBS 176.71).

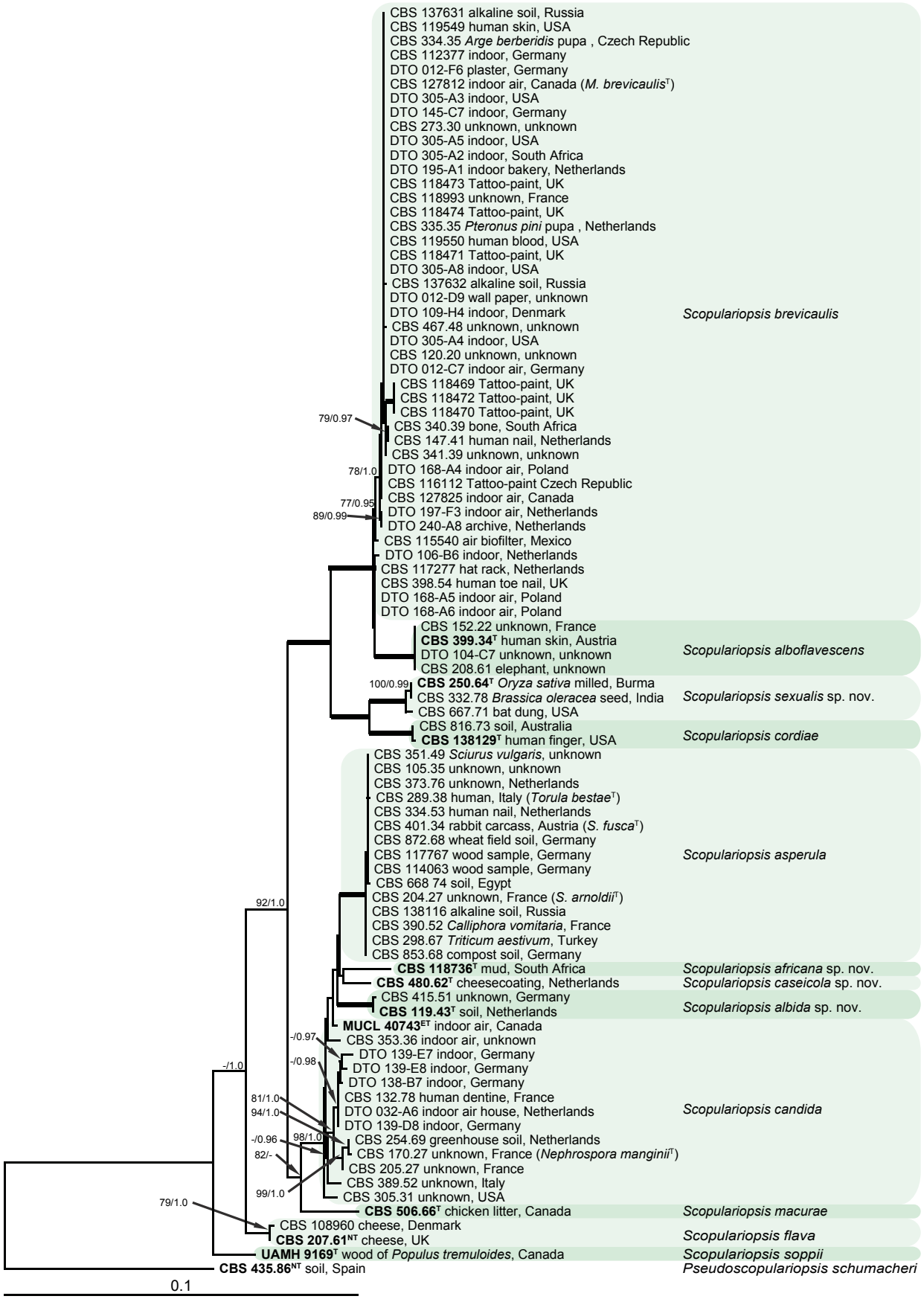


Fig. 2. Maximum likelihood tree based on the ITS, *tub2* and *tef1* sequences of 89 isolates representing the genus *Scopulariopsis*. The RAxML bootstrap support values ≥75 % (BS) and Bayesian posterior probabilities ≥0.95 (PP) are given at the nodes. Thickened lines indicate a BS of 100 % and a PP of 1.0. Ex-type strain numbers are in **bold** face and indicated with ^{T} (or ^{NT} or ^{ET} when ex-neotype or ex-epitype respectively). Species names between parentheses represent synonymised species names. The tree was rooted to *Pseudoscopulariopsis schumacheri* (CBS 435.86).

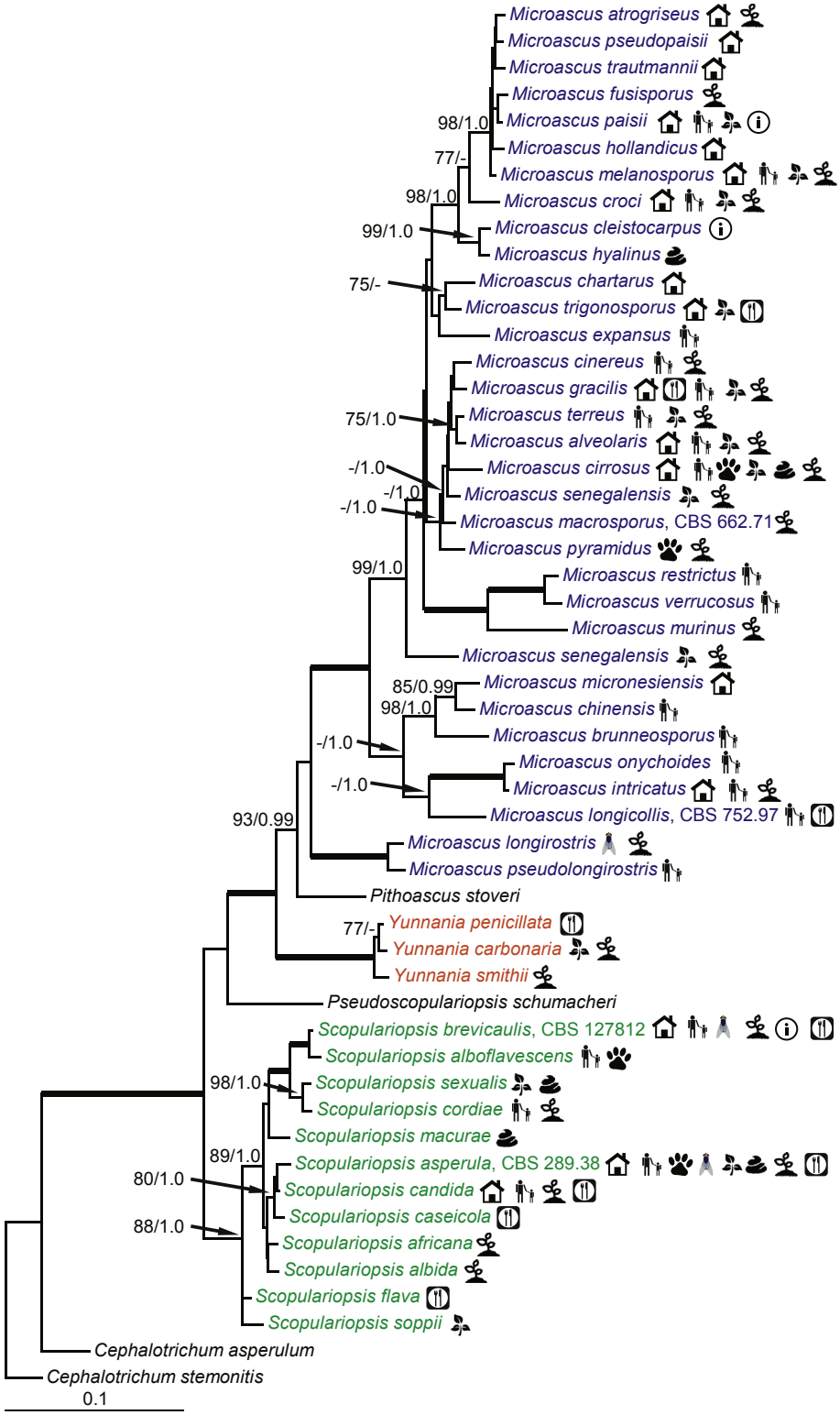


Fig. 3. Maximum likelihood tree based on the LSU, ITS and *tef1* sequences of 52 isolates. The RAxML bootstrap support values ≥75 % (BS) and Bayesian posterior probabilities ≥0.95 (PP) are given at the nodes. Thickened lines indicate a BS of 100 % and a PP of 1.0. When no collection number is mentioned behind the species name, the type-isolate is used. The tree was rooted to *Cephalotrichum stemonitis* (CBS 103.19). The habitats where the species are found are plotted behind the species names: = indoor; = animal; = dung; = food; = human; = insect; = plant; = soil; = others.

distributed rate variation was suggested as model for the ITS and *tef1* alignments and the TrN model with a gamma-distributed rate variation for the LSU alignment. After discarding the burn-in phase trees, the multi-gene Bayesian analysis resulted in 1 180 trees from two runs from which the majority rule consensus tree and posterior probabilities were calculated. The habitats are plotted behind the species names in the genus tree (Fig. 3) and placed in an overview table depicting the species per habitat (Table 2). No specific clustering of habitat preference related to phylogenetic relationships can be found, the different habitats are scattered over the phylogenetic tree (Fig. 3).

Seventeen species are found in the indoor environment, 14 *Microascus* species and three *Scopulariopsis* species (Table 2). Most of them are only occasionally found in the indoor environment. *Scopulariopsis brevicaulis* (22 indoor isolates) and *M. melanosporus* (19 indoor isolates) are the most common indoor

Table 2. Current species within *Microascus*, *Scopulariopsis* and *Yunnania* per habitat.

Habitat	Species
Indoor	*M. alveolaris*, *M. atrogriseus*, *M. chartarus*, *M. cirrosus*, *M. croci*, *M. gracilis*, *M. hollandicus*, *M. intricatus*, *M. melanosporus*, *M. micronesiensis*, *M. paisii*, *M. pseudopaisii*, *M. trautmannii*, *M. trigonosporus*, *S. asperula*, *S. brevicaulis*, *S. candida*
Animal	*M. cirrosus*, *M. pyramidus*, *S. alboflavescens*, *S. asperula*
Dung	*M. cirrosus*, *M. hyalinus*, *S. asperula*, *S. sexualis*, *S. macurae*
Food	*M. gracilis*, *M. longicollis*, *M. trigonosporus*, *S. asperula*, *S. brevicaulis*, *S. candida*, *S. caseicola*, *S. flava*, *Y. penicillata*
Human	*M. alveolaris*, *M. appendiculatus*, *M. brunneosporus*, *M. chinensis*, *M. cinereus*, *M. cirrosus*, *M. croci*, *M. expansus*, *M. gracilis*, *M. intricatus*, *M. longicollis*, *M. melanosporus*, *M. onychoides*, *M. paisii*, *M. restrictus*, *M. terreus*, *M. verrucosus*, *M. pseudolongirostris*, *S. alboflavescens*, *S. asperula*, *S. brevicaulis*, *S. candida*, *S. cordiae*
Insect	*M. longirostris*, *S. asperula*, *S. brevicaulis*
Plant	*M. alveolaris*, *M. cirrosus*, *M. croci*, *M. gracilis*, *M. melanosporus*, *M. paisii*, *M. senegalensis*, *M. terreus*, *M. trigonosporus*, *S. asperula*, *S. sexualis*, *S. soppii*, *Y. carbonaria*
Soil	*M. alveolaris*, *M. atrogriseus*, *M. cinereus*, *M. cirrosus*, *M. croci*, *M. fusisporus*, *M. gracilis*, *M. intricatus*, *M. longirostris*, *M. macrosporus*, *M. melanosporus*, *M. murinus*, *M. pyramidus*, *M. senegalensis*, *M. terreus*, *S. africana*, *S. albida*, *S. asperula*, *S. brevicaulis*, *S. candida*, *S. cordiae*, *Y. carbonaria*, *Y. smithii*
Others	*M. paisii*, *M. cleistocarpus*, *S. brevicaulis*

species, in number of isolates, followed by *M. paisii* (8 indoor isolates), *S. candida* (7 indoor isolates), and *M. croci* (5 indoor isolates). Ten species which are found indoor are also found in relation with humans (Fig. 3), but mostly only from skin or nail infections, and more rarely in other tissues like pulmonary tissue (e.g. *M. cirrosus*) or blood culture (e.g. *S. brevicaulis*). This needs to be taken into account when trying to indicate the risk for human health.

Scopulariopsis asperula can be found in all included habitats, followed by *S. brevicaulis* and *M. cirrosus* which both are found in six different habitats and *M. gracilis* found in five different habitats (Fig. 3). These species are all also found indoor, which is not surprisingly considering their non-selective habitats. Five species, *M. chartarus*, *M. hollandicus*, *M. micronesiensis*, *M. pseudopaisii* and *M. trautmannii*, are only found in the indoor environment. Of these five species, three are single isolate species and the other two only include two isolates (*M. micronesiensis* and *M. pseudopaisii*). The two isolates of *M. pseudopaisii* are isolated from the same place, and could be seen as duplicates. *Microascus micronesiensis* has been found in two different houses in Micronesia in different cities on separate occasions, and has therefore the most potential in being a true indoor species.

TAXONOMY

Based on the multi-gene species phylogenies (Figs 1 and 2) 33 *Microascus* species, 12 *Scopulariopsis* species, and three *Yunnania* species are recognised. In total 12 new species (four *Scopulariopsis*, seven *Microascus* and one *Yunnania* species), and a new name and two new name combination are proposed, which descriptions are provided below. Additionally, all recent name changes are summarised in an overview table (Table 3).

Microascus appendiculatus Woudenb. & Samson **sp. nov.** MycoBank MB818278. Fig. 4.

Etymology: name refers to its conidia with a basal appendage.

Ascomata abundant, immersed, ostiolate, globose to subglobose with a short (up to 45 µm long) cylindrical ostiolar neck, (134–)158–208(–218) µm diam., black, glabrous; peridium with a *textura angularis*. *Asci* irregularly ellipsoidal, (19.5–)21–24.5(–25) × (10–)12.5–17.5(–20) µm. *Ascospores* fusiform, (5.5–)6.5–7.5(–8) × (3.5–)4–4.5(–5) µm, honey, pale luteous in mass, smooth, with a single inconspicuous germ pore. *Conidiophores* arising from substrate mycelium, indistinctive or simple, rarely branched, bearing terminally a single annellide. *Annellides* lageniform to ampulliform, (6–)7.5–11(–13.5) µm long, (2–)2.5–3(–3.5) µm broad at the widest part, tapering abruptly to a cylindrical annellate zone 0.5–1(–1.5) µm wide, hyaline to subhyaline, smooth-walled. *Conidia* subglobose with small basal appendage, (5–)5.5–7 × (3.5–)4–5(–5.5) µm, subhyaline, older conidia covered with hazel mucilaginous coating, smooth, thick-walled, arranged in short chains.

Culture characteristics: Colonies on OA attaining a diameter of 27–28 mm after 14 d at 25 °C, flat, white to cream-coloured with smoke grey zones and olivaceous grey ascomata, margin undulated. On MEA attaining a diameter of 17–19 mm, convex, white to cream-coloured, radially striated with dentate margin. On DG18 attaining a diameter of 19 mm, low convex, white to cream-coloured with partly a grey olivaceous ring close to the edge, margin undulate. On OA able to grow at 36 and 40 °C.

Specimen examined: **Algeria**, from human skin, collection date and collector unknown, (**holotype** CBS H-22744, culture **ex-type** CBS 594.78).

Notes: The ex-type strain of *M. appendiculatus* (CBS 594.78) was recently published as *M. senegalensis* (Jagielski *et al.* 2016). However, the sequences of their two included *M. senegalensis* isolates deposited on GenBank (which are confirmed by resequencing the isolate) only have 94 % identity based on ITS, 99 % on LSU, 90 % on *tub2* and 96 % on *tef1*. Although they seem to cluster together in their phylogenetic tree, our phylogenies (all single gene phylogenies, and the combined phylogeny Fig. 2) places CBS 594.78 as a separate species, which is described here as *M. appendiculatus*. Also morphologically it is distinct from *M. senegalensis* with the subglobose conidia with small basal appendage and the hazel mucilaginous coating around the older conidia.

Microascus atrogriseus Woudenb. & Samson **nom. nov.** MycoBank MB818284. Fig. 5.

Basionym: *Masonia grisea* G. Sm., Trans. Brit. Mycol. Soc. 35: 149. 1952, non *Microascus griseus* P.N. Mathur & Thirum,. 1963.
≡ *Masoniella grisea* (G. Sm.) G. Sm., Trans. Brit. Mycol. Soc. 35: 237. 1952.

