Aspergillus, Penicillium and Talaromyces isolated from house dust samples collected around the world

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ABSTRACT: As part of a worldwide survey of the indoor mycobiota, dust was collected from nine countries. Analyses of dust samples included the culture-dependent dilution-to-extinction method and the culture-independent 454-pyrosequencing. Of the 7,904 isolates, 2,717 isolates were identified to species level and describe the new species found. Secondly, we wanted to create a reliable reference sequence database to be used for next-generation sequencing projects. Isolates represented 59 Aspergillus species, including eight undescribed species, 49 Penicillium species of which seven were undescribed and 18 Talaromyces species including three described here as new. In total, 568 ITS barcodes were generated, and 391 β-tubulin and 507 calmodulin sequences, which serve as alternative identification markers.

Key words: Environmental metagenomics, Indoor moulds, Eurotiomycetes, Trichocomaceae.

Taxonomic novelties: New species: Aspergillus arenariae Isagase, Hirooka & Samson, A. capensis Hirooka, Seifert & Samson, A. griseoaurantiacus Hirooka, Seifert & Samson, A. micronesiensis Visagie, Hirooka & Samson, A. porphyrosporangitatus Visagie, Hirooka & Samson, A. sloani Visagie, Hirooka & Samson, A. subaethus Visagie, Hirooka & Samson, A. templicola Visagie, Hirooka & Samson, Penicillium alfredi Visagie, Seifert & Samson, P. dunnemense Visagie, Seifert & Samson, P. infrapurpureum Visagie, Seifert & Samson, P. lenticrescens Visagie, Seifert & Samson, P. magneliipitatum Visagie, Seifert & Samson, P. mexiticanum Visagie, Seifert & Samson, P. singorense Visagie, Seifert & Samson, Talaromyces oumae-anneae Visagie, Yilmaz, Seifert & Samson, T. sayulitensis Visagie, Yilmaz, Seifert & Samson, T. yelensis Visagie, Yilmaz, Seifert & Samson.

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INTRODUCTION

Indoor environments provide humans with a protective habitat in which they spend up to 90 % of their time (Höppe & Martinac 1998). These environments reportedly have unique microbial communities, which have adapted to the specific carbon, temperature and humidity constraints of these environments (Flannigan et al. 2011). Indoor environments, especially in first world countries, are well regulated with regards to temperature and are generally dry. Carbon sources available to fungi include damaged building materials (Flannigan et al. 2011), textiles, various food products and dust (Samson et al. 2010, Flannigan et al. 2011). When actively growing on these substrates, fungi often release high concentrations of spores and fungal fragments into the air that could affect humans as pathogens (Li et al. 2011). When actively growing on these substrates, fungi often release high concentrations of spores and fungal fragments into the air that could affect humans as pathogens (Li et al. 2011). When actively growing on these substrates, fungi often release high concentrations of spores and fungal fragments into the air that could affect humans as pathogens (Li et al. 2011). When actively growing on these substrates, fungi often release high concentrations of spores and fungal fragments into the air that could affect humans as pathogens (Li et al. 2011). When actively growing on these substrates, fungi often release high concentrations of spores and fungal fragments into the air that could affect humans as pathogens (Li et al. 2011).
and most common causative agent of aspergillosis and myceloma; Laët 1999, de Hoog 2000, Grosjean & Weber 2007, A. penicilloides, A. restrictus, A. sydowii (a common cause of human mycoses; Takahata et al. 2008, Samson et al. 2010), A. versicolor and A. westerdijkiae (common ochratoxin A producer; Frisvad et al. 2004a). Many Penicillium species are associated with biodeterioration of specific foods and are thus commonly reported from indoor surveys. Examples include P. expansum, commonly associated with apple rot and patulin production (Frisvad et al. 2004b), while P. digitatum and P. italicum cause rots of citrus (Frisvad & Samson 2004). Other species considered very common in indoors include P. brevicompactum (produces myco phenolic acid; Frisvad et al. 2004b), P. chrysogenum (penicillin producer; Houbraken et al. 2012), P. citrinum, P. commune, P. glabrum, P. olsonii, P. oxalicum and P. rubens (penicillin producer; Houbraken et al. 2012), while common Talaromyces species include T. funiculosus, T. rugulosus (produces rugulosin; Samson et al. 2010) and T. wortmanii (produces rugulosin and wortmannin; Brian et al. 1957, Samson et al. 2010). The two species, A. versicolor and P. chrysogenum were very common in buildings with water damage and have been suggested as indicators for sick building syndrome (Andersen et al. 2011).

