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 (tefl) 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 Fuscoannelis, 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, tefl 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: Fuscoannelis, 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. traumanni Woudenb. & Samson, Scopulariopsis africana Woudenb. & Samson, S. albida Woudenb. & Samson, S. caseicola Woudenb. & Samson, S. sexualis Woudenb. & Samson, Yunnania smithii Woudenb., Houbraken & Samson.

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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 (tefl) gene regions next to LSU to identify their Scopulariopsis species (Ropers 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 tefl 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
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 Fuscoannelis 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 1996)/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 × NH4 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) MgCl2, 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 Bionumbers v. 4.61 software package (Applied Maths, St-Martens-Latem, Belgium). Several sequences obtained in this study had one or multiple nucleotide differences and length differences with already published sequences of the same isolates. All new sequences and sequences which were longer in length or had nucleotide differences with already published sequences 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 name¹ | Strain numbers² | Host/Substrate | Country          | GenBank accession number |
|-----------------------------|-----------|-----------------|----------------|------------------|--------------------------|
| **Cephalotrichum asperulum**|           |                 | Soil           | Argentina        | KX923818, KX924043, KX924027 |
| **C. stemonitis**           |           |                 | Seed           | Netherlands      | KX923819, LN850953, LN850952 |
| *Microascus alveolaris*     |           |                 | Avena sativa, grain | USA | KX923823, KX924257, KX924047 |
| *M. trignonosporus*         |           |                 | Glycine soja, seed | USA | KX923824, KX924258, KX924048 |
| *M. trignonosporus*         |           |                 | Hordeum vulgare, seed | USA | KX923825, KX924259, KX924049 |
| *M. trignonosporus*         |           |                 | Hordeum vulgare, seed | USA | KX923826, KX924260, KX924050 |
| *M. trignonosporus*         |           |                 | Avena sativa, leaf | USA | KX923827, KX924261, KX924051 |
| *M. trignonosporus*         |           |                 | Allium cepa, seed | USA | KX923828, KX924262, KX924052 |
| *M. trignonosporus*         |           | **CBS 139501**, DTO 351-E2, FMR 12252, UTHSC 07-3491 | Marine sediment | Norway | LN850757, LN850855, LN850903 |
| **M. appendiculatus sp. nov.** |       |                 | Human, BAL fluid | USA | KX923829, KX924263, KX924053, KX924029 |
| **M. senegalensis**         |           | **CBS 594.78**, DTO 354-C3 | Human, skin | Algeria | LN850781, LN850878, KX924055, LN850830 |
| **M. atrogriseus nom. nov.**|           |                 | Culture contaminant | UK | LM652433, KX924265, KX924056, KX924030 |
| **M. chartarum**            |           | **CBS 295.52**, DTO 103-H6, IFO 6795, IMI 049908, MUCL 9003 | Wheat field soil | Germany | LM652436, LM652649, LM652571 |
| **S. chartarum**            |           | **CBS 410.76**, DTO 345-B1, DTO 191-C2 | Burnt soil, Indoor horse arena | Netherlands | KX923831, KX924266, KX924057, KX923832, KX924267, KX924058, KX923833, KX924268, KX924059 |
| **M. brunneosporus**        |           | **CBS 138276**, DTO 351-D8, UTHSC 06-4312, FMR 12343 | Human, BAL fluid | USA | KX923834, KX924269, HG380420, HG380497 |
| **M. chinensis**            |           | **CBS 294.52**, IMI 049909, MUCL 9001 | Wall paper | UK | LM652393, LM652607, HG380386, HG380463 |
| **M. cinereus**             |           | **CBS 365.65**, DTO 104-A3, DTO 104-A4, ATCC 16204, HACC 1522, IMI 113680 | Soil | India | LM652399, KX924270, KX924060 |
| **S. chartarum**            |           | **CBS 264.71**, DTO 104-B8, CBS 324.72, DTO 342-G2, CBS 138709**, DTO 351-E1, UTHSC 10-2805, FMR 12217 | Human, lung, Clay, Human, BAL fluid | USA | KX923835, LN850860, KX924061, KX923836, KX924271, KX924062, KX923837, KX924272, KX924063, KX924031 |
| **M. cirrosus**             |           | **CBS 217.31**, DTO 103-G1, CBS 277.34, DTO 345-A7, MUCL 9050, MUCL 9055 | Prunus sp., leaf, Vitis vinifera, root | Italy | KX923838, KX924273, KX924064, KX924032 |
| **M. longostris**           |           | **CBS 267.49**, DTO 170-B9, IFO 7029 | Sciurus vulgaris, skin | Netherlands | KX923840, KX924275, KX924065 |
| **M. griseus**              |           | **CBS 270.58**, DTO 342-E1, IMI 088913 | Compost soil | Germany | KX923841, KX924276, KX924066 |
| **CBS 301.61**, DTO 345-A6, IMI 088914, NRRL 1689, MUCL 9054 | Unknown | Unknown | UK | KX923842, KX924277, KX924067 |
| **CBS 302.61**, DTO 345-D1 | Unknown | Unknown | Canada | KX923843, KX924278, KX924068 |
| **CBS 342.62**, DTO 345-A9 | Polyvinylchloride | Unknown | Netherlands | KX923844, KX924279, KX924069 |
| **CBS 541.74**, DTO 342-I8 | Rodent dung | Unknown | USA | KX923845, KX924280, KX924070 |
| **CBS 157.92**, DTO 342-G6, FRR 4174 | Arachis hypogaea, nut | Unknown | Indonesia | KX923846, KX924281, KX924071 |
| **CBS 115960**, DTO 345-D4, FMR 6875 | Unknown | Unknown | Spain | KX923847, KX924282, KX924072 |
| **CBS 116405**, DTO 345-D6 | Antique tapestries | Unknown | Poland | LN850763, LN850861, LN850909 |
| **Dito 342-D4, RGR 84.0007** | Helianthus annuus, cloiseed | Unknown | USA | KX923848, KX924283, KX924073 |
| **Dito 342-D5, RGR 84.0033** | Unknown | Unknown | Unknown | KX923849, KX924284, KX924074 |
| **Dito 342-D7, RGR 84.0051** | Unknown | Unknown | Unknown | KX923850, KX924285, KX924075 |