Etymology: name refers to the original description of the basionym where “atro-griseis coloniis” are described.

Table 3. Overview of recent name changes in *Scopulariopsis* and scopulariopsis-like species.

Old name	Current name	Old name	Current name
Kernia hyalinus	*Microascus hyalinus*	*Scopulariopsis brevicaulis* var. *glabra*	*Scopulariopsis candida*
Masonia chartarum	*Microascus chartarus*	*S. brumptii*	*Microascus paisii*
M. grisea	*Microascus atrogriseus*	*S. carbonaria*	*Yunnania carbonaria*
Masoniella chartarum	*Microascus chartarus*	*S. casei*	*Scopulariopsis flava*
M. croci	*Microascus croci*	*S. chartarum*	*Microascus chartarus*
M. grisea	*Microascus atrogriseus*	*S. croci*	*Microascus croci*
M. tertia	*Microascus croci*	*S. fusca*	*Scopulariopsis asperula*
Microascus brevicaulis	*Scopulariopsis brevicaulis*	*S. gracilis*	*Microascus gracilis*
M. exsertus	*Pithoascus exsertus*	*S. grylli*	*Scopulariopsis flava*
M. griseus	*Microascus cinereus*	*S. hibernica*	*Pseudoscopulariopsis hibernica*
M. intermedius	*Pithoascus intermedius*	*S. hominis*	*Scopulariopsis brevicaulis*
M. manginii	*Scopulariopsis candida*	*S. insectivora*	Scopulariopsis *brevicaulis*
M. nidicola	*Pithoascus nidicola*	*S. ivorensis*	*Scopulariopsis asperula*
M. niger	*Scopulariopsis asperula*	*S. koningii*	*Scopulariopsis brevicaulis*
M. schumacheri	*Pseudoscopulariopsis schumacheri*	*S. murina*	*Microascus murinus*
M. soppii	*Scopulariopsis soppii*	*S. paisii*	*Microascus paisii*
M. stoveri	*Pithoascus stoveri*	*S. penicilloides*	*Scopulariopsis brevicaulis*
M. stysanophorus	*Pseudoscopulariopsis schumacheri*	*S. roseola*	*Scopulariopsis asperula*
M. trigonosporus var. *terreus*	*Microascus terreus*	*S. rufulus*	*Scopulariopsis brevicaulis*
Nephrospora manginii	*Scopulariopsis candida*	*S. sphaerospora*	*Microascus paisii*
Pithoascus schumacheri	*Pseudoscopulariopsis schumacheri*	*S. stercoraria*	*Scopulariopsis brevicaulis*
P. stysanophorus	*Pesudoscopulariopsis schumacheri*	*S. trigonospora*	*Microascus trigonosporus*
Scopulariopsis arnoldii	*Scopulariopsis asperula*	*S. versicolor*	*Microascus paisii*
S. atra	*Pithoascus ater*	*Torula asperula*	*Scopulariopsis asperula*
S. aurea	*Scopulariopsis flava*	*T. bestae*	*Scopulariopsis asperula*
S. bestae	*Scopulariopsis asperula*	*T. paisii*	*Microascus paisii*
S. brevicaulis var. *alba*	*Scopulariopsis flava*		

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple or indistinctive, bearing one or multiple annellides. *Annellides* ampulliform, (4.5–)5.5–8.5(–10) µm long, 2–3 µm broad at the widest part, tapering abruptly to a cylindrical annellate zone 1–1.5(–2) µm wide, hyaline, smooth-walled. *Conidia* broadly ellipsoidal to short clavate with truncate base, (3–)3.5–4(–4.5) × (2.5–)3(–3.5) µm, hyaline when young turning hazel when ageing, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 17–20 mm after 14 d at 25 °C, flat, white to cream-coloured with (pale) olivaceous grey to iron grey centre, margin crenated. On MEA attaining a diameter of 13–14 mm, convex, white to very pale olivaceous grey, radially striated edge with crenated margin. On DG18 attaining a diameter of 10–20 mm, low convex, white to pale olivaceous grey, margin entire. On OA no growth at 36 and 40 °C.

Specimens examined: **England**, London, isolated as culture contaminant, 1946, G. smith, (culture **ex-type** CBS 295.52). **Germany**, indoor environment, before Aug. 2010, collector unknown, DTO 139-D7. **Netherlands**, from a swab sample of an indoor horse arena, Mar. 2012, Houba, DTO 191-C2.

Notes: *Microascus atrogriseus* is morphologically indistinguishable from *M. paisii*. Sequence data is necessary to distinguish it from *M. paisii*. All three genes used in this manuscript can separate the two species (ITS 5 nt difference, *tub2* 20 nt difference, and *tef1* 9 nt difference between the type isolates of both species).

Microascus cleistocarpus Woudenb., X. Wei Wang & Samson **sp. nov.** MycoBank MB803264. Fig. 6.

Etymology: named after the non-ostiolate ascomata.

Ascomata abundant, immersed, non-ostiolate, globose to subglobose, (50–)52–71(–83) µm diam., dark brown, glabrous; peridium with a *textura angularis*. *Asci* ovoid to subglobose, (11–)11.5–14(–15) × (7–)7.5–9.5(–10.5) µm. *Ascospores* broad fusiform to ellipsoidal, (6.5–)7–8 × 4–5 µm, buff to honey, smooth, with a single inconspicuous germ pore. *Conidiophores* arising from substrate mycelium, indistinctive, simple or occasionally branched, bearing terminally a single annellide. *Annellides* lageniform to ampulliform, (8–)9–14.5(–17.5) µm long, (2–)2.5–3 µm broad at the widest part, tapering gradually to a cylindrical annellate zone 1–1.5(–2) µm wide, hyaline to subhyaline, smooth-walled. *Conidia* obovoid with truncate base, (4.5–)5–6(–6.5) × 3.5–4.5 µm, hyaline, turning to hazel when ageing, smooth or finely roughened, thick-walled, arranged in chains.

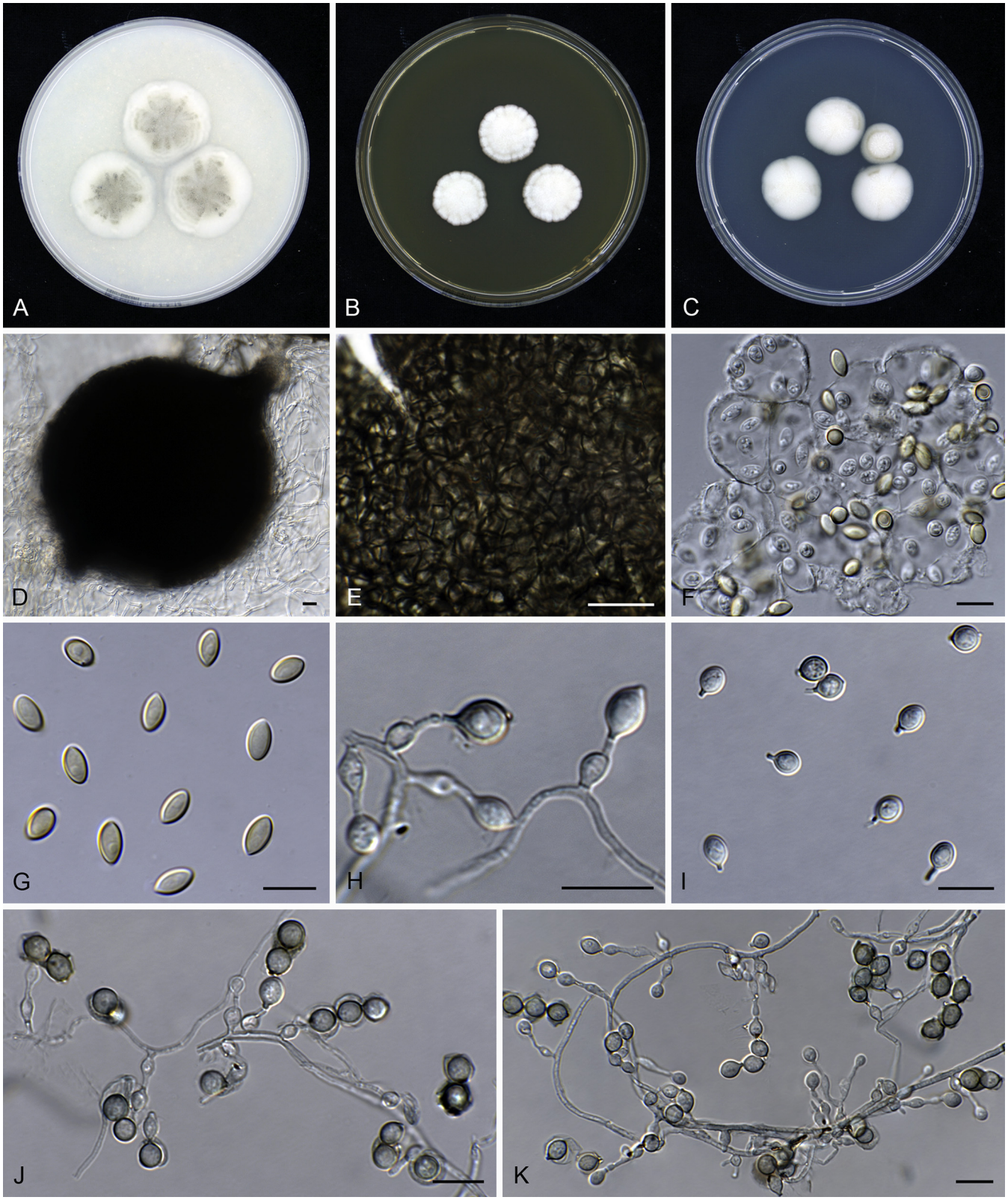


Fig. 4. *Microascus appendiculatus* sp. nov. CBS 594.78. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D.** Ascoma. **E.** Ascomatal wall. **F.** Asci and ascospores. **G.** Ascospores. **H, J–K.** Conidiophores, annellides and conidia. **I.** Conidia. Scale bars = 10 µm.

Culture characteristics: Colonies on OA attaining a diameter of 21–24 mm after 14 d at 25 °C, flat, white to cream-coloured with greenish olivaceous to olivaceous buff and pale olivaceous grey zones, radially striated with dentate margin. On MEA attaining a diameter of 18–19 mm, crateriform, pale olivaceous grey to olivaceous grey and greyish sepia, radially striated and folded in the centre, margin crenated. On DG18 attaining a diameter of 13–14 mm, crateriform, buff to rosy buff, radially striated and folded in the centre, margin undulate. On OA still growth at 36 °C, no growth at 40 °C.

Specimen examined: **China**, Inner Mongolia, Ulanqab city, Huade county, from discarded cloth, 24 Jul. 2011, Y-Y Huo, (**holotype** HMAS 2444424, culture **ex-type** CBS 134638 = CGMCC 3.15222).

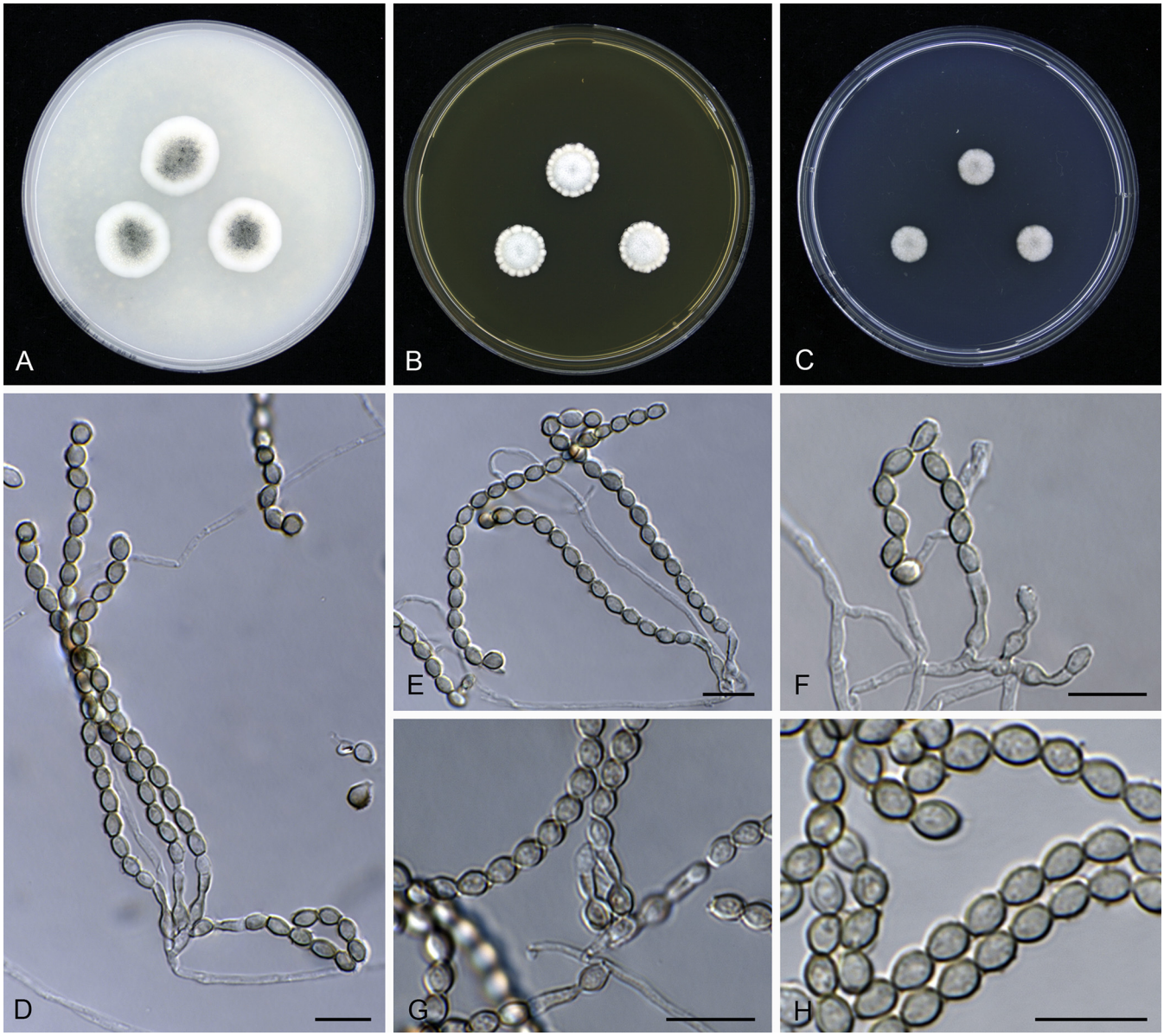


Fig. 5. *Microascus atrogriseus* nom. nov. **A–C.** Fourteen day old colonies of DTO 139-D7 on OA (A), MEA (B) and DG18 (C). **D–F.** Conidiophores, annellides and conidia CBS 295.52. **G.** Conidiophores, annellides and conidia DTO 139-D7. **H.** Conidia DTO 191-C2. Scale bars = 10 µm.

Notes: The newly described *M. cleistocarpus* is closely related to *M. hyalinus* (Fig. 1). *Microascus cleistocarpus* and *M. hyalinus* are the only two species in *Microascus* producing cleistothecial ascocarps. However, *M. hyalinus* produces hyaline conidia and *M. cleistocarpus* has hazel conidia. Based on sequence data *M. cleistocarpus* can be distinguished from *M. hyalinus* on all three genes (ITS 3 nt difference, *tub2* 5 nt difference, *tef1* 10 nt difference).

Microascus fusisporus Woudenb. & Samson **sp. nov.** MycoBank MB818280. Fig. 7.

Etymology: name refers to the fusiform conidia.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple or branched, occasionally indistinctive, bearing one to multiple annellides. *Annellides* ampulliform, (7–) 9–12(–14) µm long, 2–3(–3.5) µm broad at the widest part, tapering gradually to a cylindrical annellate zone, sometimes thickened, 1–1.5(–2) µm wide, hyaline, smooth-walled. *Conidia* obovoid to broad clavate or fusiform, with truncate base, (5–) 5.5–6.5 (–7) × 2.5–3.5 µm, hyaline or subhyaline, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 15 mm after 14 d at 25 °C, flat, white at the margin with grey olivaceous to olivaceous centre, margin crenated. On MEA attaining a diameter of 10–12 mm, convex, olivaceous grey with white to cream-coloured sectors and margin, margin crenated. On DG18 attaining a diameter of 15–18 mm, crateriform, cinnamon with buff tufts of mycelium at the outer ring, olivaceous grey with white velvet mycelium at the centre, margin dentate. On OA no growth at 36 and 40 °C.

Specimen examined: **Germany**, Schleswig-Holstein, Kiel-Kitzeberg, from wheat-field soil, collection date unknown, K.H. Domsch & W. Gams, (**holotype** CBS H-22743, culture **ex-type** CBS 896.68 = ATCC 16278 = IFO 31244 = MUCL 8989).