As of 1 January 2013, single name nomenclature for fungi was enforced in the International Code of Nomenclature for algae, fungi, and plants (ICN) (McNeill & Turland 2011, McNeill et al. 2012). The abandonment of dual nomenclature resulted in significant changes in the taxonomy and nomenclature of Aspergillus, Penicillium and Talaromyces. Based on a four gene phylogeny, Houbraken & Samson (2011) showed that species formerly classified in Penicillium subgenus Biverticillium are resolved in a monophyletic clade with the former teleomorph genus Talaromyces, while the remaining Penicillium species are associated with the younger teleomorph genus name Eupenicillium. As such, Samson et al. (2011) transferred the accepted species of Penicillium subgenus Biverticillium into Talaromyces and Houbraken & Samson (2011) transferred Eupenicillium species into Penicillium. This was well received by the general community working on these fungi (Houbraken et al. 2011a,b, Visagie & Jacobs 2012, Visagie et al. 2012, Yilmaz et al. 2012, Manoeh et al. 2013, Visagie et al. 2013, Peterson & Jurjevic 2013, Sang et al. 2013, Fuji et al. 2013, Frisvad et al. 2013, Devi et al. 2014, Dufossé et al. 2014, Kanse et al. 2014).

The single name solution for Aspergillus and its large number of younger associated teleomorphic genera (such as Emericella, Neurosartorya, Eurotium etc.) is controversial, although phylogenetic data seems to suggest that Aspergillus and its associated teleomorphic genera collectively represent a monophyletic clade based on Bayesian analysis of a four gene (Houbraken & Samson 2011) and 25 gene (Houbraken et al. 2014a) dataset. The International Commission of Penicillium and Aspergillus (ICPA) voted on this nomenclatural issue on 14 April 2012 and chose to retain a broad but monophyletic concept of Aspergillus, rather than splitting the genus into smaller clades correlating with the teleomorphic names.

To achieve stability in names, the opportunity exists to have them protected in the ICN. With this in mind, lists for Aspergillus, Penicillium and Talaromyces were published in Visagie et al. (2014a), Samson et al. (2014) and Yilmaz et al. (2014), with updates to these lists available on ICPA’s website (http://www.aspergilluspenicillium.org). In addition to providing accepted species lists, it also provides information such as culture collection numbers for living ex-type material and GenBank accession numbers for sequences linked to these ex-types. This is considered an important step towards enabling correct species identifications in these large genera; there are currently 331 species in Aspergillus, 319 in Penicillium and 85 in Talaromyces.

The ITS barcodes from this list are incorporated in the RefSeq data set intended to enhance reliable fungal identifications using the GenBank database (Schoch et al. 2014).

This paper is focused on the identification of Aspergillus, Penicillium and Talaromyces species isolated from house dust collected from nine countries and the creation of a DNA barcode database for these species. We describe 18 new species, including eight in Aspergillus, seven in Penicillium, and three in Talaromyces. This work contributes to the Alfred P. Sloan research network on the Microbiology of the Built Environment, by providing authoritative taxonomic and molecular data to be used for metagenomic studies, thereby helping bridge the gap between culture-dependent and -independent detection techniques. This is the second of a series of reports on the taxonomy of fungi isolated using dilution to extinction in the survey, the first being the brief description of a new species of Rasamsonia (Tanney & Seifert 2013). The taxonomy of the other fungi isolated, reporting a taxonomically broad and diverse range of fungi, will be the subject of future publications.

MATERIALS AND METHODS
Isolations and identifications

Settled dust was collected in April of 2009 using sterilised Duststream® collectors (Indoor Biotechnologies) attached to vacuum cleaners. Buildings from nine countries, including Australia, Indonesia, Mexico, Micronesia, New Zealand, South Africa, Thailand, United Kingdom and Uruguay, were included in the survey. Samples from Canada and the United States were not included in this taxonomic study. Isolations were made using a dilution-to-extinction (d2e) method modified from Collado et al. (2007), using microplates composed of capped 1.5 mL micro tubes instead of 48-well microplates (Seifert et al. unpubl.). Malt extract agar (MEA, 20 g malt extract, 15 g agar, 1.000 mL dH2O) and 20 % sucrose MEA (20SMEA) with chloramphenicol were used as isolation media and 1.0 mL of medium was dispensed into each micro tube using a multi-channel pipette. House dust was suspended in a carboxymethylcellulose solution and diluted stepwise up to 1:64; the dilution yielding the maximum number of single-species colonies in the isolation was selected for subsequent study. For preliminary screening, cultures that appeared to represent Penicillium, Aspergillus, or Talaromyces were plated onto MEA in 6 cm Petri dishes and purified as necessary. All selected cultures from each country were sorted into putative species groups based on colony characters on MEA, and then up to five strains per culture-group per country were selected for more detailed study.