(continued on next page)
| Name                             | Old name | Strain numbers | Host/Substrate | Country         | GenBank accession number |
|---------------------------------|----------|----------------|----------------|-----------------|--------------------------|
| **M. cleistocarpus sp. nov.**    |          | CBS 134638<sup>4</sup>, DTO 342-D2, CMGMC 3.15222 | Discarded cloth | China            | XX923851 XX924286 XX924076 XX924033 |
| **M. croci**                     | S. croci | CBS 158.44<sup>4</sup>, DTO 103-H3, IMI 078261, MUCL 9002 | Crocus sp.      | Netherlands     | XX923852 XX924287 XX924077 LM652508 |
| Masoniella tertia<sup>7</sup>    |          | CBS 296.61, DTO 103-H6, IMI 109550, MUCL 9005 | Air             | Brazil           | XX923853 XX924288 XX924078 |
| S. chartarum                    |          | CBS 522.69, DTO 342-C7 | Forest soil   | Canada           | XX923854 XX924289 XX924079 |
| M. expansus                     |          | DTO 225-NT, DTO 252-DB, DTO 305-B3, DTO 305-B5 | Indoor         | Mexico           | XX923857 XX924292 XX924082 |
| M. expansus                     |          | CBS 138127, DTO 351-D6, UTHSC 06-472, FMR 12266 | Human, sputum | USA              | XX923859 XX924294 XX924084 HG380492 |
| M. fusiisporus sp. nov.          | M. paisii | CBS 896.68<sup>4</sup>, DTO 356-C2, ATCC 16278, IFO 3114, MUCL 8989 | Wheat-field soil | Germany | LM652432 LM652645 HG380372 LN850825 |
| M. gracilis                     | M. cinereus | CBS 126.14, DTO 347-C4, IMI 086916 | Unknown        | Unknown          | XX923860 XX924295 XX924085 |
| M. gracilis                     | M. cinereus | CBS 195.61, DTO 345-C8, IMI 075542, MUCL 9048 | Soil           | UK              | LM652416 LM652629 HG380391 |
| M. gracilis                     | M. cinereus | CBS 300.61, DTO 345-C9 | Zea mays, stored seed | USA | LM652417 XX924296 LM652563 |
| M. gracilis                     | M. cinereus | CBS 369.70<sup>7</sup>, DTO 104-B3, IFO 7561 | Wheat flour | Japan           | XX923861 XX924297 XX924086 HG380467 |
| M. hollandicus sp. nov.         |          | CBS 141582<sup>4</sup>, DTO 191-C3 | Indoor horse arena | Netherlands | XX923869 XX924304 XX924094 XX924034 |
| M. hyalinus                     |          | CBS 766.70<sup>7</sup>, DTO 170-F2 | Cow dung       | USA              | XX923870 XX924305 LM652564 LM652513 |
| M. intricatus                   |          | CBS 134639, DTO 342-I9 | Goat dung       | China            | XX923871 XX924306 XX924095 |
| M. intricatus                   |          | CBS 138128<sup>7</sup>, DTO 351-D7, UTHSC 07-156, FMR 12264 | Human BAL fluid | USA              | XX923872 XX924307 HG380419 HG380496 |
| M. macrosporus                  |          | DTO 223-A6 | Indoor         | Micronesia       | XX923873 XX924308 XX924096 |
| M. macrosporus                  |          | CBS 752.97, DTO 338-G8 | Anacardium occidentale, nut | Brazil | XX923874 XX924309 XX924097 XX924035 |
| M. macrosporus                  |          | CBS 196.61<sup>7</sup>, IMI 086908, MUCL 9058, NRRL 1717 | Wasp's nest    | USA              | LM652421 LM652634 LM652566 LM652515 |
| M. macrosporus                  |          | 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. cirrus                       |          | CBS 540.74, DTO 347-D1 | Soil           | USA              | XX923875 XX924310 XX924098 |
| M. melanosporus comb. S. melanospora nov. |          | CBS 272.60<sup>7</sup>, DTO 103-H1, IFO 6441, IMI 078257, LCP 59.1590, MUCL 9040, NHL 6045 | Oryza sativa, milled | USA | XX923876 XX924311 LM652572 XX924036 |
| S. fusca                        |          | CBS 854.68, DTO 220-H7 | Compost soil  | Germany          | XX923877 XX924312 XX924099 |
| M. melanosporus comb. S. melanospora nov. |          | CBS 102829, DTO 342-E7, CBS 116060, DTO 136-G8 | Cheese warehouse, Antique tapestries | Netherlands | XX923878 XX924313 XX924100 |
| DTO 043-A1                      | Unknown | Unknown       | Unknown        | Unknown          | XX923879 XX924314 XX924102 |
| DTO 043-A2                      | Unknown | Unknown | Unknown        | Unknown          | XX923880 XX924315 XX924103 |
| DTO 049-E4                      | Archive | Unknown    | Unknown        | Netherlands      | XX923881 XX924316 XX924104 |
| DTO 049-E5                      | Archive | Unknown | Unknown        | Netherlands      | XX923882 XX924317 XX924105 |
| DTO 049-F2                      | Office   | Unknown | Unknown        | Netherlands      | XX923883 XX924318 XX924106 |
| DTO 053-H2                      | Between concrete Floor and carpet | Unknown | Unknown        | Netherlands      | XX923884 XX924319 XX924107 |
| DTO 067-G7                      | Bakery   | Unknown | Unknown        | Netherlands      | XX923885 XX924320 XX924108 |
| DTO 138-B6                      | Indoor   | Unknown | Unknown        | Germany           | XX923886 XX924321 XX924109 |
### Table 1. (Continued).