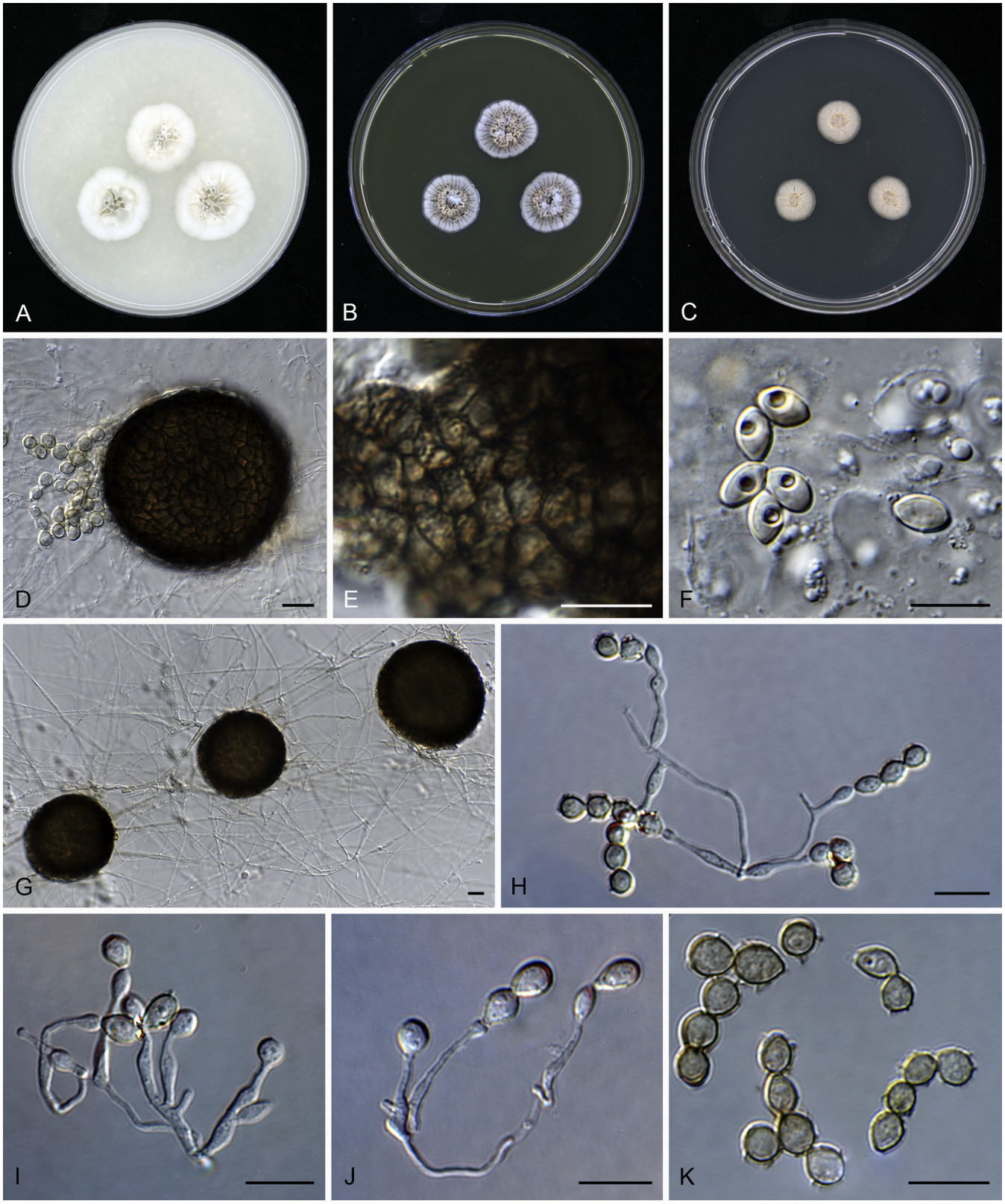


Fig. 6. *Microascus cleistocarpus* sp. nov. CBS 134638. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D, G.** Ascomata. **E.** Ascomatal wall. **F.** Asci and ascospores. **H–J.** Conidiophores, annellides and conidia. **K.** Conidia. Scale bars = 10 µm.

Notes: Morphologically *M. fusisporus* resembles *M. trautmannii*, but can be distinguish based on its shorter annellides (9–12 µm long in *M. fusisporus* against 16–22 µm long in *M. trautmannii*) and the ability to grow on OA at 36 °C of *M. trautmannii*. Both species can easily be distinguished from the other *M. paisii*-like species based on their obovoid to broad clavate or fusiform conidia with truncate base.

Microascus hollandicus Woudenb. & Samson **sp. nov.** MycoBank MB818279. Fig. 8.

Etymology: name refers to the country of isolation, the Netherlands.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple or indistinctive, bearing one or multiple

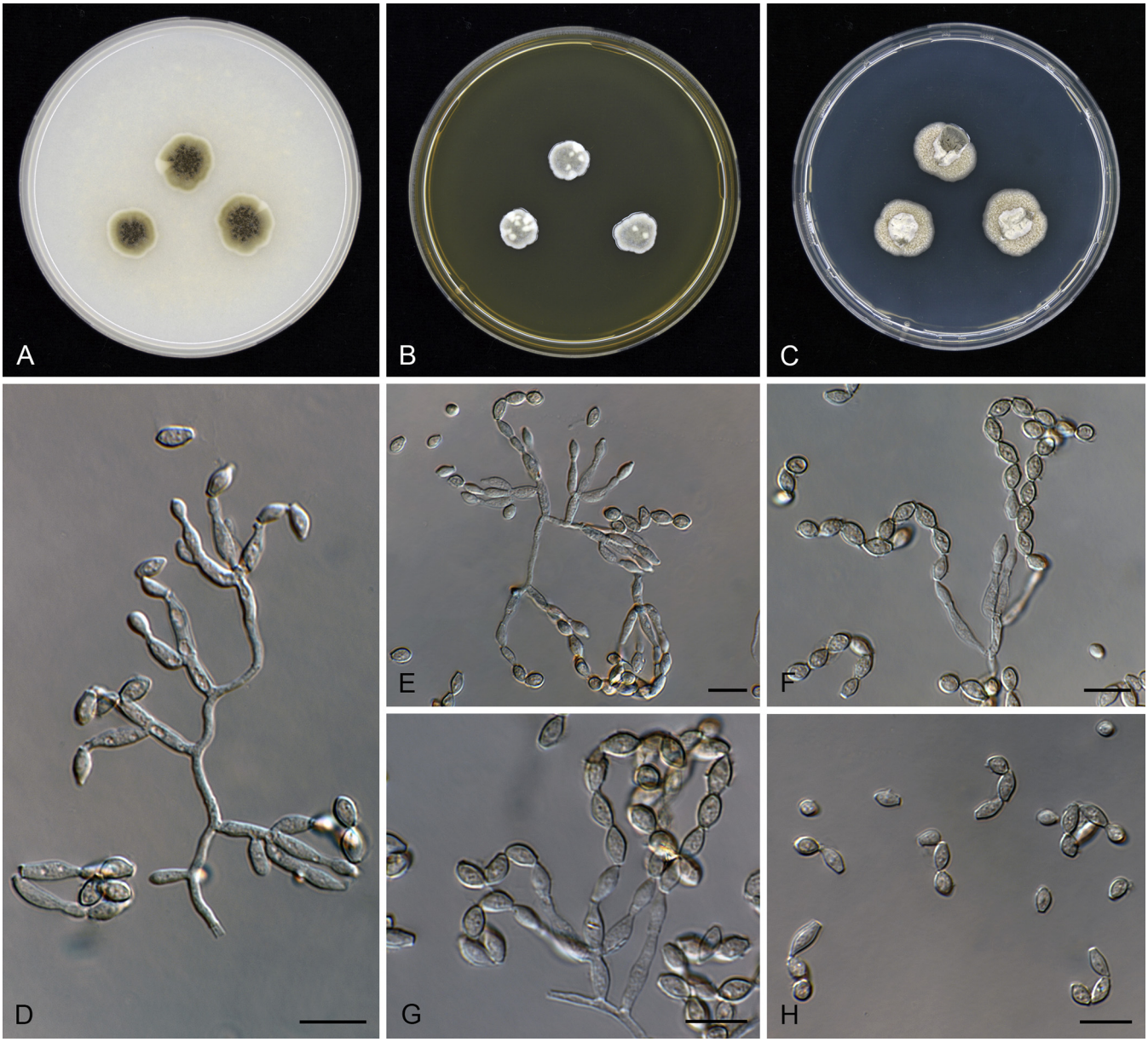


Fig. 7. *Microascus fusisporus* sp. nov. CBS 896.68. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–G.** Conidiophores, annellides and conidia. **H.** Conidia. Scale bars = 10 µm.

annellides. *Annellides* ampulliform, (3.5–)4–6(–8) µm long, (2.0–)2.5–3(–3.5) µm broad at the widest part, tapering abruptly to a cylindrical annellate zone 1–1.5 µm wide, hyaline, smooth-walled. *Conidia* broadly ellipsoidal to short clavate with truncate base, (3.5–)4–4.5(–5) × (2.5–)3–3.5(–4) µm, hyaline when young turning honey when ageing, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 17–18 mm after 14 d at 25 °C, flat to slightly raised, white to cream-coloured with olivaceous grey to olivaeous buff centre, margin dentate. On MEA attaining a diameter of 12–13 mm, raised, white to very pale olivaceous grey, radially striated with crenated margin. On DG18 attaining a diameter of 10–11 mm, raised, olivaceous grey, woolly with long white mycelium hairs growing out, margin entire. On OA no growth at 36 and 40 °C.

Specimen examined: **Netherlands**, from a swab sample of an indoor horse arena, Mar. 2012, Houba, (**holotype** CBS H-22716, culture **ex-type** CBS 141582).

Notes: *Microascus hollandicus* morphologically resembles *M. pseudopaisii*. Sequence data is necessary to distinguish both species. All three genes used in this manuscript can separate the two species (ITS 8 nt difference, *tub2* 21 nt difference, and *tef1* 10 nt difference between the type isolates of both species). *Microascus hollandicus* and *M. pseudopaisii* can be differentiated from the other *M. paisii*-like species by their shorter annellides (4–6 µm long).

Microascus melanosporus (Udagawa) Woudenb. & Samson **comb. nov.** MycoBank MB817657. Fig. 9.

Basionym: *Scopulariopsis melanospora* Udagawa, J. agric. Sci. (Tokyo) 5: 18. 1959.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple or indistinctive, bearing one to multiple annellides. *Annellides* ampulliform, (5.5–)7.5–11(–13) µm long, (2–)2.5–3.5(–4) µm broad at the widest part, tapering abruptly

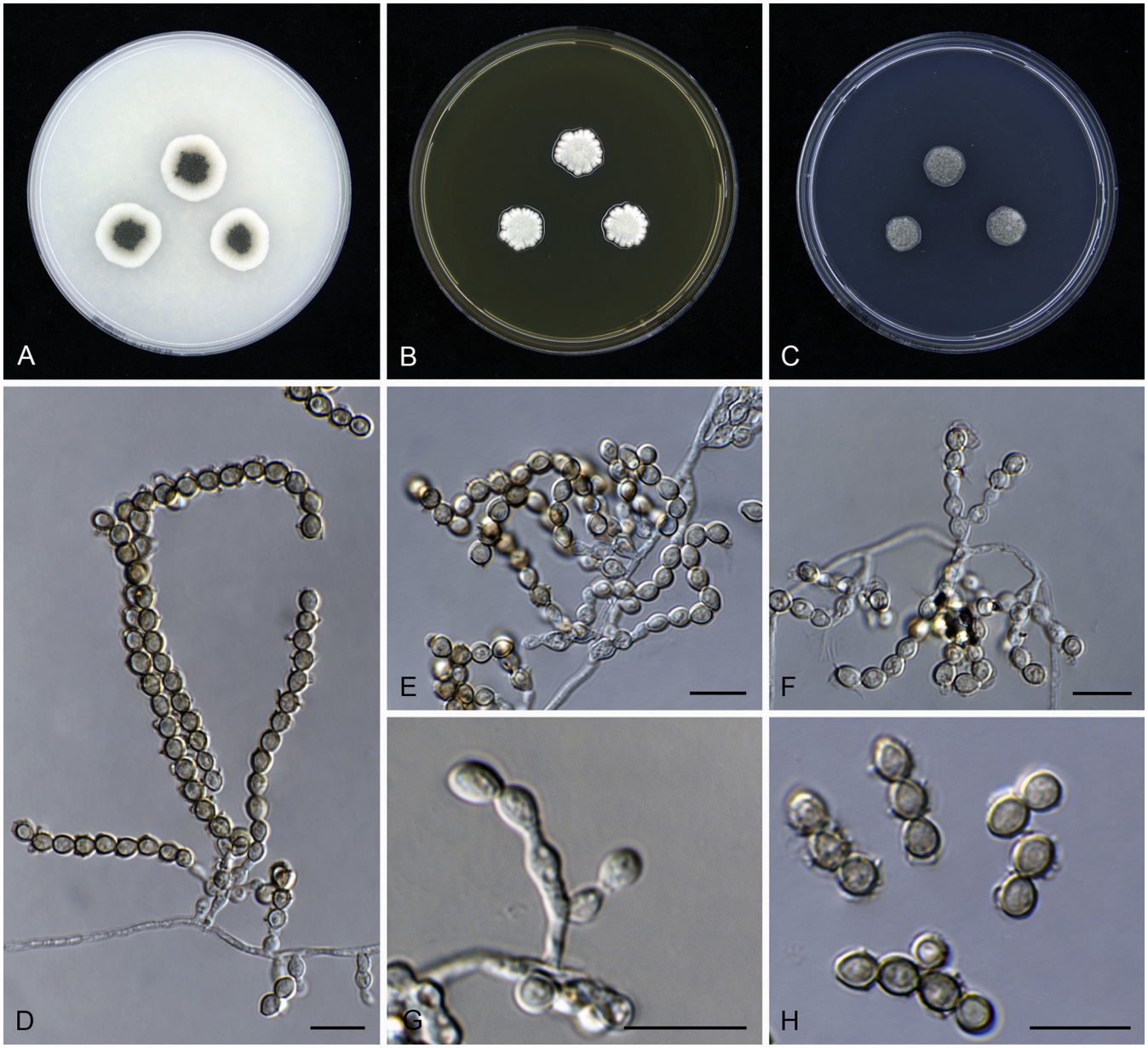


Fig. 8. *Microascus hollandicus* sp. nov. CBS 141582. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–F.** Conidiophores, annellides and conidia. **H.** Conidia. Scale bars = 10 µm.

to a cylindrical annellate zone 1–1.5(–2) µm wide, hyaline, smooth-walled. *Conidia* broadly ellipsoidal to short clavate with truncate base, 4–4.5(–5) × (2.5–)3–3.5 µm, hyaline when young turning hazel when ageing, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 21–25 mm after 14 d at 25 °C, low convex, white to cream-coloured with olivaceous grey to iron grey zones, margin crenated. On MEA attaining a diameter of 19–23 mm, convex or crateriform, pale olivaceous grey to olivaceous grey, margin undulate. On DG18 attaining a diameter of 20–24 mm, crateriform, white to cream-coloured with grey olivaceous to greyish sepia and vinaceous grey zones, margin undulate. On OA some isolates grow at 36 °C, no growth at 40 °C.

Specimens examined: **Germany**, from indoor air sample, 2013, C. Trautmann, DTO 255-A5; from indoor air sample, 2013, C. Trautmann, DTO 255-A7; from plaster, 2013, C. Trautmann, DTO 255-B1. **South Africa**, Somerset West, from house dust, 12 Feb. 2009, Karin Jacobs, DTO 220-H9. **USA**, from milled *Oryza sativa*, 1955, S. Udagawa, (culture **ex-type** CBS 272.60 = MUCL 9040 = IMI 078257).

Notes: *Microascus melanosporus* is morphologically and phylogenetically closely related to *M. paisii*. Morphologically it can be differentiated from the other *M. paisii*-like species by its faster growth on OA and MEA at 25 °C (21–25 mm versus 16–20 mm and 19–23 versus 15–18 mm in diam. respectively). Based on sequence data both the *tub2* and *tef1* can separate *M. melanosporus* from the other *M. paisii*-like species. The ITS sequence is identical to *M. paisii*.

Microascus micronesiensis Woudenb., Seifert & Samson **sp. nov.** MycoBank MB818281. Fig. 10.