For our analyses of the prevalence of particular species in specific countries (Table 1), samples collected from different sites were considered to represent one sample.

Isolates from each country were placed into morpho-groups based on their characters on Czapek Yeast Autolysate agar
Table 1. Aspergillus, Penicillium and Talaromyces species distribution in house dust from around the world.

| Species           | United Kingdom | Mexico | Thailand | Indonesia | South Africa | Uruguay | Australia | New Zealand |
|-------------------|----------------|--------|---------|-----------|--------------|---------|-----------|-------------|
| Aspergillus species | 7              | 23     | 19      | 6         | 23           | 5       | 0         | 7           |
| Penicillium species | 4              | 5      | 9       | 7         | 16           | 0       | 8         | 22          |
| Talaromyces species | 0              | 4      | 10      | 2         | 0            | 8       | 0         | 2           |

Specie distribution:
- United Kingdom: +
- Mexico: +
- Thailand: +
- Indonesia: +
- South Africa: +
- Uruguay: +
- Australia: +
- New Zealand: +
Netherlands. Strains representing new species were deposited in the Applied and Industrial Mycology department (DTO) housed at the CBS-KNAW Fungal Biodiversity Centre, Utrecht, the Netherlands. Strains representing new species were deposited into the public collection of the CBS-KNAW (CBS).

DNA extraction, sequencing and phylogenetic analysis

DNA was extracted from 10-day-old strains grown on MEA (some Aspergillus species on DG18) using the Ultraclean™ Microbial DNA isolation Kit (MoBio, Solano Beach, USA), with DNA preps stored at −20 °C. PCR reactions were prepared as described in Houben & Samson (2011). Amplification of ITS was done using the primer set ITS1 and ITS4 (White et al. 1990), primer pair Bt2a and Bt2b for BenA (Glass & Donaldson 1995) and cmd5 and cmd6 for CaM (Hong et al. 2006). A standard amplification cycle was used, which ran 35 cycles with an annealing temperature of 55 °C. Sequencing reactions were set up using the BigDye Terminator v. 3.1 Cycle Sequencing Kit (Applied Biosystems, California, USA). Sequence contigs were assembled using Segman Pro v. 9.0.4 (DNASTar Inc.) and newly generated sequences deposited into GenBank.

The phylogenies presented here were prepared using a subset of representative strains of each species. The ITS phylogenies for Aspergillus, Penicillium and Talaromyces were used to direct the allocation of sequences into the correct genera and into smaller clades (indicated by different colours in the large scale trees), to allow more robust alignments of the alternative genes BenA and CaM.

Data sets were aligned in MAFFT v. 7.058b (Katoh & Standley 2013) using the L-INS-i algorithm. When needed, manual adjustments to alignments were made in MEGA v. 5.2.2 (Tamura et al. 2011). Maximum-likelihood (ML) trees were calculated for aligned data sets using MEGA. For the multigene phylogenies presented in the Taxonomy section for new species below, data sets were concatenated in Seaview v. 4.4.1 (Gouy et al. 2010). The most suitable model was determined in MEGA based on the lowest Bayesian Information Criterion (BIC). ML analyses were run by calculating the initial tree with the Bio-Neighbour-Joining (BioNJ) option, followed by a Heuristic search with the Nearest-Neighbour-Interchange (NNI) option. Support in nodes was calculated using a bootstrap analysis with 1000 replicates. In the phylogenies presented, thickened branches indicate bootstrap support above 80 %.

Morphology

Species were characterised using standard growth conditions (Okuda et al. 2000; Visagie et al. 2013, Visagie et al. 2014a). Strains were inoculated in three-point fashion onto CYA, MEA, Yeast Extract Sucrose agar (YES), DG18, CYA with 5 % NaCl (CYAS), Oatmeal agar (OA) and Creatine Sucrose agar (CREA). Plates were incubated in plastic boxes for 7 d in the dark at 25 °C. Additional CYA plates were incubated at 30 and 37 °C. Colour names and alphanumeric codes used in descriptions refer to Körnerup & Wanscher (1967).

Microscopic preparations were made from colonies grown on MEA, with DG18 also used for Aspergillus, after 1 to 2 wk. Lactic acid (60 %) was used as mounting fluid and excess conidia were washed away with 70 % ethanol. Characters were captured using a Zeiss SteREO Discovery.V20 dissecting microscope and Zeiss AX10 Imager.A2 compound microscope, both equipped with AxioCam MRC5 cameras using AxioVs40 v. 4.8.2.0. Microscopic measurements were done using Nikon NIS-elements D v. 4.0. Photo plates were prepared in Adobe® Photoshop® CS6 with photomicrographs cleaned up using the healing brush tool, for aesthetic reasons, without altering areas of scientific significance.