| Name                        | Old name¹ | Strain numbers² | Host/Substrate | Country            | GenBank accession number |
|-----------------------------|-----------|-----------------|----------------|--------------------|--------------------------|
| DTO 220-H9                  | Indoor    | South Africa    | KX923887       | KX923832           | KX924110                |
| DTO 220-I1                  | Indoor    | South Africa    | KX923888       | KX923832           | KX924111                |
| DTO 220-I2                  | Indoor    | South Africa    | KX923889       | KX923832           | KX924112                |
| DTO 220-I3                  | Indoor    | South Africa    | KX923890       | KX923832           | KX924113                |
| DTO 223-A9                  | Indoor    | Germany         | KX923891       | KX923832           | KX924114                |
| DTO 240-A9                  | Archive   | Netherlands     | KX923892       | KX923832           | KX924115                |
| DTO 240-B1                  | Archive   | Netherlands     | KX923893       | KX923832           | KX924116                |
| DTO 240-B3                  | Archive   | Netherlands     | KX923894       | KX923832           | KX924117                |
| DTO 240-B4                  | Archive   | Netherlands     | KX923895       | KX923832           | KX924118                |
| DTO 252-D7                  | Indoor    | Germany         | KX923896       | KX923832           | KX924119                |
| DTO 255-A5                  | Airsampling| Germany        | KX923897       | KX923832           | KX924120                |
| DTO 255-A6                  | Airsampling| Germany        | KX923898       | KX923832           | KX924121                |
| DTO 255-A7                  | Airsampling| Germany        | KX923899       | KX923832           | KX924122                |
| DTO 255-B1                  | Plaster   | Germany         | KX923900       | KX923832           | KX924123                |
| DTO 255-B3                  | Polystyrene| Germany        | KX923901       | KX923832           | KX924124                |
| DTO 255-B5                  | Oriented strand board| Germany | KX923902       | KX923832           | KX924125                |
| DTO 255-B6                  | Wood      | Germany         | KX923903       | KX923832           | KX924126                |
| DTO 255-C3                  | Unknown   | Germany         | KX923904       | KX923832           | KX924127                |