Etymology: name refers to the country of isolation, Micronesia.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, indistinctive, simple or branched, bearing terminally one or occasionally two annellides. *Annellides*

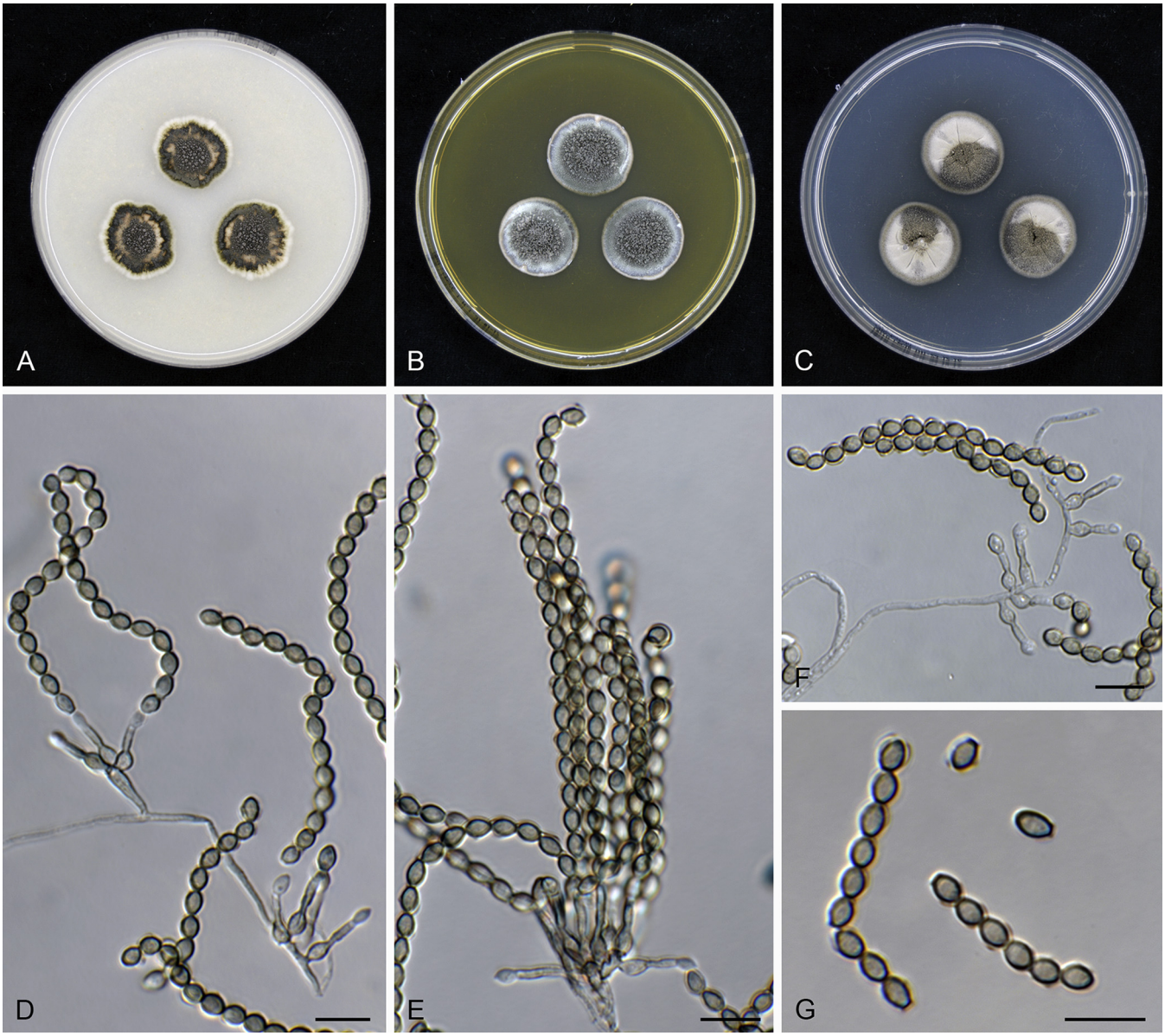


Fig. 9. *Microascus melanosporus* comb. nov. DTO 255-B1. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–F.** Conidiophores, annellides and conidia. **G.** Conidia. Scale bars = 10 µm.

ampulliform, (6–)7–11(–14) µm long, 2–2.5(–3) µm broad at the widest part, tapering gradually to a cylindrical annellate zone (0.5–)1–1.5 µm wide, hyaline, smooth-walled. *Conidia* broadly obovoid with truncate base, 3–4(–4.5) × (2–)2.5–3(–3.5) µm, hyaline or subhyaline, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 15–17 mm after 14 d at 25 °C, flat, white to cream-coloured with pale grey olivaceous to grey olivaceous rings, margin undulated. On MEA attaining a diameter of 16–17 mm, low convex, white to cream-coloured, margin undulate. On DG18 attaining a diameter of 10–11 mm, low convex, white to cream-coloured, margin undulate. On OA reduced growth at 36, no growth at 40 °C.

Specimens examined: **Micronesia**, Kosrae, Kosrae Island, Malem, from house dust, 15 Mar. 2009, Wayne Law, (**holotype** CBS H-22739 culture **ex-type** CBS 141523); Kosrae, Kosrae Island, Tofol, from house dust, 2009, Wayne Law, DTO 223-A5.

Notes: Phylogenetically *M. micronesiensis* is closely related to the two recently described sexual species *M. brunneosporus* (Sandoval-Denis *et al.* 2016) and *M. chinensis* (Jagielski *et al.* 2016). Morphologically *M. micronesiensis* can be distinguished from *M. brunneosporus* and *M. chinensis* by the lack of producing sexual structures in culture and its much slower growth on OA at 25 °C (15–17 mm for *M. micronesiensis* versus 21–25 and 25–28 mm for *M. brunneosporus* and *M. chinensis* respectively after 14 d). *Microascus micronesiensis* has been found in house-dust samples from two different houses in Micronesia in different cities on separate occasions.

Microascus paisii (Pollacci) Sandoval-Denis, Gené & Guarro, Persoonia 36:21. 2016. Fig. 11.

Basionym: *Torula paisii* Pollacci (as 'pais'), Atti Ist. Bot. Univ. Pavia, ser. 2, 18:130. 1921.

≡ *Phaeoscopulariopsis paisii* (Pollacci) M. Ota, Jap. J. Dermatol. Urol. 28:5. 1928. nom. inval.

≡ *Scopulariopsis paisii* (Pollacci) Nann., Repert. Sist. dei Miceti dell'Uomo e degli Anim.: 259. 1934.

= *Scopulariopsis sphaerospora* Zach, Oesterr. Bot. Z. 83: 180. 1934.

= *Scopulariopsis brumptii* Salv.-Duval, Thèse Fac. Pharm. Paris. 23: 58. 1935.

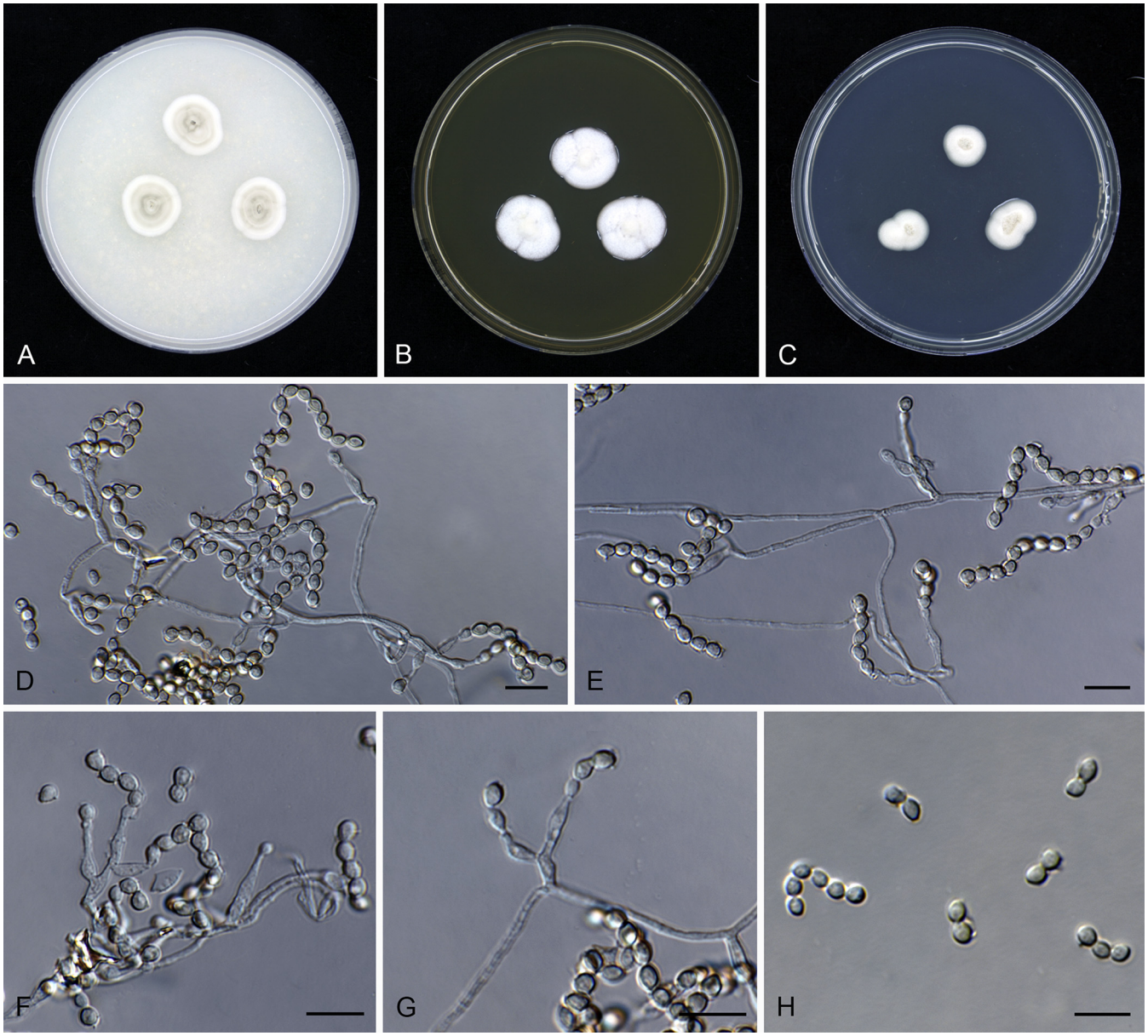


Fig. 10. *Microascus micronesiensis* sp. nov. CBS 141523. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–G.** Conidiophores, annellides and conidia. **H.** Conidia. Scale bars = 10 µm.

= *Scopulariopsis versicolor* Salv.-Duval, Thèse Fac. Pharm. Paris 23: 63.1935.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple or indistinctive, bearing one or multiple annellides. *Annellides* ampulliform, (5.5–)6.5–9.5(–12) µm long, (2–)2.5–3(–3.5) µm broad at the widest part, tapering abruptly to a cylindrical annellate zone 1–1.5(–2) µm wide, hyaline, smooth-walled. *Conidia* broadly ellipsoidal to short clavate with truncate base, 3.5–4(–4.5) × 3–3.5(–4) µm, hyaline when young turning hazel when ageing, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 17–20 mm after 14 d at 25 °C, low convex, white to cream-coloured with olivaceous grey to iron grey centre, margin crenated. On MEA attaining a diameter of 15–18 mm, crateriform, olivaceous grey to iron grey, radially striated, margin crenated. On DG18 attaining a diameter of 19–22 mm, crateriform, vinaceous buff with purplish grey zones at the margin and greyish sepia centre, margin entire. On OA some isolates grow at 36 °C, no growth at 40 °C.

Specimens examined: **Austria**, from unknown substrate, 1934, F. Zach, (*S. sphaerospora* culture **ex-type** CBS 402.34 = MUCL 9045). **France**, from small-pox vaccine, 1935, M. Langeron, (probably *S. brumptii* culture **ex-type** CBS 333.35). **Germany**, from plaster, 2013, C. Trautmann, DTO 255-B2; from oriented strand board, 2013, C. Trautmann, DTO 255-B8. **Italy**, from human, 1927, G. Pollacci (*T. paisii* culture **ex-type** CBS 213.27 = MUCL 7915).

Notes: The new name combination *Microascus paisii* for *Torula paisii* was recently proposed, together with the synonymy of several well-known species underneath it (Sandoval-Denis *et al.* 2016). In this manuscript two synonymies are reinstated, namely *Masonia grisea* as *Microascus atrogriseus* and *Scopulariopsis melanospora* as *Microascus melanosporus*, and four new species are described, *M. fusisporus*, *M. hollandicus*, *M. pseudopaisii* and *M. trautmannii*. Morphologically *M. fusisporus* and *M. trautmannii* can be distinguished from *M. paisii* by their shape of conidia (see notes of the respective species), and *M. pseudopaisii* and *M. hollandicus* by their shorter

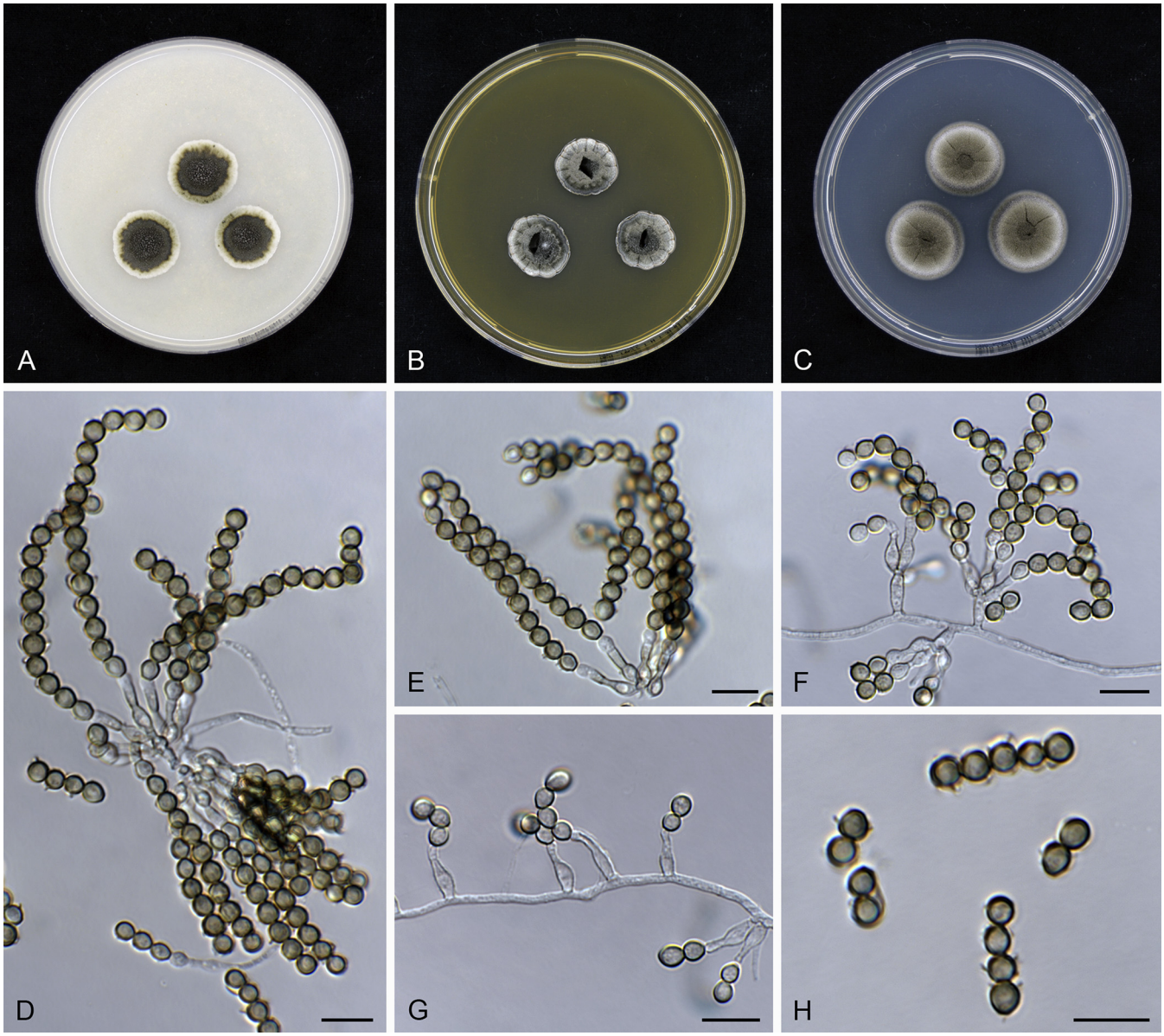


Fig. 11. *Microascus paisii* DTO 255-B2. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–G.** Conidiophores, annellides and conidia. **H.** Conidia. Scale bars = 10 µm.

annellides (see notes of the respective species). *Microascus melanosporus* can be distinguished by its faster growth rate on OA and MEA at 25 °C (see notes of *M. melanosporus*). *Microascus atrogriseus* is morphological identical to *M. paisii*, molecular data is necessary to distinguish the species (see notes of *M. atrogriseus*). CBS 333.35 isolated from small-pox vaccine in France is recognised here as the probable ex-type isolate of *S. brumpti*. It was deposited to the CBS in 1935 by Prof. Dr. Langeron who worked in the Université de Paris, Faculté de Médecine. The original description of *S. brumptii* by Salvanet-Duval was published in Thése Faculté de Pharmacie at the Université de Paris, on research on the small-pox vaccine (Salvanet-Duval 1935). All three studied ex-type isolates (CBS 213.27, CBS 402.34 and CBS 333.35) showed reduced growth and are therefore excluded from the culture descriptions.