RESULTS

Isolations and identifications

D2E dust isolations resulted in 7 904 isolates, including 1160 Aspergillus, 1459 Penicillium and 98 Talaromyces isolates. Isolates represented 59 Aspergillus, 49 Penicillium and 18 Talaromyces species. Of these, 18 displayed unique characters deviating from known species of these genera and are described below as new species in the taxonomy section. Species identities and their presence/absence at a country scale are provided in Table 1.

High species richness was observed in dust collected in South Africa (47 species), Thailand (44 species), Mexico (32 species), New Zealand (31 species) and Micronesia (28 species). Countries with low species richness included the United Kingdom (11 species), Australia (8 species), Indonesia (7 species) and Uruguay (5 species).

Aspergillus diversity was high in Thailand (25 species), South Africa (23 species), Mexico (23 species) and Micronesia (19 species), while no Aspergillus species were isolated from Australian house dust. Penicillium species richness was highest in New Zealand (22 species) and South Africa (16 species), with no Penicillium species isolated from Uruguay. For Talaromyces, Thailand (10 species) and South Africa (8 species) had the highest species richness, while none were isolated from Australia, Indonesia, the United Kingdom and Uruguay.

Several species were common in the house dust (Table 1), with 13 Aspergillus species isolated from more than two countries. Aspergillus sydowii occurred in dust from six countries, A. fumigatus in five and A. subramanianii, A. niger and A. versicolor in four. Six Penicillium species were isolated from more than two countries. Penicillium brevicompactum, P. citrinum
Table 2. Strains used for phylogenetic analyses of new *Aspergillus*, *Penicillium* and *Talaromyces* species described from house dust.