**M. micronesiensis** sp. nov.  
CBS 14152³, DTO 220-I9  
Indoor Micronesia  
KX923905 KX924340 KX924128 KX924037

**M. murinus** CBS 621.70, DTO 347-C8  
Composted municipal waste Germany  
LN850868

**M. onychoides**  
CBS 13962⁹, BMU 03911  
Human, nail China  
LN850774 LN850871 LN850920 LN850823

**M. paisii** Torula paisii  
CBS 213.27, DTO 103-F9, IMI 036480, MUCL 7915, VKM F-424  
Human Italy  
LM652434 KX924343 KX924133

**S. sphaerospora**³  
CBS 402.34, DTO 103-G8, MUCL 9046  
Unknown Austria  
LM652437 KX924344 LM652651

**S. brumptii**²  
CBS 333.35, DTO 220-H5  
Small-pox vaccine France  
KX923910 KX924345 KX924134

**M. pseudolongirostris**  
CBS 462.97, DTO 351-D5  
Human, nail Netherlands  
LN850782 LN850879 LN850924 LN850831

**M. pseudopaisii** sp. nov.  
CBS 14158¹, DTO 116-A3  
Air, basement Netherlands  
KX923925 KX924346 KX924138

**M. pyramidus**  
CBS 212.65, DTO 104-A1, DTO 104-A2, ATCC 36763, IMI 109887  
Desert soil USA  
KX923925 KX924360 KX924150 HG380435