Microascus pseudopaisii Woudenb. & Samson **sp. nov.** MycoBank MB818282. Fig. 12.

Etymology: name refers to the morphological and phylogenetic close relationship to *M. paisii*.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple or branched, occasionally indistinctive, bearing one to multiple annellides. *Annellides* lageniform to ampulliform, (3.5–)4.5–6(–6.5) µm long, 2–3(–3.5) µm broad at the widest part, tapering abruptly to a cylindrical annellate zone 1–1.5 µm wide, hyaline, smooth-walled. *Conidia* broadly ellipsoidal to short clavate with truncate base, (3–)3.5–4.5(–5) × 2.5–3(–3.5) µm, hyaline when young turning honey when ageing, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 17–20 mm after 14 d at 25 °C, slightly raised, white to cream-coloured with olivaceous grey centre, margin crenated. On MEA attaining a diameter of 14–15 mm, crateriform, olivaceous grey with white to cream-coloured edge, radially striated with crenated margin. On DG18 attaining a diameter of 10–12 mm, crateriform, pale olivaceous grey, woolly with long white mycelium hairs growing out, margin entire. On OA no growth at 36 and 40 °C.

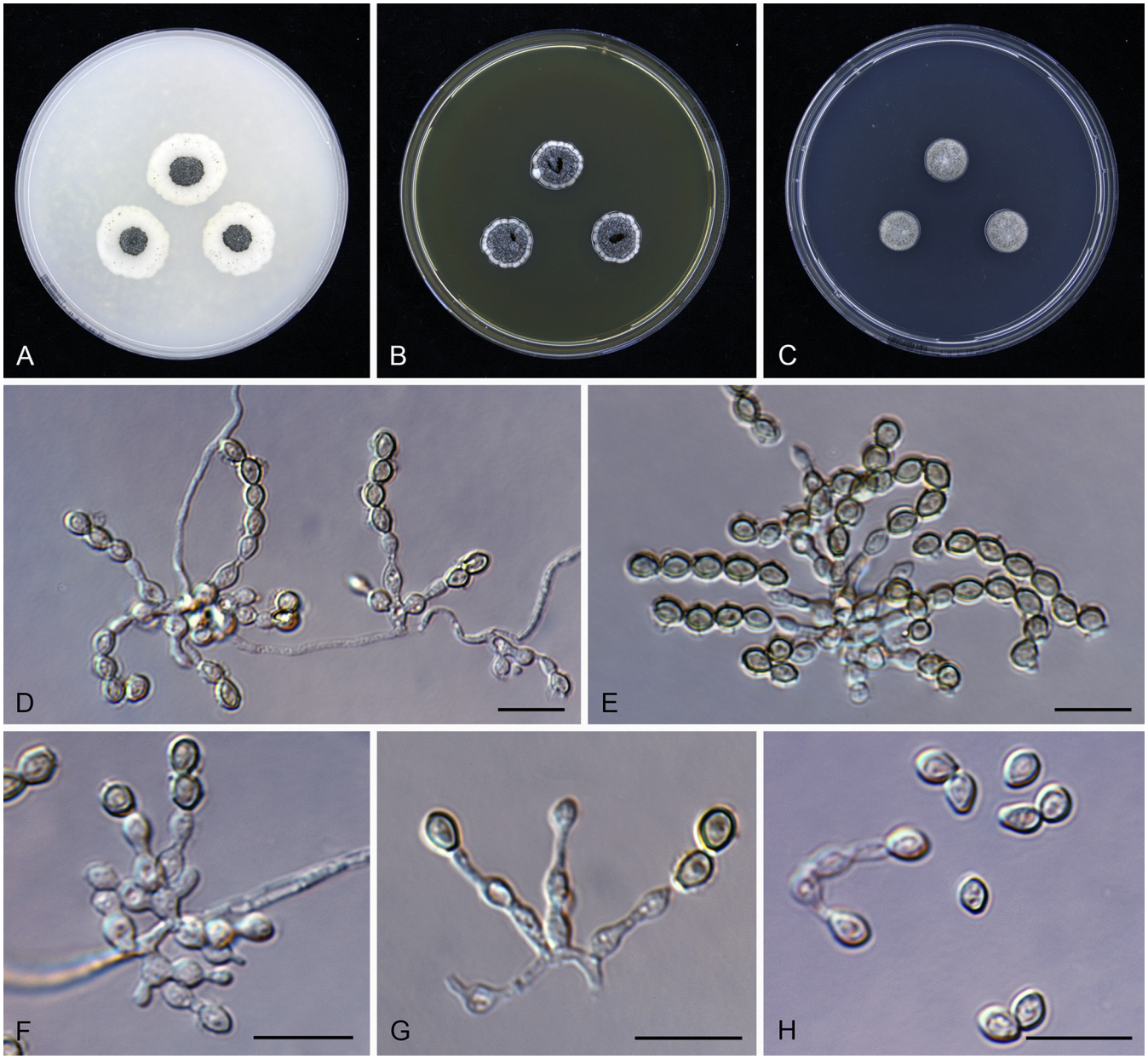


Fig. 12. *Microascus pseudopaisii* sp. nov. CBS 141581. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–H.** Conidiophores, annellides and conidia. Scale bars = 10 µm.

Specimens examined: **Netherlands**, Nederwetten, from an air sample of the basement of a house, 16 Dec. 2009, J. Houbraken, (**holotype** CBS H-22715, culture **ex-type** CBS 141581); additional strain from the same source, DTO 116-A4.

Notes: *Microascus pseudopaisii* morphologically resembles *M. hollandicus*. Sequence data is necessary to distinguish both species (see notes *M. hollandicus*). *Microascus hollandicus* and *M. pseudopaisii* can be differentiated from the other *M. paisii*-like species by their shorter annellides (4–6 µm long).

Microascus trautmannii Woudenb. & Samson **sp. nov.** MycoBank MB818283. Fig. 13.

Etymology: named after Dr. Christoph Trautmann, who collected numerous *Microascus* isolates from the indoor environment.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple or indistinctive, bearing terminally one or multiple annellides. *Annellides* slender ampulliform, (13.5–)16–22(–25) µm long, (1.5–)2–2.5(–3) µm broad at the widest part, with a sometimes thickened cylindrical annellate zone (1–)1.5–2(–2.5) µm wide, hyaline, smooth-walled. *Conidia* obovoid to broad clavate or fusiform, with truncate base, (5–)5.5–6.5(–7) × (2–)2.5–3 µm, hyaline or subhyaline, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 17 mm after 14 d at 25 °C, flat to slightly raised, white to cream-coloured with olivaceous grey centre, margin dentate. On MEA attaining a diameter of 13–16 mm, raised, buff to (pale) olivaceous grey with zones of white woolly mycelium, edge radially striated with crenated margin. On DG18 attaining a diameter of 10–11 mm, crateriform, pale olivaceous grey to pale greenish grey, margin entire. On OA reduced growth at 36 °C, no growth at 40 °C.

Specimen examined: **Germany**, from oriented strand board, C. Trautmann, 2013 (**holotype** CBS H-22717, culture **ex-type** CBS 141583).

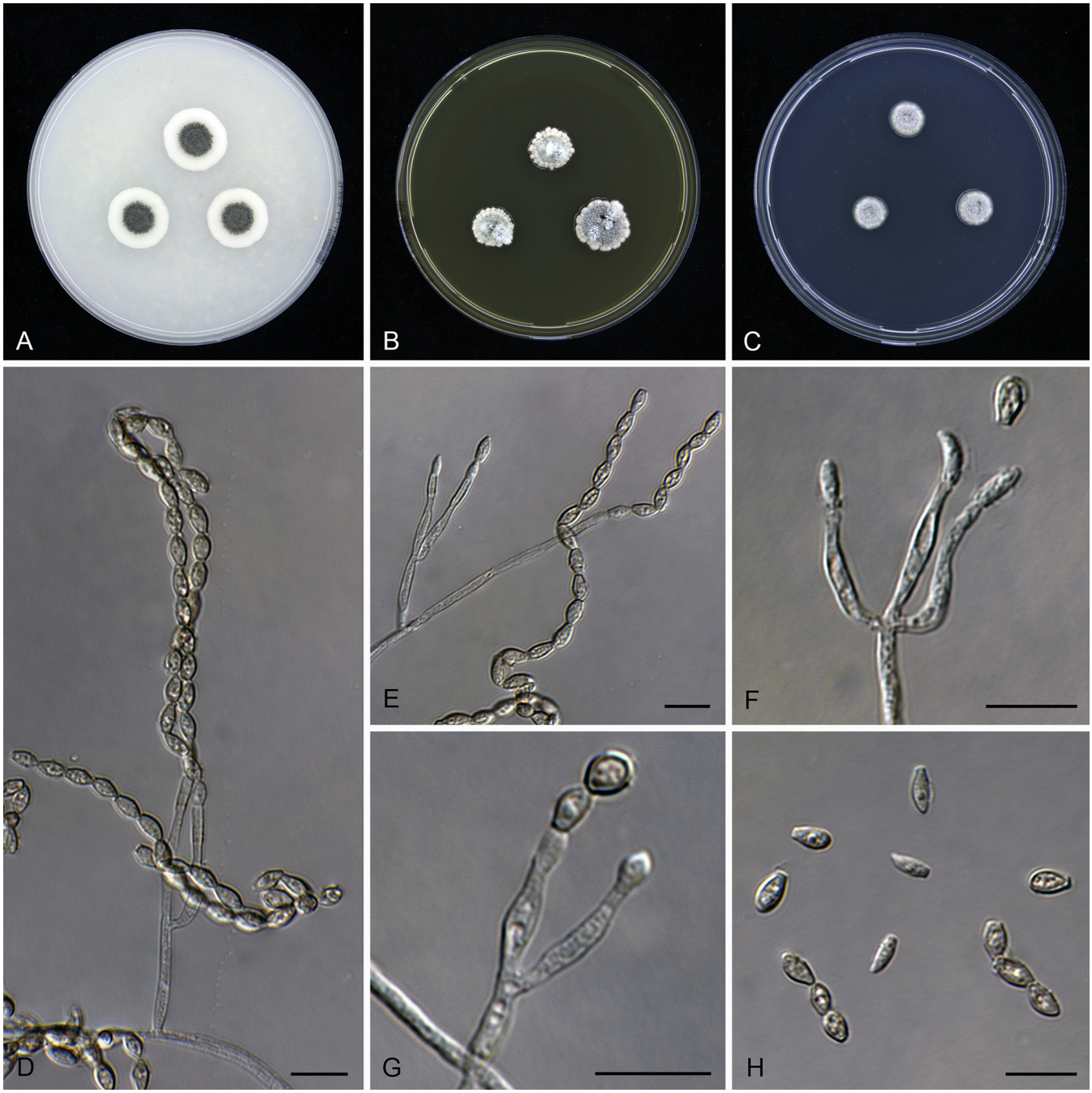


Fig. 13. *Microascus trautmannii* sp. nov. CBS 141583. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–G.** Conidiophores, annellides and conidia. **H.** Conidia. Scale bars = 10 µm.

Notes: Morphologically *M. trautmannii* resembles *M. fusisporus*, but they can be distinguished based on the size of their annellides and the growth at 36 °C on OA (see notes *M. fusisporus*). Both species can easily be distinguished from the other *M. paisii*-like species based on their obovoid to broad clavate or fusiform conidia with truncate base.

Scopulariopsis africana Woudenb. & Samson **sp. nov.** MycoBank MB818274. Fig. 14.

Etymology: name refers to the country of isolation, South Africa.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple to indistinctive, occasionally branched. *Annellides* cylindrical to slight ampulliform, (5–)8–15(–21.5) µm long, (2–)3–4(–4.5) µm broad at the widest part, tapering gradually to a cylindrical annellate zone 2– 3(–3.5) µm wide, hyaline, smooth-walled. *Conidia* subglobose to broadly ovoid with truncate base, (5.5–)6–7(–8) × (4–)4.5–5.5(–6) µm, hyaline, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 35 mm after 14 d at 25 °C, flat, white to cream-coloured with olivaceous zones, margin crenated. On MEA attaining a diameter of 12–14 mm, crateriform, white to cream-coloured, folded, margin crenated. On DG18 attaining a diameter of 25–28 mm, low convex, white to cream-coloured, margin undulate to erose to fimbriate. On OA no growth at 36 and 40 °C.

Specimen examined: **South Africa**, Free State, Lemoenskloof, from mud sample from salt pan, before Sep. 2004, M.E. Setati, (**holotype** CBS H-22741, culture **ex-type** CBS 118736).

Fig. 14. *Scopulariopsis africana* sp. nov. CBS 118736. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–F.** Conidiophores, annellides and conidia. **G–H.** Conidia. Scale bars = 10 µm.

Notes: Morphologically *S. africana* resembles *S. albida*, *S. candida* and *S. alboflavescens*, although *S. africana* shows olivaceous zones on OA (*S. albida* and *S. candida* are characterised by white colonies, *S. alboflavescens* by white-cream to pale yellowish colonies). Molecularly, *S. africana* can be distinguished from other *Scopulariopsis* species based on its *tub2* and *tef1* sequence.

Scopulariopsis albida Woudenb. & Samson **sp. nov.** MycoBank MB818275. Fig. 15.

Etymology: name refers to the white colonies.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple to indistinctive. *Annellides* cylindrical to slight ampulliform, (6)8.5–19.5(–29.5) µm long, (2.5–)3–5(5.5) µm broad at the widest part, annellate zone (2–)2.5–3.5(–4) µm wide, single, hyaline, smooth-walled. *Conidia* globose to subglobose with truncate base, (5–)6.5–8(–8.5) × (6–)6.5–7.5(–8) µm, hyaline, smooth, thick-walled, arranged in chains.

Culture characteristics: Colonies on OA attaining a diameter of 55–60 mm after 14 d at 25 °C, flat, white to cream-coloured, margin entire. On MEA attaining a diameter of 20–23 mm, crateriform, white to cream-coloured, folded, margin undulate. On DG18 attaining a diameter of 21–25 mm, low convex, white to cream-coloured, folded, margin undulate to erose to fimbriate. On OA no growth at 36 and 40 °C.

Specimens examined: **Netherlands**, from soil, collection date and collector unknown (**holotype** CBS H-22740, culture **ex-type** CBS 119.43). **Germany**, substrate and collection date unknown, P. Höhle, CBS 415.51.

Notes: Morphologically *S. albida* resembles *S. candida*. Although *S. candida* does not form a monophyletic clade, *S. albida* can molecularly be distinguished from *S. candida* based on its *tub2* and *tef1* sequence. Also *S. africana* and *S. alboflavescens* morphologically resemble *S. albida*. Here the olivaceous zones on OA of *S. africana* isolates and the cream-white to pale yellowish colonies and subhyaline conidia of *S. alboflavescens* isolates can be used to distinguish the species.