| Species            | Culture collection number | GenBank accession nr. |
|--------------------|---------------------------|-----------------------|
|                    |                           | ITS                  | BenA     | CaM      |
| **Aspergillus**     |                           |                      |          |
| *A. amoenus*        | NRRL 4838                 | EF652480             | JN853946 | JN854035 |
| *A. arenarioides*   | CBS 138195 = DTO 129G8    | KJ775557             | KJ775070 | KJ775256 |
| *A. arenarius*      | CBS 138196 = DTO 267B6    | KJ775558             | KJ775082 | KJ775347 |
|                     | CBS 138197 = DTO 267C7    | KJ775559             | KJ775083 | KJ775349 |
|                     | CBS 138198 = DTO 268E1    | KJ775560             | KJ775089 | KJ775388 |
|                     | CBS 138199 = DTO 268E2    | KJ775561             | KJ775090 | KJ775389 |
|                     | CBS 138200 = DTO 268E3    | KJ775562             | KJ775091 | KJ775390 |
| *A. arenarius*      | CBS 463.65 = NRRL 5012 = ATCC 16830 = IMI 055632 = IMI 055632ii = WB 4429 = WB 5012 | EU021615 | EU021674 | EU021681 |
| *A. aureofulgens*   | CBS 653.74 = NRRL 6326    | EF669582             | EU014078 | EF669540 |
| *A. austroafricanus*| NRRL 233                 | JQ301891             | JN853963 | JN854025 |
| *A. baeticus*       | NRRL 62501 = CCF 4226 = CMFISB 2153 | HE615086                  | HE615092                  | HE615117 |
| *A. brevijanus*     | CBS 111.46 = NRRL 1935 = ATCC 16828 = CBS 119.45 = IMI 016066ii = IMI 16066 = NCTC 6971 = QB 7417 = WB 1935 | EF669582 | EU014078 | EF669540 |
| *A. brunneus*       | CBS 112.26 = CBS 524.65 = NRRL 131 = NRRL 134 = ATCC 1021 = IFO 5662 = IMI 211378 = QM 7406 = Thom 4481 = Thom 5633.4 = WB 131 | KJ775560 | KJ775089 | KJ775389 |
| *A. capensis*       | CBS 348.81 = NRRL 13001 = ATCC 44563 = IMI 259099 | HE615086                  | HE615092                  | HE615117 |
| *A. candidus*       | CBS 566.65 = NRRL 303 = ATCC 1022 = IMI 16264 = IMI 91889 = LSHBA c .27 = NCTC 595 = QM 995 = Thom 106 = WB 303 | EF652483 | EF652307 | EF652361 |
|                     | CBS 138188 = DTO 179E6    | EF669592             | EU014089 | EF669550 |
| *A. creber*         | NRRL 56592                | JQ301898             | JN853900 | JN854043 |
| *A. cvjetkovicii*   | NRRL 227                 | EF652440             | EF652264 | EF652352 |
| *A. flavipes*       | NRRL 302 = ATCC 24487 = IMI 171885 = QM 9566 = Thom 4640.474 = WB 302 | EF669591 | EU014085 | EF669549 |
| *A. fructus*        | NRRL 239                 | EF652449             | EF652273 | EF652361 |
| *A. fruticans*      | CBS 486.65 = NRRL 4903 = ATCC 16823 = IMI 139279 = O-1077 = QM 8033 = WB 4903 | EF652483 | EF652307 | EF652395 |
| *A. glaucus*        | CBS 516.65 = NRRL 116 = ATCC 16469 = IMI 211383 = LCP 64.1859 = Thom 5629.C = WB 116 | EF652052 | EF651887 | EF651989 |
|                     | NRRL 120                 | EF652054             | EF651889 | EF651991 |
|                     | NRRL 121                 | EF652055             | EF651890 | EF651992 |
| *A. griseoaurantiacus* | CBS 138189 = DTO 245F5 | KJ775551             | KJ775079 | KJ775319 |
|                     | CBS 138190 = DTO 267D2    | KJ775552             | KJ775084 | KJ775352 |
|                     | CBS 138191 = DTO 267D8    | KJ775553             | KJ775086 | KJ775357 |
| *A. iizukae*        | CBS 541.69 = NRRL 3750 = IMI 141552 = QM 9325 | EF669597 | EU014086 | EF669555 |
|                     | NRRL 35046               | EF669596             | EU014087 | EF669554 |
| *A. j anus*          | CBS 116.45 = NRRL 1787 = IMI 16065 = NCTC 6970 | EF669587 | EU014076 | EF669536 |
| *A. jensenii*       | NRRL 58600               | JQ301892             | JN854007 | JN854046 |
| *A. micronesiensis* | CBS 138182 = DTO 245D7    | KJ775546             | KJ775078 | KJ775318 |
|                     | CBS 138183 = DTO 267D5    | KJ775548             | KJ775085 | KJ775355 |
|                     | CBS 138186 = DTO 267H5    | KJ775549             | KJ775086 | KJ775372 |
| *A. niveoglaucus*   | CBS 101750               | HE801233             | HE801233                  | HE801233 |
|                     | CBS 114.27 = CBS 517.65 = NRRL 127 = ATCC 10075 = IMI 32050 = LSHBA 16 = NRRL 129 = NRRL 130 = QM 1977 = Thom 562.16 = Thom 5633. = Thom 5633.7 = Thom 7053.2 = WB 127 = WB 130 | EF652058 | EF651905 | EF651993 |
|                     | NRRL 128                 | EF652059             | EF651906 | EF651994 |
|                     | NRRL 136                 | EF652062             | EF651909 | EF651995 |
|                     | NRRL 137                 | EF652063             | EF651910 | EF651996 |