**M. restrictus** M. trigonosporus  
CBS 13827⁷, DTO 342-E4,  
Pocket mouse, hair USA  
KX923926 LN850876 LN850925

**M. senegalensis**  
CBS 277.74⁴, DTO 351-E4  
Mangrove soil Senegal  
KX923929 KX924363 KX924153 LM652523

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(continued on next page)
| Name                               | Old name | Strain numbers | Host/Substrate | Country          | GenBank accession number |
|------------------------------------|----------|----------------|----------------|------------------|-------------------------|
| **ITS tef1**                       |          |                |                |                  |                         |
| M. terreus                         | CBS 601.67, 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             | USA                     |
| M. trigonosporus                   | CBS 807.73, DTO 342-E5 |                | Saline desert soil | Kuwait          | USA                     |
| M. trigonosporus                   | CBS 138275, UTHSC 07-1823, FMR 12342 |                | Human, sputum  | USA             | USA                     |
| M. trigonosporus                   | DTO 342-D3, RGR 85.0058 |                | Helianthus annuus, confectionary seed | USA | USA                     |
| M. trigonosporus                   | DTO 343-A1, RGR 84.0003 |                | Helianthus annuus, seed | USA | USA                     |
| M. trautmannii sp. nov.            | CBS 141983, DTO 255-C1 |                | oriented strand board | Germany          | USA                     |
| M. trigonosporus                   | CBS 218.31, DTO 103-G2, HACC 178, IMI 113702 |                | Unknown        | Puerto Rico      | HG380436 HG380359 HG380436 |
| Pithoascus stoveri                 | CBS 176.71, DTO 104-B6, ATCC 1117 |                | Beta vulgaris, root seedling | USA | LM652532 |
| Pseudoscopulariopsis schumacheri   | CBS 435.86, DTO 170-H5 |                | Soil           | Spain            | LM652534 |
| Scopulariopsis africana sp. nov.   | CBS 118736 |                | Mud, salt pan  | South Africa     | USA                     |
| S. altida sp. nov.                 | CBS 210.61, DTO 347-B3, IMI 086939 |                | Unknown        | Unknown          | USA                     |
| S. flavescens                      | CBS 152.22, DTO 347-C5, IMI 086928, MUCL 9044 |                | Unknown        | France           | USA                     |
| S. koningii                        | CBS 399.34, DTO 103-G6, UAMH 934 |                | Human, skin    | Austria          | USA                     |
| S. koningii                        | CBS 208.61, DTO 170-C6, IMI 086926, FMR 3654 |                | Elephant       | Unknown          | LM850786 LM850883 LM850931 |
| S. asperula                        | CBS 204.27, DTO 334-F5, MUCL 9009, UAMH 923 |                | Unknown        | France           | USA                     |
| S. fusca                           | CBS 401.34, DTO 103-G7, IFO 8181, IMI 086934, MUCL 9032, UAMH 930 |                | Rabbit carcass | Australia        | LM652463 LM652492 LM652482 |
| S. fusca                           | CBS 105.35, DTO 334-F8, IMI 086925 |                | Unknown        | Unknown          | LM652463 LM652492 LM652482 |
| Torula bestae                      | CBS 289.38, DTO 103-H1, IMI 086927, MUCL 9012, UAMH 924 |                | Human          | Italy            | USA                     |
| S. fusca                           | CBS 351.49, DTO 342-C4, MUCL 9033 |                | Sciurus vulgaris, dead | France          | USA                     |

**Notes:**
- ITS: Internal Transcribed Spacer
- tub2: Tubulin subunit 2
- tef1: Translation elongation factor 1
- LSU: Large Subunit
| Name         | Old name | Strain numbers | Host/Substrate | Country       | GenBank accession number |
|--------------|----------|----------------|----------------|---------------|--------------------------|
| *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 334-15 | Compost soil | Germany      | KX923963 JG434558 KX924188 |
|              | CBS 872.88, DTO 334-H6 | Wheat field soil | Germany      | KX923964 KX924397 KX924189 |
|              | ATCC 16281 |                |               |               |
|              | CBS 668.74, DTO 335-A5 | Soil | Egypt        | KX923965 KX924348 KX924190 |
|              | CBS 373.76, DTO 170-G6 | Unknown | Netherlands | KX923966 KX924399 KX924191 |
|              | CBS 114063, DTO 038-B3, DTO 334-I4 | Wood sample | Germany      | KX923967 KX924400 KX924192 |
|              | D TO 335-B3 |                |               |               |
|              | CBS 117767, DTO 038-B6 | Wood sample | Germany      | KX923968 LN850884 KX924193 |
|              | CBS 131816, DTO 335-D1 | Alkaline soil | Russia       | KX923969 KX924401 KX924194 |
|              | 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 |
|              | CBS 334.35, 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 |
| *M. brevicaulis* | CBS 127812, DTO 138-E6, UAMH 7770, D TO 138-E7, UAMH 7770, MUCL 40726 | Indoor air | Canada      | LM652465 KX924423 HG380363 HG380440 |
|              | CBS 127925, DTO 138-E8 | 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)
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 analyses including 500 bootstrap replicates using RAxML v. 7.2.6 (Stamatakis & Alachiotis 2010) were additionally run on both the
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 ascocarp 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. traumanni), 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 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. aibida, 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. flavia, 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.
**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 Pilthoascus stoveri (CBS 176.71).