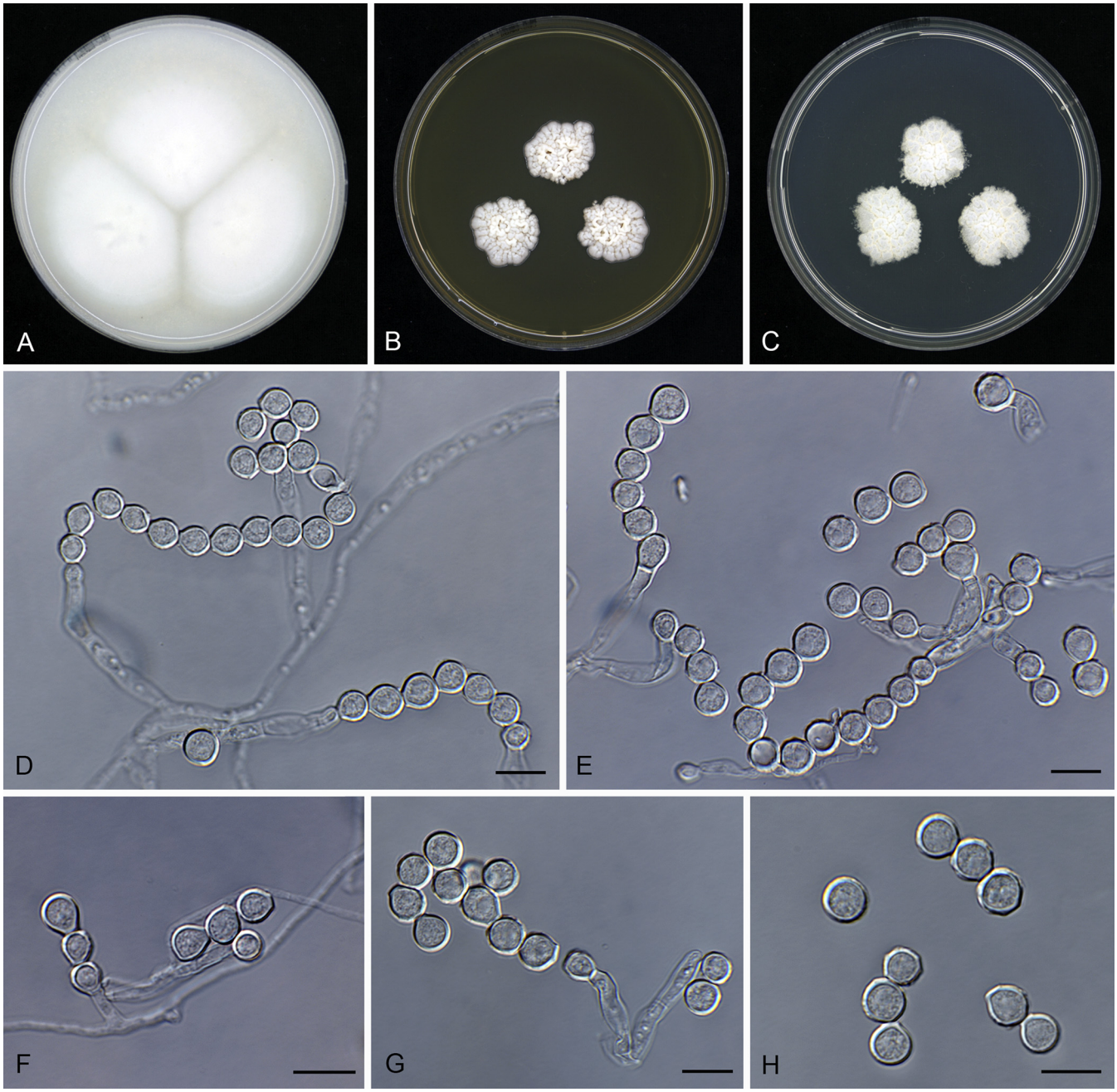


Fig. 15. *Scopulariopsis albida* sp. nov. CBS 119.43. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–G.** Conidiophores, annellides and conidia. **H.** Conidia. Scale bars = 10 µm.

Scopulariopsis caseicola Woudenb. & Samson **sp. nov.** MycoBank MB818276. Fig. 16.

Etymology: name refers to the substrate of isolation, cheese.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, simple or branched, bearing terminally a single annellide (at each branch). *Annellides* cylindrical, (10.5–)22.5–47.5(–67.5) × (2.5–)3–4(–5) µm, tapering gradually to a cylindrical annellate zone 2–3.5(–4) µm wide, subhyaline becoming darker with age, smooth-walled. *Conidia* broad ovoid with truncate base, (4.5–)6–7(–8) × (4–)5–6(–7) µm, buff to honey, smooth, thick-walled, arranged in long chains.

Culture characteristics: Colonies on OA attaining a diameter of 30 mm after 14 d at 25 °C, flat, white to opaque, margin entire. On MEA attaining a diameter of 22–23 mm, low convex, white to cream-coloured, margin undulate. On DG18 attaining a diameter of 7 mm, flat, pale olivaceous grey to smoke grey, margin fimbriate. On OA no growth at 36 and 40 °C.

Specimen examined: **Netherlands**, from cheese-coating, collection date unknown, M.B. Schol-Schwarz, (**holotype** CBS H-22738, culture **ex-type** CBS 480.62).

Note: Sporulation was only observed on OA after 2 months cultivation, re-isolation of a fresh culture might influence the morphological description. Morton & Smith (1963) discussed the synonyms of *S. flava*, a species frequently found on cheese. Among the synonyms they also discussed *S. casei* Loubière of which no type material is known to exist.

Scopulariopsis sexualis Woudenb. & Samson **sp. nov.** MycoBank MB818277. Fig. 17.

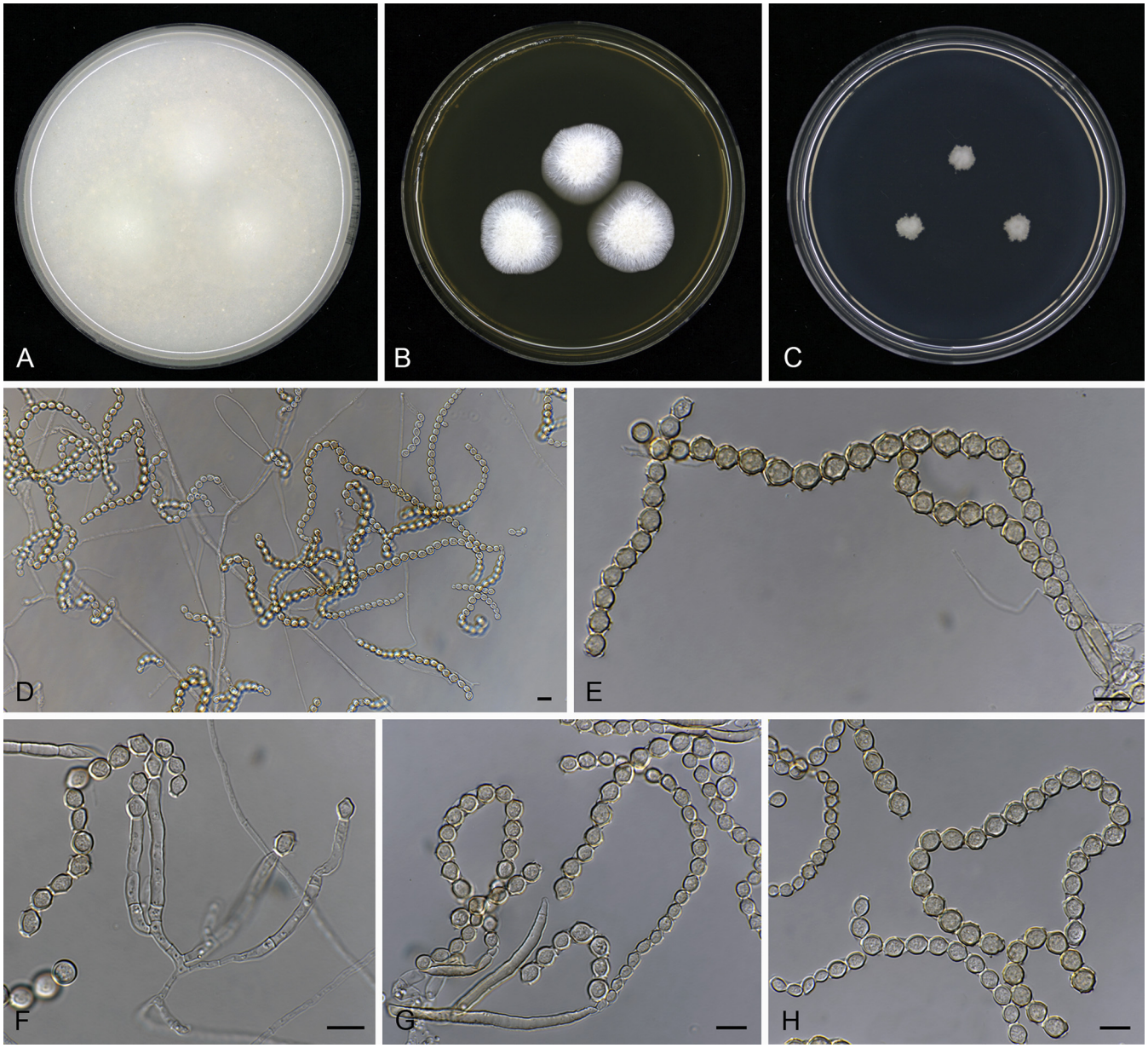


Fig. 16. *Scopulariopsis caseicola* sp. nov. CBS 480.62. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–G.** Conidiophores, annellides and conidia. **H.** Conidia. Scale bars = 10 µm.

Etymology: name refers to the presence of only sexual structures and lack of asexual structures.

Ascomata abundant, superficial or immersed, ostiolate, globose with a short cylindrical ostiolar neck (up to 20 µm) or ovoid, 108–145(171) µm diam., dark brown to black, glabrous; peridium with a *textura angularis*. *Asci* irregularly ellipsoidal, (9.5–) 10.5–12(–13) × 9–11.5(–13) µm. *Ascospores* reniform to broadly lunate, (4.5–)5–5.5(–6.5) × 3.5–4.5(–5) µm, buff to honey, luteous to orange in mass, smooth, with a single inconspicuous germ pore. Asexual morph not observed.

Culture characteristics: Colonies on OA attaining a diameter of 60–67 mm after 14 d at 25 °C, flat, dull green with white edge, margin entire. On MEA attaining a diameter of 47–57 mm, crateriform, white to cream-coloured with olivaceous grey to iron grey centre, radially striated with entire margin. On DG18 attaining a diameter of 38–40 mm, flat, white to cream-coloured, margin undulate to crenated. On OA still growth at 36 °C, no growth at 40 °C.

Specimens examined: **Burma**, from milled rice, 1954, S. Udagawa, (**holotype** CBS H-14445, culture **ex-type** CBS 250.64 = IFO 7555 = UAMH 1923 = NHL 2278). **India**, Delhi, from seed of *Brassica oleracea* (*Brassicaceae*), collection date unknown, K.G. Mukerji, CBS 332.78. **USA**, Arizona, Tucson, from bat dung, collection date unknown, G.F. Orr, CBS 667.71 = NRRL A-8022.

Note: Morphologically *S. sexualis* resembles the sexual morph of *S. cordiae*. *Scopulariopsis sexualis* can be differentiated from *S. cordiae* by its much faster growth on OA (60–70 mm for *S. sexualis*, 35–36 mm for *S. cordiae* at 25 °C after 14 d) and shorter cylindrical ostiolar neck (*S. sexualis* up to 20 µm, *S. cordiae* up to 390 µm).

Yunnania H.Z. Kong, Mycotaxon 69: 320. 1998.

= *Fuscoannellis* Sandoval-Denis, Jagielski, Jin Yu & Gené, Fungal Biol. 120: 593. 2016.

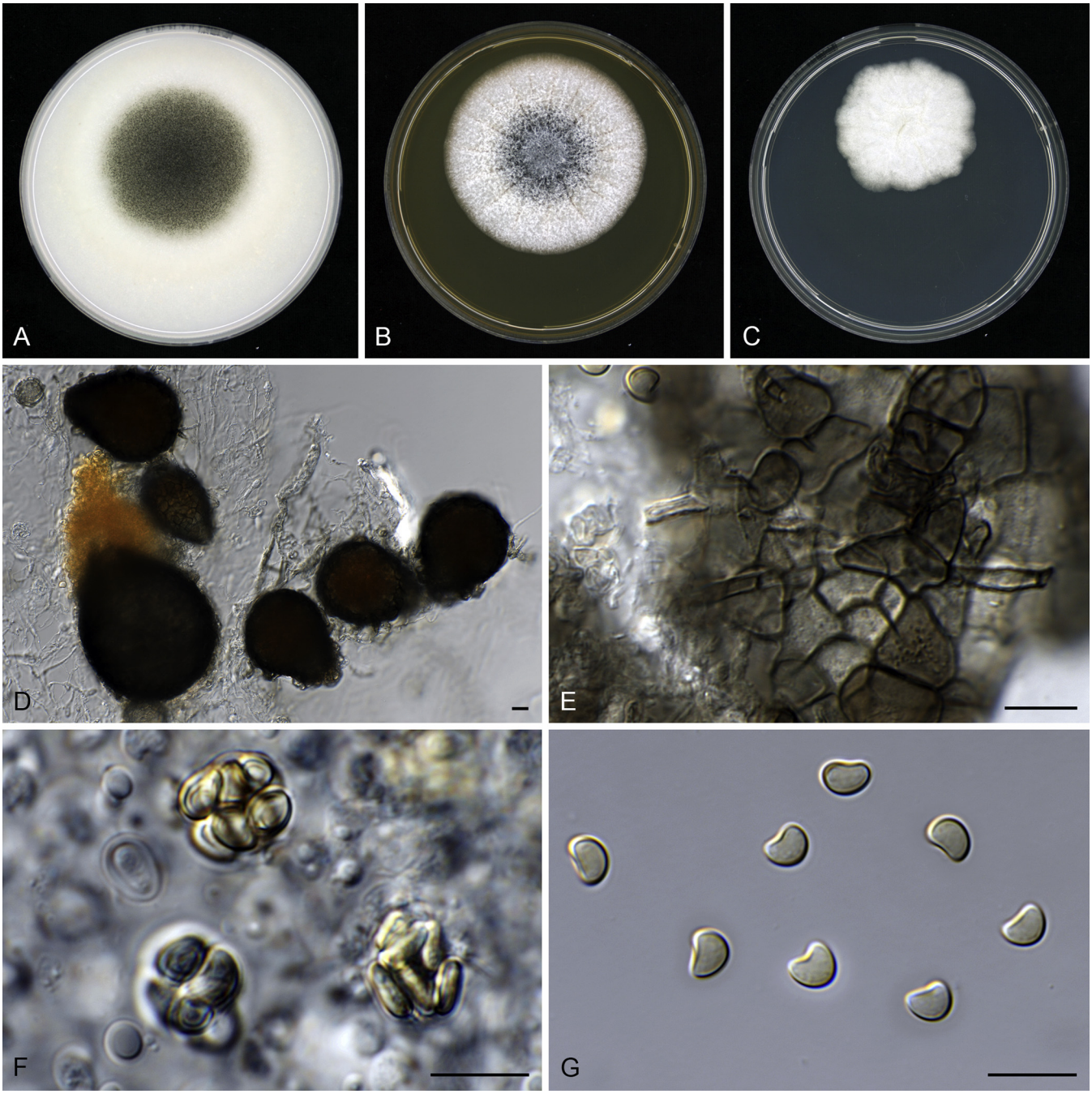


Fig. 17. *Scopulariopsis sexualis* sp. nov. CBS 250.64. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D.** Ascomata. **E.** Ascomatal wall. **F.** Asci. **G.** Ascospores. Scale bars = 10 µm.

Yunnania carbonaria (F.J. Morton & G. Sm.) Woudenb., Houbraken & Samson **comb. nov.** MycoBank MB820189.

Basionym: *Scopulariopsis carbonaria* F.J. Morton & G. Sm., Mycol. Pap. 86: 59. 1963.

≡ *Fuscoannellis carbonaria* (F.J. Morton & G. Sm.) Sandoval-Denis, Jagielski, Jin Yu & Gené, Fungal Biol. 120: 593. 2016.

Specimens examined: **Panama**, from soil, collection date unknown, R. Cogill, (culture **ex-type** CBS 205.61 = NRRL 1860 = IFO 8116 = MUCL 9027 = IMI 086941); **USA**, Hawaii, on dead hardwood branch, 3 Nov. 2002, D.T. Wicklow, CBS 121662.

Yunnania smithii Woudenb. & Samson **sp. nov.** MycoBank MB818273. Fig. 18.

Etymology: named after late George Smith (1895–1967), a British mycologist who extensively studied the closely related fungal genera *Microascus* and *Scopulariopsis*, and collected the type isolate.

Sexual morph not observed. *Conidiophores* arising from substrate mycelium, frequently branched, bearing terminally a group of annellides (at each branch). *Annellides* ampulliform, (4–) 5–7 µm long, 2–2.5(–3) µm broad at the widest part, with a short annellate zone, (1–)1.5–2 µm wide, hyaline to subhyaline, smooth-walled. *Conidia* ovoid to ellipsoidal with truncate base, 4–5(–5.5) × 2–2.5(–3) µm, vinaceous buff to hazel, smooth, thick-walled, arranged in (long) chains.