(continued on next page)
| Species          | Culture collection number | GenBank accession nr. |
|------------------|---------------------------|----------------------|
| **A. porphyreostipitatus** | CBS 138202 = DTO 132D1 | KJ775563 KJ775071 KJ775260 |
|                  | CBS 138203 = DTO 266D9   | KJ775564 KJ775080 KJ775338 |
| **A. proliferans**     | CBS 121.45 = NRRL 1908 = IMI 016105ii = IMI 16105 = LSHB 5624 = NCTC 7462 = UC 4303 = WB 1908 | EF652064 EF651891 EF651988 |
|                  | NRRL 114                  | EF652051 EF651886 EF651987 |
| **A. protuberus**      | CBS 602.74 = NRRL 3505 = ATCC 18990 = QM 9804 | EF652460 EF652284 EF652372 |
| **A. pseudoglaucus**   | CBS 123.28 = NRRL 40 = ATCC 10066 = IMI 016122 = IMI 016122ii = LSHB 19 = MUCL 15624 = QM 7463 = WB 40 | EF652498 EF652322 EF652410 |
| **A. pseudoustus**     | CBS 123904 = NRRL 5856 = IBT 28161 | FJ531147 FJ531168 FJ531129 |
| **A. puniceus**        | CBS 495.65 = NRRL 5077 = ATCC 16800 = IMI 9812 = WB 5077 | EF652425 EF652249 EF652337 |
| **A. puulaauensis**    | NRRL 35641                | JQ301893 JN853979 JN854034 |
| **A. ruber**           | CBS 530.65 = NRRL 52 = ATCC 16441 = IMI 211380 = QM 1973 = Thom 55988 = WB 52 | EF652066 EF651920 EF652009 |
| **A. saccharolyticus** | CBS 127449 = IBT 28509  | HM853552 HM853553 HM853554 |
| **A. sloani**          | CBS 138176 = DTO 244I8   | KJ775539 KJ775073 KJ775308 |
| **A. subalbidus**      | CBS 567.65                | KJ866983 EU076295 EF669561 |
| **A. subversicolor**   | CBS 138192 = DTO 129E3    | KJ775554 KJ775068 KJ775249 |
| **A. sydowi**          | CBS 138193 = DTO 129F9    | KJ775555 KJ775069 KJ775250 |
| **A. tabacinus**       | CBS 138194 = DTO 266I9    | KJ775556 KJ775081 KJ775251 |
| **A. taichungensis**   | CBS 138190 = DTO 266G2    | KJ775572 KJ866980 KJ775252 |
| **A. tanneri**         | CBS 138171 = DTO 245A1    | KJ775540 KJ775074 KJ775309 |
| **A. templicola**      | CBS 138177 = DTO 245A6    | KJ775541 KJ775075 KJ775311 |
| **A. tennesseensis**   | CBS 138178 = DTO 245A8    | KJ775542 KJ775076 KJ775313 |
| **A. tennesseensis**   | CBS 138179 = DTO 245A9    | KJ775543 KJ775077 KJ775314 |
| **A. tonophilus**      | CBS 138180 = DTO 245G2    | KJ775573 KJ866981 KJ775253 |
| **A. tritici**         | CBS 138181 = DTO 270C9    | KJ775573 KJ866981 KJ775253 |
| **A. ustus**           | CBS 261.67 = NRRL 250 = IMI 211384 = NRRL 254 | EF652450 EF652274 EF652362 |
| **A. venenatus**       | CBS 583.65 = NRRL 5212 = ATCC 16440 = ATCC 36504 = IMI 108299 = QM 5699 = WB 52 | EF652081 EF651919 EF652000 |
| **A. versicolor**      | CBS 266.81                | KJ775032 KJ786305 KJ786305 |
| **P. alfredii**        | CBS 138190 = DTO 266A4    | KJ775684 KJ775177 KJ775411 |
Table 2. (Continued)