**Fig. 1.** (Continued).
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).
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 1180 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

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.
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. hollanicus, M. microesiensis, 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. microesiensis and M. pseudopaisii). The two isolates of M. pseudopaisii are isolated from the same place, and could be seen as duplicates. Microascus microesiensis 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.

Ascospora abundant, immersed, ostiolate, globose to subglobe 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. Anellides 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 subglobe with small basal appendage, (5–)5.5–7 × (3.5–)4–5.5 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 undulate. 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 (Jagelski 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 tuf2 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 subglobe 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 colonis” are described.

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**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. hollanicus, M. intricatus, M. melanosporus, M. microesiensis, M. paisii, M. pseudopaisii, M. trautmannii, M. tricuspidatus, S. brevicaulis, S. candida, S. brevicausa, S. candida, S. caseicolor, S. flavus, Y. carbonaria |
| Animal    | M. cirrusus, M. pyramidalis, S. albiflavescens, S. asperula               |
| Dung      | M. cirrusus, M. hyalinus, S. asperula, S. sexualis, S. maculatus          |
| Food      | M. gracilis, M. longicollicia, M. trigonusporus, S. asperula, S. brevicaulis, S. candida, S. caseicolor, S. flavus, Y. penicillata |
| Human     | M. alveolaris, M. appendiculatus, M. bruneosporus, M. chinenesis, M. cinereus, M. cirrusus, M. croci, M. expansus, M. gracilis, M. intricatus, M. longicollicia, M. melanosporus, M. onychoides, M. paisii, M. restrictus, M. terreus, M. verrucosus, M. pseudolongostris, S. albiflavescens, S. asperula, S. brevicaulis, S. candida, S. cordiae |
| Insect    | M. longirostris, S. asperula, S. brevicaulis                              |
| Plant     | M. alveolaris, M. cirrusus, M. croci, M. gracilis, M. melanosporus, M. paisii, M. senegalensis, M. terreus, M. trigonusporus, S. asperula, S. sexualis, S. soppi, Y. carbonaria |
| Soil      | M. alveolaris, M. atrogriseus, M. cinereus, M. cirrusus, M. croci, M. fusissorus, M. gracilis, M. intricatus, M. longirostris, M. macrosporus, M. melanosporus, M. muninus, M. pyramidis, M. senegalensis, M. terreus, S. africana, S. albida, S. asperula, S. brevicaulis, S. candida, S. cordiae, Y. carbonaria, Y. smithii |
| Others    | M. paisii, M. cercotropus, S. brevicaulis                                 |
Sexual morph not observed. Conidiophores arising from substrate mycelium, simple or indistinctive, bearing one or multiple anellides. Anellides ampulliform, (4.5–)5–8.5(–10) μm long, 2–3 μm broad at the widest part, tapering abruptly to a cylindrical anellate 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 cream-coloured with (pale) olivaceous grey, radially striated edge with crenated margin. On OA no growth at 36 °C. On DG18 attaining a diameter of 10 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 anellide. Anellides 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 anellate 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.

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–)7×4–5 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 anellide. Anellides 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 anellate 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.