Culture characteristics: Colonies on OA attaining a diameter of 33–35 mm after 14 d at 25 °C, flat, olivaceous to olivaceous grey, margin crenated. On MEA attaining a diameter of 26–30 mm, crateriform, greyish blue to (pale) olivaceous grey

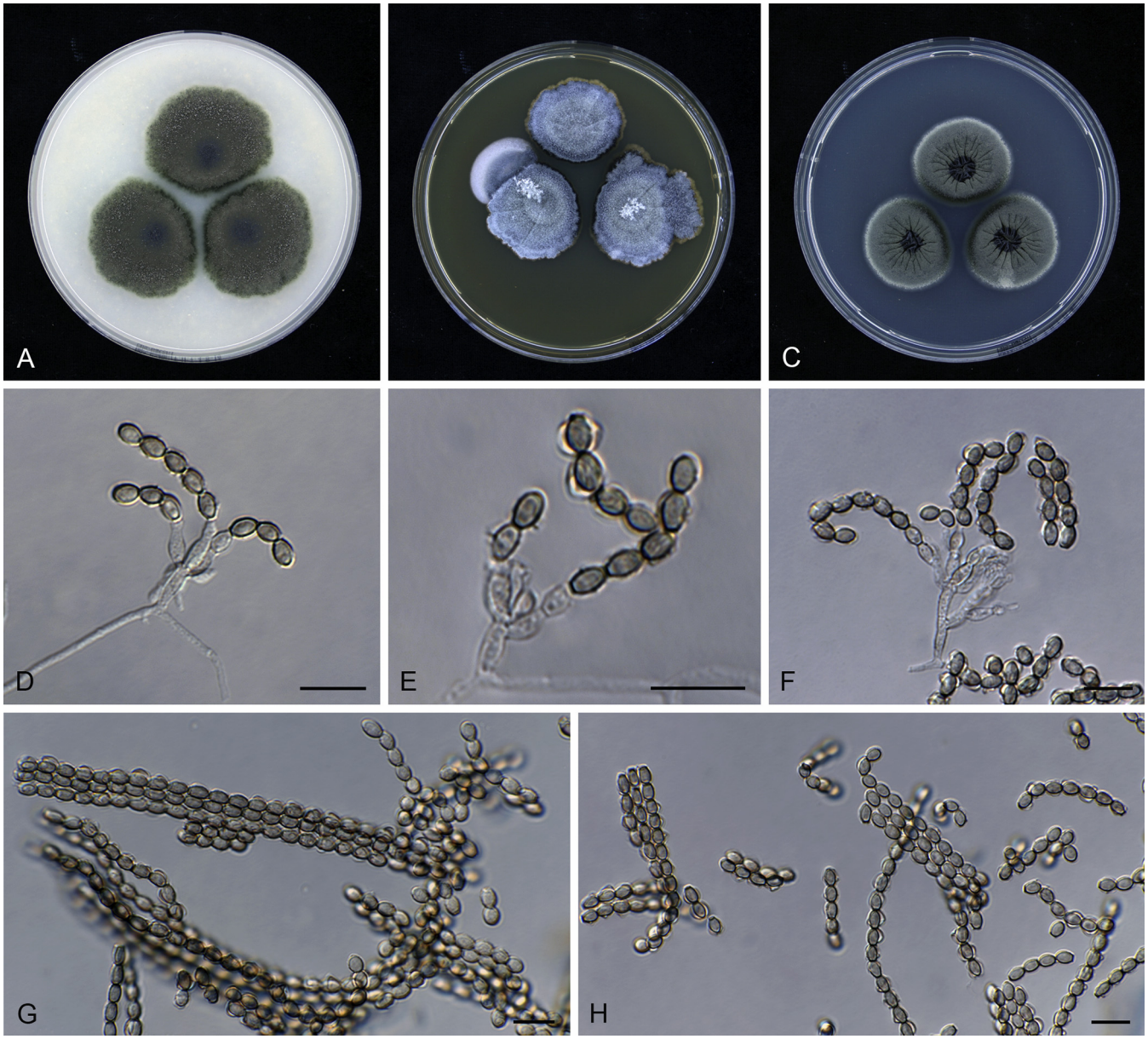


Fig. 18. *Yunnania smithii* sp. nov. CBS 855.68. **A–C.** Fourteen day old colonies on OA (A), MEA (B) and DG18 (C). **D–F.** Conidiophores, annellides and conidia. **G–H.** Conidia. Scale bars = 10 µm.

and slate blue, radially striated with dentate margin. On DG18 attaining a diameter of 29–30 mm, crateriform, pale olivaceous grey to olivaceous grey, radially striated, margin entire. On OA no growth at 36 and 40 °C.

Specimen examined: **Germany**, Kiel-Kitzeberg, from garden soil, 1963, G. Smith, (**holotype** CBS H-22742, culture **ex-type** CBS 855.68).

Notes: *Yunnania smithii* morphologically resembles the other two species in the genus *Yunnania*, *Y. carbonaria* and *Y. penicillata*. It can be distinguished from *Y. penicillata* by its faster growth on OA in 7 d (*Y. smithii* 33–35 mm, *Y. penicillata* 20 mm). The colour of the conidiophores and annellides can be used to distinguish it from *Y. carbonaria* (hyaline in *Y. smithii*, pale brown to brown in *Y. carbonaria*). Molecularly *Y. smithii* can best be distinguished based on its *tef1* sequence (19 nt difference *Y. carbonaria*, 19 nt difference *Y. penicillata*), followed by its *tub2* sequence (12 nt difference *Y. carbonaria*, 14 nt difference *Y. penicillata*). The LSU and ITS sequences are not suited for identification, the LSU sequences are all 100 % identical and the ITS sequence of *Y. smithii* is identical to *Y. penicillata* and has only 1 nt difference with the type isolate of *Y. carbonaria*.

DISCUSSION

This manuscript presents a molecular phylogenetic study of species in the genera *Microascus* and *Scopulariopsis* known from culture, with the intention to identify the common indoor species. Since fungi present in indoor environments can produce toxins or carry allergens which cause health hazards, it is important to know which fungal species are present indoors. *Scopulariopsis* and scopulariopsis-like species are mainly found in soil, but also frequently isolated from food and building materials like drywall paper and wood (Samson *et al.* 2010). Little is known about the health effects of these fungi, although several species seem to be able to cause human onychomycosis and superficial tissue infections (*e.g.* Tosti *et al.* 1996, Wu *et al.* 2009). Rare cases of more severe diseases are reported, but only in immunocompromised patients (*e.g.* Baddley *et al.* 2000,

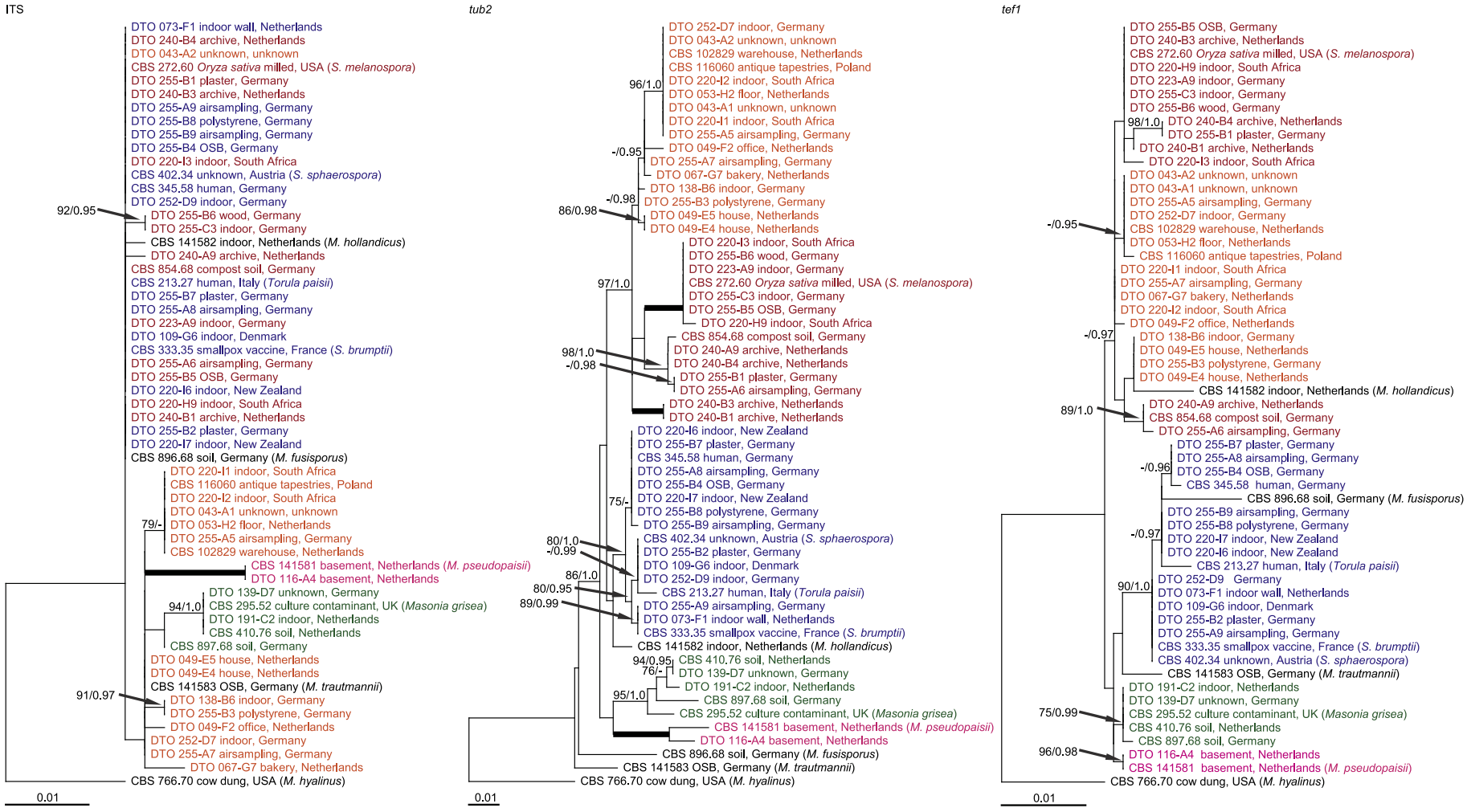


Fig. 19. Maximum likelihood trees based on respectively the ITS, *tub2* or *tef1* sequences of 56 isolates, representing the *Microascus paisii* clade and the out-group isolate *M. hyalinus* (CBS 766.70). The RAxML bootstrap support values ≥75 % (BS) and Bayesian posterior probabilities ≥0.95 (PP) are given at the nodes. Thickened lines indicate a BS of 100 % and a PP of 1.0. Species names between parentheses indicate the ex-type isolates of those species names. The red and orange printed isolates represent *M. melanosporus*, the blue printed isolates represent *M. paisii*, the green printed isolates represent *M. atrogriseus* and the pink printed isolates represent *M. pseudopaisii*.

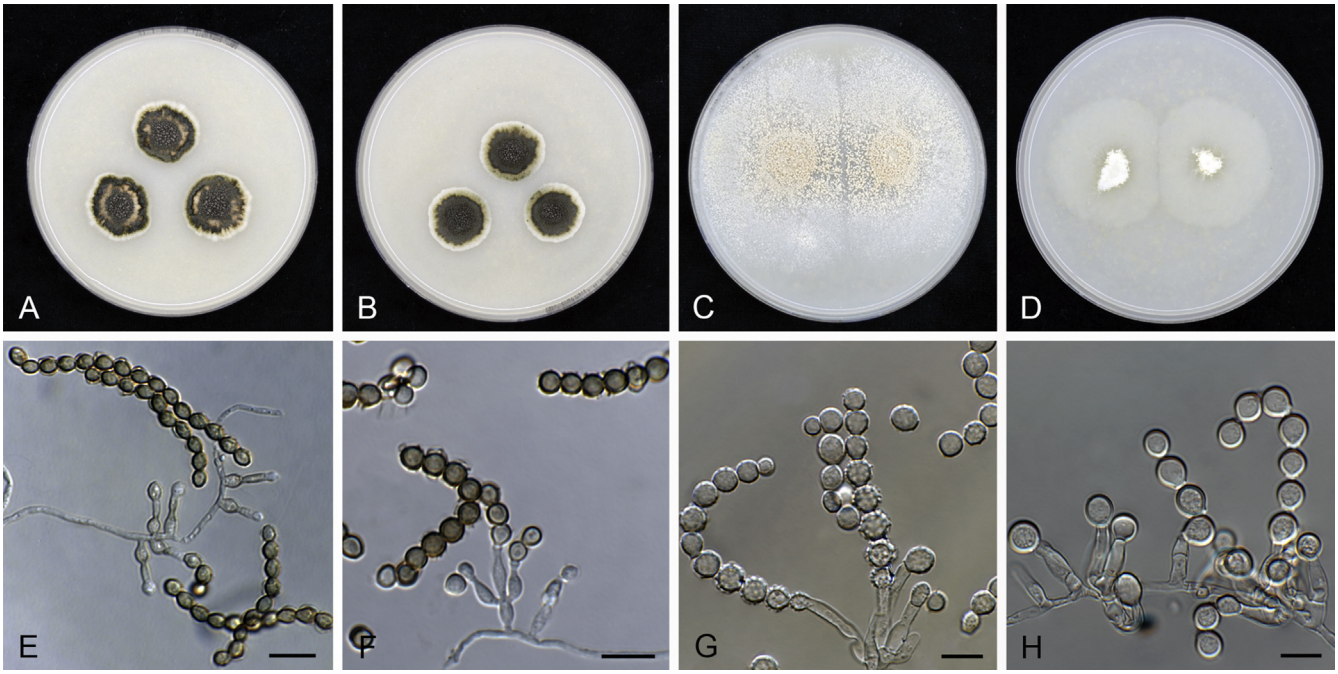


Fig. 20. Most common indoor *Microascus* and *Scopulariopsis* species. **A, E.** *M. melanosporus* DTO 255-B1. **B, F.** *M. paisii* DTO 255-B2. **C, G.** *S. brevicaulis* CBS 118474. **D, H.** *S. candida* DTO 138-B7. **A–D.** Fourteen day old colonies on OA. **E–H.** Conidiophores, annellides and conidia. Scale bars = 10 µm.

Miossec *et al.* 2011). The ability of *Scopulariopsis* species to deteriorate building materials (Gutarowska 2014, Lavin *et al.* 2016), and to accumulate various elements and turning these into toxic volatiles (Cheng & Focht 1979, Boriová *et al.* 2014) also makes them an important group to study in the indoor environment.

As stated in the results section, 17 species are mentioned in this manuscript to occur in the indoor environment (Table 2), but most of them are only occasionally found indoors. Besides the number of isolates found indoors, the substrate of isolation should also be taken into consideration when labelling species as indoor species. The isolates assigned to the indoor habitat include swab samples and house dust or air samples. Since swab sample are mostly taken from sites suspicious of fungal growth, they can (often) be related to actual indoor growth. A dust or air sample only implies the presence of the fungus. Since the concentration of fungal spores in the indoor air is to certain extent dependent on the outside spore concentration, it is recommended to also sample the outside air for comparison (Samson *et al.* 2010). This information is not known for our isolates, and also information on the abundance of the species in the air or dust sample is unknown. Ten of the species which are mentioned here to occur in the indoor environment are also found in relation with humans (Fig. 3). However, isolates assigned in this study to the human habitat are mainly isolated from human-derived specimens, which is merely an indication of a possible pathogenic role. For the majority of the species known from human specimens there is no proven relation with disease (Sandoval-Denis *et al.* 2013). Especially for isolates obtained from superficial sites and the upper respiratory tracts it should be taken into account that these can be environmental contaminants. Another point of attention is the indoor environment in which the species are found. How much time people spend in the different indoor environments (archives, homes, offices, stables, animal pens, etc.) varies, although all of them are treated here as indoor habitat. As example we will take *M. alveolaris*, only 1 out of 9 studied isolates is isolated from the indoor environment. This indoor isolate came from a house-dust sample, but no additional information is known on the abundance of the fungus in the dust sample. Additional information is needed to label *M. alveolaris* as true indoor species, although this study shows it can be found in homes. One other *M. alveolaris* isolate was human-derived, although an earlier study linked multiple human-derived isolates to this species (Sandoval-Denis *et al.* 2016). Most of them are bronchoalveolar lavage isolates, as the name of the fungus already applies. Although for most of these isolates their relation with disease is not known, the finding of multiple isolates from the respiratory tract of human patients, and the ability of the species to grow at 40 °C are good indications of the potential pathogenicity of the species.

The most commonly found indoor species, both in swab and air/dust samples are *M. melanosporus*, *M. paisii*, *S. brevicaulis* and *S. candida*. All four are also placed in relation with the human habitat. *Scopulariopsis brevicaulis* and *S. candida* are known to be involved in onychomycosis, and *S. brevicaulis* is also recognised as important human opportunistic pathogens, as well as *S. brumptii* (now *M. paisii*) (De Hoog *et al.* 2011). For *M. melanosporus*, which was previously regarded a synonym of *S. brumptii* (Morton & Smith 1963, as *S. melanospora*), the pathogenic abilities are unknown. However, one can expect that it can also act as opportunistic pathogen, as it close relatives, especially with the ability of some isolates to grow at 36 °C.