| Species              | Culture collection number | GenBank accession nr. |
|----------------------|---------------------------|-----------------------|
|                      |                           | ITS | BenA     | CaM     |
| P. atramentosum      | CBS 109588 = DTO 249C3    | n.a. | KJ866976 | KJ866996 |
|                      | CBS 109601 = DTO 249C4    | n.a. | KJ866977 | KJ866987 |
|                      | CBS 109611 = IBT 10565    | n.a. | KJ866972 | KJ866988 |
|                      | CBS 109612 = IBT 14762    | n.a. | KJ866973 | KJ866989 |
|                      | CBS 109613 = DTO 250G3    | n.a. | KJ866978 | KJ866990 |
|                      | CBS 194.88 = IBT 21504    | n.a. | KJ866974 | KJ866999 |
|                      | CBS 291.48 = ATCC 10104 = FRR 795 = IFO 8137 = IMI 039752 = IMI 039752ii = LSHBP 1 = MUCL 29071 = MUCL 29126 = NRRL 795 = QM 7483 | n.a. | KY674402 | FJ530964 |
|                      | CBS 490.84 = IBT 11800    | n.a. | KJ866975 | KJ867017 |
|                      | DTO 178G2                 | n.a. | KJ775095 | KJ867019 |
| P.atrovenetum        | CBS 241.56 = ATCC 13352 = FRR 2571 = IFO 8138 = IMI 061837 = LSHBSm683 = QM 6963 | n.a. | JX140944 | KJ867004 |
|                      | CBS 243.56                | n.a. | KJ866971 | KJ867005 |
| P. brefeldianum      | CBS 235.81 = NRRL 710 = FRR 710 = IFO 31731 = IMI 216896 = LCP 89.2573 = LCP 89.2578 = MUCL 38762 = QM 1872 = Thom 5296 | n.a. | AF033435 | GU981623 |
|                      | CBS 300.48 = ATCC 10419 = DSM1215 = IMI 028260 = MUCL 29169 = NCTC 6607 = NRRL 910 = QM 7550 = VKMF-1148 | n.a. | JX140946 | KJ867009 |
|                      | CBS 231.81 = NRRL 2048 = FRR 2048 = IFO 31745 = IMI 099159 = LCP 58.1674 = NRRL 35656 | n.a. | DQ658166 | DQ658167 |
| P. cinnamopurpureum  | CBS 429.65 = CBS 847.68 = NRRL 162 = ATCC 18489 = CSIR 936 = FAT 362 = IAM 7016 = IFO 6032 = NHL 6359 = QM 7888 | n.a. | EF626950 | EF626948 |
|                      | CBS 114.69                | n.a. | KJ866970 | KJ866991 |
| P. coralligerum      | CBS 123.65 = NRRL 5082 = ATCC 16833 = IMI 139270 | n.a. | KJ834444 | KJ866994 |
| P. crystallinum      | CBS 479.65 = NRRL 5082 = ATCC 16833 = IMI 139270 | n.a. | EF626962 | FJ530973 |
| P. dunedinense       | CBS 138218 = DTO 244G1    | n.a. | KJ775171 | KJ775405 |
| P. echinulatum       | NRRL 917                  | n.a. | KJ866964 | KJ867021 |
| P. ellipsodeascoporum| CBS 112493 = AS 3.5688    | n.a. | JX012224 | AQ65104 | AY78559 |
| P. granatense        | CBS 166.81                | n.a. | KJ866967 | KJ866998 |
| P. guizhouanum       | AS 3.5215                 | KJ890410 | KJ890408 | KJ890406 |
| P. idahoense         | CBS 341.68 = NRRL 5274 = ATCC 22055 = FRR 881 = IMI 148393 | KC411747 | EF626953 | EF626954 |
| P. incoloratum       | CBS 101753 = AS 3.4672    | KJ834508 | KJ834457 | KJ866994 |
|                      | DTO 129G5                 | KJ775689 | KJ775182 | KJ775415 |
|                      | DTO 129I1                 | KJ775690 | KJ775183 | KJ775416 |
| P. infrapurpureum    | CBS 138219 = DTO 235F6    | KJ775679 | KJ775172 | KJ775406 |
|                      | CBS 138220 = DTO 235G2    | KJ775680 | KJ775173 | KJ775407 |
|                      | CBS 138221 = DTO 235G5    | KJ775681 | KJ775174 | KJ775408 |
|                      | CBS 138222 = DTO 235G6    | KJ775682 | KJ775175 | KJ775409 |
|                      | CBS 138223 = DTO 235HS    | KJ775683 | KJ775176 | KJ775410 |
| P. janesonlandense   | CBS 102888 = DAOM 234087 = IBT 21984 = IBT 24411 | DQ267912 | DQ309448 | KJ866985 |
| P. janczewskii       | CBS 221.28 = FRR 919 = IMI 191499 = NRRL 919 | n.a. | KJ834460 | KJ867001 |
|                      | CBS 279.47                | n.a. | KJ866968 | KJ867008 |
|                      | CBS 413.68                | n.a. | KJ866969 | KJ867014 |
|                      | CBS 414.68                | n.a. | KJ866960 | KJ867015 |
|                      | CBS 458.69                | n.a. | KJ866961 | KJ867016 |
| P. janthinellum      | CBS 340.48 = ATCC 10455 = IMI 040238 = NRRL 2016 = QM 6865 | GU981658 | GU981625 | KF296401 |
| P. javanicum         | CBS 341.48 = ATCC 9099 = CSIR 831 = FRR 707 = IFO 31735 = IMI 039733 = MUCL 29099 = NRRL 707 = QM 1876 | GU981613 | GU981657 | KF296387 |
| P. jensenii          | CBS 216.28                | n.a. | KJ866963 | KJ867000 |
|                      | CBS 327.59 = ATCC 18317 = FRR 909 = IFO 5764 = IMI 039768 = LCP 89.1389 = NRRL 909 = QM 7587 | n.a. | JX140954 | AY443490 |
| P. jianxiense        | AS 3.6521                 | KJ890411 | KJ890409 | KJ890407 |
Table 2. (Continued).