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

| Old name                  | Current name                  | Old name           | Current name                  |
|---------------------------|-------------------------------|--------------------|-------------------------------|
| Kernia hyalina            | Microascus hyalina            | Scopulariopsis brevicaulis var. glabra | Scopulariopsis candida |
| Masonia chartarum         | Microascus chartarus          | S. brunntii        | 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 chartarust         |
| M. grisea                 | Microascus atrogriseus        | S. croci           | Microascus croci              |
| M. teria                  | Microascus croci              | S. fusca           | Scopulariopsis asperula       |
| Microascus brevicaulis    | Scopulariopsis brevicaulis    | S. gracilis        | Microascus gracilis          |
| M. exsertus               | Pithoascus exsertus           | S. Gryllis         | Scopulariopsis flava          |
| M. griseus                | Microascus cinereus           | S. hibernica       | Pseudoscopulariopsis hibernum |
| 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. kongingii       | Scopulariopsis brevicaulis    |
| M. schumacheri            | Pseudoscopulariopsis schumacheri | S. munina       | Microascus murinus           |
| M. soppii                 | Scopulariopsis soppii         | S. paisii          | Microascus paisii             |
| M. stoveri                | Pithoascus stoveri            | S. penicilloides   | Scopulariopsis brevicaulis    |
| M. styssanophorus         | 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. styssanophorus         | Pseudoscopulariopsis schumacheri | S. trigonospora | Microascus trigonosporus      |
| Scopulariopsis Arnoldii   | Scopulariopsis asperula       | S. versicolor      | Microascus paisii             |
| S. atra                   | Pithoascus ater               | Torula asperula    | Scopulariopsis asperula       |
| S. aurea                  | Scopulariopsis asperula       | T. bestae          | Scopulariopsis asperula       |
| S. bestae                 | Scopulariopsis asperula       | T. paisii          | Microascus paisii             |
| S. brevicaulis var. alba  | Scopulariopsis asperula       |                    |                               |

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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. 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.
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. *Anellides* 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, cratenniform, 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).

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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:** Morphologically M. fusisporus resembles M. trautmannii, but can be distinguished 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...
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 oliveaceous 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.

**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 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.

**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).

Specimen examined: Netherlands, from a swab sample of an indoor horse arena, Mar. 2012, Houba, (holotype CBS H-22716, culture ex-type CBS 141582).
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
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. Dermatol. Urol. 26:5. 1928. nom. inval.

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

≡ Scopulariopsis aphaespora Zach, Oesterr. Bot. Z. 83: 180. 1934.

≡ Scopulariopsis brumptii Salv.-Duval, Thèse Fac. Pharm. Paris. 23: 58. 1935.
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...
annelides (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 morphologically 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. brumptii*. 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 Thèse 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 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. 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.
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 anellides (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 anellides. Anellides 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 anellate zone (1–) 1.5–2(–2.5) μm wide, hyaline, smooth-walled. Conidia obvoid 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).

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**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, anellides and conidia. Scale bars = 10 μm.
Notes: Morphologically *M. trautmannii* resembles *M. fusisporus*, but they can be distinguished based on the size of their annel- lides and the growth at 36 °C on OA (see notes *M. fusisporus*). Both species can easily be distinguished from the other *M. paisi-* 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 sub- strate 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, hy- aline, 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 di- ameter 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).
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* Woudemb. & Samson sp. nov. Myco-Bank MB818275. Fig. 15.

Etymology: name refers to the white colonies.

Sexual morph not observed. Conidiophores arising from substrate mycelium, simple to indistinctive. Anellides 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.
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 Loubier of which no type material is known to exist.

Scopulariopsis sexualis Woudenb. & Samson sp. nov. MycoBank MB818277. Fig. 17.
**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 & Genie, *Fungal Biol.* 120: 593. 2016.
**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 & Gé, Fungal Biol. 120: 593. 2016.

Specimens examined: **Panama**, from soil, collection date unknown, R. Cogill, (culture ex-type CBS 205.61 = NRRL 1860 = 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). *Anellides* 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. 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.** Ascii. **G.** Ascospores. 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 (BS) and Bayesian posterior probabilities (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.
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, Boriov et al. 2016) 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. traummannii) 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

![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.](image-url)
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. traumanni 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 holländicus 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. paisi and M. holländicus 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. teresus 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 distin-
guished 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 distin-
guished 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 Fuscoannelis 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. Conidia obovoid to broad clavate or fusiform .......... Microascus, 3
2b. Conidia broadly ellipsoidal to short clavate ........... 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 .......... M. fusiporus
4b. Conidia broadly ellipsoidal to short clavate ..........  8
5a. Annellides 9–12 μm long .................................. M. pseudopaisii
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 distinctly rough ................................ C. verrucissorum
9b. Conidia smooth ........................................... 10
10a. Conidia 3.5–5 × 2–3 μm ........................................ C. microsporum
10b. Conidia larger ................................ C. pseudopurpureofuscum or C. purpureofuscum

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