Based on the multi-gene phylogeny (Fig. 2) and congruent single gene trees (Fig. 19) the newly combined *M. paisii* (Sandoval-Denis *et al.* 2016) is split in this study into seven species of which four (*M. fusisporus*, *M. hollandicus*, *M. pseudopaisii*, and *M. trautmannii*) are newly described, one was given a new name (*M. atrogriseus*) and one a new name combination (*M. melanosporus*). *Scopulariopsis brumptii* is still regarded as synonym of *M. paisii* (Table 3). Based on their *tub2*

and *tef1* sequences all seven *M. paisii*-like species can be molecularly identified (Fig. 19). *Microascus melanosporus* seems to be the most prevalent species found indoor, and *M. paisii* is recognised as second most common indoor *Microascus* species. For the studied isolates *M. melanosporus* can morphologically be distinguished from *M. paisii* based on the growth rate and colony colour after 2 wk incubation on OA at 25 °C (Fig. 20). *Microascus melanosporus* grows slightly faster than *M. paisii* (21–25 mm versus 16–20 mm in diam. respectively), and *M. melanosporus* has slightly lighter grey colonies than *M. paisii* (Fig. 20A, B). *Microascus fusisporus* and *M. trautmannii* can be distinguished from the other *M. paisii*-like species based on their obovoid to broad clavate or fusiform conidia versus the broadly ellipsoidal to short clavate conidia from the other *M. paisii*-like isolates. *Microascus hollandicus* and *M. pseudopaisii* can be distinguished by their shorter annellides (4–6 µm long versus 6–11 µm long on average for the other *M. paisii*-like isolates). To distinguish *M. atrogriseus* from *M. paisii* and *M. hollandicus* from *M. pseudopaisii* molecular data is needed. The two most common indoor *Scopulariopsis* species, *S. brevicaulis* and *S. candida*, are both molecularly as morphologically easy to distinguish. Morphologically the growth rate and colony colour after 2 wk incubation on OA at 25 °C, and the conidia morphology can be used to distinguish the species (Fig. 20). *Scopulariopsis brevicaulis* grows faster than *S. candida* (75 mm and 38–48 mm in diam. respectively), and *S. brevicaulis* has buff to rosy buff colonies versus white colonies in *S. candida* (Fig. 20C, D). Another distinction are the roughened conidia of *S. brevicaulis*, versus the smooth conidia of *S. candida* (Fig. 20G, H). A growth test at 36 °C can also be used to distinguish the species since *S. brevicaulis* is able to grow at 36 °C and *S. candida* is not.

Below we will discuss some phylogenetic unclarities which we encountered during this molecular phylogenetic study of *Scopulariopsis* and scopulariopsis-like species.

The phylogenetic position of *M. longirostris* and *M. pseudolongirostris* is doubtful. In our *Microascus* phylogeny, based on the ITS, *tub2* and *tef1* sequences, *M. longirostris* and *M. pseudolongirostris* cluster closest to the genus *Yunnania* rather than *Microascus* but without phylogenetic support (Fig. 2). In the genus tree, based on the LSU, ITS and *tef1* sequences, *M. longirostris* and *M. pseudolongirostris* cluster closest to *Microascus*, although again without phylogenetic support (Fig. 3). We choose to keep them in the genus *Microascus* following earlier publications (Jagielski *et al.* 2016, Sandoval-Denis *et al.* 2016) although they will need further study. The genus *Yunnania* is supported as separate genus in the genera tree, which is congruent with the study of Jagielski *et al.* (2016). They already stated that the *S. carbonaria* isolates did not belong to *Scopulariopsis*, and proposed the new genus *Fuscoannellis*. However, since the genus *Yunnania* was described earlier (Kong 1998), this genus name has priority according to the rules of the ICN and *Fuscoannellis* will become a synonym of *Yunnania*. The CBS collection contained four isolates named *Scopulariopsis carbonaria*, including the type isolate CBS 205.61. However, the type isolate only clustered together with CBS 121662 (Fig. 2), which was originally stored as *S. brumptii* in the CBS collection (as was already noticed by Jagielski *et al.* 2016). Two other '*S. carbonaria*' isolates, CBS 687.68 and 253.69, cluster together in the genus *Kernia* (data not shown). CBS 855.68 does cluster with the type isolate of *S. carbonaria* based on its ITS sequence (only 1 nt difference), but based on its *tub2* (12 nt difference) and *tef1* (19 nt difference) sequence, in combination with morphological study, we describe it here as a new species *Y. smithii*. These "*S. carbonaria*" isolates form a good example of the problems with morphological identification in these genera. The isolate DTO 223-A6 clusters close to the type isolates of the recent described species *M. intricatus* and *M. onychoides*. These two species have identical ITS sequences, but differ 9 nt in their *tub2* sequences, and 10 nt in their *tef1* sequences. Isolate DTO 223-A6 clusters closest to *M. onychoides*, although it is not 100 % molecularly identical. Also based on morphology we could not clearly place DTO 223-A6 in one of the two species, since the measurements of the spores did not exactly match one of them. We choose however to name DTO 223-A6 *M. onychoides* for now, but collection of more isolates will be necessary to establish the species boundaries of *M. intricatus* and *M. onychoides*. The phylogenetic species *M. terreus* contains two supported clades (Fig. 2). Because the isolates in these two clades are morphologically identical, and are isolated from the same substrates, we choose to keep them as one species. Also in the species *M. croci* there is some sequence variation. Isolates CBS 158.44 and DTO 220-I5 deviate from the other *M. croci* isolates in their ITS sequence only (3 nt in a short stretch). DTO 305-B5 deviates on all three loci from the other isolates (ITS 3 nt, *tub2* 6 nt and *tef* 8 nt difference). We choose to keep it as a *M. croci* for now, since there is no support in the tree for the split. With the collection of more isolates, *M. croci* might split into two or maybe three *Microascus* species. The new species *M. longicollis* was published while preparing this manuscript (Crous *et al.* 2016, Fungal Planet description sheet 444). The morphological description matches the morphology of isolate CBS 752.97, stored as *S. gracilis* in the CBS collection. Sequence comparison of CBS 752.97 with the ex-type isolate of *M. longicollis* gave 99 % identity matches between all three sequenced loci. We therefore named CBS 752.97 *M. longicollis*. Multiple isolates stored as *M. trigonosporus* are now identified as *M. alveolaris* (Table 1). Also many stored as *M. manginii* now cluster in different species clades than the type isolate of *M. manginii* which falls within the *S. candida* clade. Four of them actually cluster within *Scopulariopsis*, corresponding to two new species (*S. sexualis* and *S. africana*). These are more examples of the problems with identification based on morphology in these genera. *Microascus campaniformis* CBS 138126 has been omitted from the study awaiting a new culture deposit. The isolate deposited to the CBS collection turned out to be a *M. melanosporus* isolate. The published sequences from the ex-type isolate were also not included in this study, since the *tef1* sequence (GenBank HG380418) seems to belong to the *M. melanosporus* clade. The deposited ITS (GenBank LM652391), and *tub2* (GenBank LM652606) sequences are unique sequences suggesting it is indeed a new species in *Microascus*. The ex-type isolate need to be recovered and re-sequenced to place it into the phylogenetic tree. *Scopulariopsis candida* has a lot of molecular variation and is non-monophyletic in the species phylogeny (Fig. 1). This is congruent with previous publications (Jagielski *et al.* 2016, Sandoval-Denis *et al.* 2016). No solution for this problem could be provided in this study, since the single gene trees were not congruent. Further study including more isolates will be necessary to solve this (for now) non-monophyletic species.

CONCLUSIONS

In the genus *Microascus* 33 phylogenetic species can be distinguished based on (parts) of the ITS, *tub2* and *tef1* gene regions. From these 33 species, seven are described here as new species, and one new name and new combination are proposed. Thirteen *Microascus* species are found in the indoor environment of which *M. melanosporus* is most commonly found, followed by *M. paisii*. In the genus *Scopulariopsis* 12 phylogenetic species can be distinguished based on (parts) of the ITS, *tub2* and *tef1* gene regions. From these 12 species, four are described here as new species. Three *Scopulariopsis* species are found in the indoor environment of which *S. brevicaulis* and *S. candida* are most common. No correlation was found between phylogenetic relationships and habitat preference in the genera *Microascus* and *Scopulariopsis*. The genus *Fuscoannellis* is placed in synonymy with *Yunnania*. The genus *Yunnania*, which is not known for indoor environments, now includes three species of which one is described here as new and one has a new name combination proposed.

Key to the most common *Microascus*, *Scopulariopsis* and *Cephalotrichum* species from the indoor environment

1a. Synnemata absent 2
1b. Synnemata present ..... ***Cephalotrichum***, 8
2a. Annellides lageniform or ampulliform ..... ***Microascus***, 3
2b. Annellides cylindrical ..... ***Scopulariopsis***, 7
3a. Colony diam. on OA after 14 d at 25 °C > 20 mm ..... ***M. melanosporus***
3b. Colony diam. on OA after 14 d at 25 °C < 20 mm 4
4a. Conidia obovoid to broad clavate or fusiform 5
4b. Conidia broadly ellipsoidal to short clavate 6
5a. Annellides 9–12 µm long ..... ***M. fusisporus***
5b. Annellides 16–22 µm long ..... ***M. trautmannii***
6a. Annellides 4–6 µm long ..... ***M. hollandicus*** or ***M. pseudopaisii***
6b. Annellides 6–11 µm long ..... ***M. atrogriseus*** or ***M. paisii***
7a. Roughened conidia, able to grow at 36 °C on OA ..... ***S. brevicaulis***
7b. Smooth conidia, no growth at 36 °C on OA ..... ***S. candida***
8a. Coiled setae present on the upper part of the synnemata ..... ***C. gorgonifer***
8b. Setae absent 9
9a. Conidia distinctively rough ..... ***C. verrucisporum***
9b. Conidia smooth 10
10a. Conidia 3.5–5 × 2–3 µm ..... ***C. microsporum***
10b. Conidia larger ..... ***C. pseudopurpureofuscum*** or ***C. purpureofuscum***

ACKNOWLEDGEMENTS

This research was supported by a grant from the Alfred P. Sloan Foundation Program on the Microbiology of the Built Environment (Grant No. G-2014-14529). The authors would like to thank Dr. Christoph Trautmann (Umweltmykologie, Germany), Prof. Dr. Keith Seifert (Agriculture and Agri-Food, Canada), Dr. Kinga Plewa (Poland) and the Technical University of Denmark (DTU) for sending/depositing their indoor isolates into the working collection of the Westerdijk Fungal Biodiversity Institute Applied and Industrial Mycology Group. Dr. Konstanze Bensch (Westerdijk Institute, the Netherlands) is thanked for her help with naming the new species and Dr. Marcelo Sandoval-Denis (Westerdijk Institute) for helpful discussions on the manuscript.

REFERENCES

Amend AS, Seifert KA, Samson R, Bruns TD (2010). Indoor fungal composition is geographically patterned and more diverse in temperate zones than in the tropics. *Proceedings of the National Academy of Sciences of the United States of America* **107**: 13748–13753.
Baddley JW, Moser SA, Sutton DA, Pappas PG (2000). *Microascus cinereus* (Anamorph *Scopulariopsis*) brain abscess in a bone marrow transplant recipient. *Journal of Clinical Microbiology* **38**: 395–397.
Boriová K, Čerňansky S, Matríš P, *et al.* (2014). Bioaccumulation and biovolatilization of various elements using filamentous fungus *Scopulariopsis brevicaulis*. *Letters in Applied Microbiology* **59**: 217–223.
Cheng C-N, Focht DD (1979). Production of arsine and methylarsines in soil and in culture. *Applied and Environmental Microbiology* **38**: 494–498.
Crous PW, Wingfield MJ, Richardson DM, *et al.* (2016). Fungal planet description sheets: 400–468. *Persoonia* **36**: 316–458.
De Hoog GS, Gerrits van den Ende AHG (1998). Molecular diagnostics of clinical strains of filamentous *Basidiomycetes*. *Mycoses* **41**: 183–189.
De Hoog GS, Guarro J, Gené J, Figueras MJ (2011). *Atlas of clinical fungi*. CD-ROM version 3.1, CBS-KNAW Fungal Biodiversity Centre, Utrecht, the Netherlands.
Glass L, Donaldson GC (1995). Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. *Applied and Environmental Microbiology* **61**: 1323–1330.
Gutarowska B (2014). Moulds in biodeterioration of technical materials. *Folia Biologica et Oecologica* **10**: 27–39.
Höppe P, Martinac I (1998). Indoor climate and air quality. Review of current and future topics in the field of ISB study group 10. *International Journal of Biometeorology* **42**: 1–7.
Huelsenbeck JP, Ronquist F (2001). MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* **17**: 754–755.
Issakainen J, Jalava J, Hyvönen J, *et al.* (2003). Relationships of *Scopulariopsis* based on LSU rDNA sequences. *Medical Mycology* **41**: 31–42.
Jagielski T, Kosim K, Skóra M, *et al.* (2013). Identification of *Scopulariopsis* species by partial 28S rRNA gene sequence analysis. *Polish Journal of Microbiology* **62**: 303–306.
Jagielski T, Sandoval-Denis M, Yu J, *et al.* (2016). Molecular taxonomy of scopulariopsis-like fungi with description of new clinical and environmental species. *Fungal Biology* **120**: 586–602.
Kong H-Z (1998). *Yunnania* gen. nov. of hyphomycetes. *Mycotaxon* **69**: 319–325.
Lavin P, de Saravia SG, Guiamet P (2016). *Scopulariopsis* sp. and *Fusarium* sp. in the documentary heritage: evaluation of their biodeterioration ability and antifungal effect of two essential oils. *Microbial Ecology* **71**: 628.
Masclaux F, Guého E, de Hoog GS, Christen R (1995). Phylogenetic relationships of human-pathogenic *Cladosporium* (*Xylophyla*) species inferred from partial LS rRNA sequences. *Journal of Medical and Veterinary Mycology* **33**: 327–338.
Miossec C, Morio F, Lepoivre T, *et al.* (2011). Fatal invasive infection with fungemia due to *Microascus cirrosus* after heart and lung transplantation in a patient with cystic fibrosis. *Journal of Clinical Microbiology* **49**: 2743–2747.
Morton FJ, Smith G (1963). The genera *Scopulariopsis* Bainier, *Microascus* Zukal, and *Doratomyces* Corda. *Mycological Papers* **8**: 1–96.
Page RDM (1996). TreeView: an application to display phylogenetic trees on personal computers. *Computer Applications in the Biosciences* **12**: 357–358.
Rambaut A, Drummond AJ (2009). *Tracer v. 1.5*. Available from: http://tree.bio.ed.ac.uk/software/tracer/.
Rayner RW (1970). *A mycological colour chart*. Commonwealth Mycological Institute, Kew, UK.
Rehner SA, Buckley E (2005). A *Beauveria* phylogeny inferred from nuclear ITS and EF1-α sequences: evidence for cryptic diversification and links to *Cordyceps* teleomorphs. *Mycologia* **97**: 84–98.
Rehner SA, Samuels GJ (1994). Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. *Mycological Research* **98**: 625–634.
Ronquist F, Huelsenbeck JP (2003). MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**: 1572–1574.
Ropars J, Cruaud C, Lacoste S, Dupont J (2012). A taxonomic and ecological overview of cheese fungi. *International Journal of Food Microbiology* **155**: 199–210.

Salvanet-Duval G (1935). *Recherches sur la flore adventice du vaccine anti-variolique*. Librairie E. le François, Paris, France.

Samson RA, Houbraken J, Thrane U, *et al*. (2010). *Food and indoor fungi*. CBS Laboratory Manual Series 2. CBS-KNAW Fungal Biodiversity Centre, Utrecht, the Netherlands.

Sandoval-Denis M, Gené J, Sutton DA, *et al*. (2016). Redefining *Microascus*, *Scopulariopsis* and allied genera. *Persoonia* **36**: 1–36.

Sandoval-Denis M, Sutton DA, Fothergill AW, *et al*. (2013). *Scopulariopsis*, a poorly known opportunistic fungus: spectrum of species in clinical samples and *in vitro* responses to antifungal drugs. *Journal of Clinical Microbiology* **51**: 3937–3943.

Schubert K, Groenewald JZ, Braun U, *et al*. (2007). Biodiversity in the *Cladosporium herbarum* complex (*Davidiellaceae*, *Capnodiales*) with standardisation of methods for *Cladosporium* taxonomy and diagnostics. *Studies in Mycology* **58**: 105–156.

Stamatakis A, Alachiotis N (2010). Time and memory efficient likelihood-based tree searches on phylogenomic alignments with missing data. *Bioinformatics* **26**: i132–i139.

Tosti A, Piraccini BM, Stinchi C, Lorenzi S (1996). Onychomycosis due to *Scopulariopsis brevicaulis*: clinical features and response to systemic antifungals. *The British Journal of Dermatology* **135**: 799–802.

Vilgalys R, Hester M (1990). Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* **172**: 4239–4246.

Wu C-Y, Lee C-H, Lin H-L, Wu C-S (2009). Cutaneous granulomatous infection caused by *Scopulariopsis brevicaulis*. *Acta Dermato-Venereologica* **89**: 103–104.