| Species | Culture collection number | GenBank accession nr. |
|---------|---------------------------|---------------------|
|         |                           | GenBank accession nr. |
| P. kojigenum | CBS 345.61 = ATCC 18227 = CCR 31515 = FRR 3442 = IFO 9581 = IMI 086562 = LSHBB394 = MUC 2457 = NRRL 3442 = QM 7951 | AF033489 KJ834463 KJ867011 |
| P. lanosum | CBS 106.11 = ATCC 10458 = FRR 2009 = IFO 5851 = IFO 6099 = IMI 040224 = LSHBP 86 = MUC 29232 = NRRL 2009 = QM 7591 | DQ304540 DQ285627 FJ530974 |
| P. lenticrescens | CBS 138215 = DTO 129A8 | KJ775675 KJ775168 KJ775404 |
| P. magnielliptisporum | CBS 138225 = DTO 128H8 | n.a. KJ775179 KJ775413 |
| P. malacaense | CBS 160.81 = NRRL 35754 = ATCC 42241 = IJFM 7093 = IMI 253801 = VKMF-2197 | EU427300 EU427268 KJ866997 |
| P. malodoratum | CBS 490.65 = NRRL 5083 = IMI 172289 = ATCC 16834 | n.a. EF696881 FJ530972 |
| P. lenticrescens | CBS 138226 = DTO 128I1 | n.a. KJ775180 KJ775414 |
| P. nigricans var. sulphureum | CBS 744.70 | n.a. KJ866966 KJ867018 |
| P. nodulum | CBS 227.89 | n.a. KJ834477 KJ866996 |
| P. novae-zeelandiae | CBS 137.41 = ATCC 10473 = IFO 31748 = IMI 040584ii = NRRL 2128 = QM 1934 = VKMF-2886 | KJ866966 |
| P. oxalicum | CBS 219.30 = ATCC 1126 = FRR 787 = IMI 192332 = MUC 29047 = NRRL 787 = QM 7600 | AF033438 KF296462 KF296367 |
| P. paradoxum | CBS 113178 = IIT 2362 | GU81570 GU981646 KF296381 |
| P. parvulum | CBS 138285 = NRRL 35504 | EF422845 EF506218 EF506225 |
| P. penarojense | CBS 362.48 = ATCC 10482 = FRR 1075 = IFO 8111 = IMI 040032 = NRRL 1075 = VKMF-1823 | GU981600 GU981668 KF296379 |
| P. radiatolobatum | CBS 340.79 | n.a. KJ866962 KJ867010 |
| P. raistrickii | CBS 261.33 = ATCC 10490 = FRR 1044 = IFO 6104 = IMI 040221 = LSHBB100 = NRRL 2128 = QM 1934 = VKMF-2886 | AY373927 KJ834485 KJ867006 |
| P. ribeum | CBS 219.30 = ATCC 1126 = FRR 787 = IMI 192332 = MUC 29047 = NRRL 787 = QM 7600 | n.a. EF696881 EF696992 |
| P. sajarovii | CBS 683.89 = FRR 2950 = IBT 3736 = IMI 285533 = DAOM 214786 | n.a. EF696881 EF696992 |
| P. scabrosum | CBS 138227 = DTO 270F1 | n.a. KJ866966 KJ867018 |
| P. shennangjianum | CBS 228.89 | n.a. KJ866966 KJ867018 |
| P. simplicissimum | CBS 129191 = ATCC MYA-4591 | KJ834485 KJ867006 |
| P. singorense | CBS 138211 = DTO 129H7 | n.a. KJ866962 KJ867010 |
| P. skrjabinii | CBS 114838 = BBA 65745 | AJ748692 KJ834500 KJ867012 |
| P. swiecickii | CBS 112616 = IBT 23023 | GU981574 GU981647 KF296382 |
| P. virgatum | CBS 114838 = BBA 65745 | AJ748692 KJ834500 KJ867012 |
| P. wotroi | CBS 118171 = IBT 23253 | GU981574 GU981647 KF296382 |
| P. yarmokense | CBS 410.69 = FRR 520 = IMI 140346 = VKMF-1076 | n.a. KJ834502 KJ867013 |
| P. zonatum | CBS 992.72 = ATCC 24353 | GU981574 GU981651 KF296380 |
| P. zonatum | CBS 289.48 = ATCC 10499 = IFO 7766 = IMI 040217 = MUCL 29233 = NRRL 2023 = QM 1936 = IBT 18220 | DQ267906 DQ285610 FJ509087 |
| P. zonatum | CBS 119391 = FRR 918 = IBT 27865 = IMI 191500 = NRRL 918 | AF033490 KJ834494 KJ866993 |
| T. aculeatus | CBS 255.31 = NRRL 1052 = FRR 1052 = Thom 4640.439 = ATCC 52257 | KF294192 KF741975 |
| T. allahabadensis | CBS 439.75 = NRRL 13055 = FRR 1945 = IMI 196528 = VKMF-1940 | GU981576 GU981626 KF296370 |
| T. apiculatus | CBS 126.28 = ATCC 10496 = FRR 2023 = IFO 7766 = IMI 040217 = MUCL 29233 = NRRL 2023 = QM 1936 = IBT 18220 | AF033488 DQ285616 KJ867002 |
| T. atricola | CBS 126216 = IBT 23203 | GU981574 GU981647 KF296382 |
| T. brunneus | CBS 118171 = IBT 23253 | GU981574 GU981647 KF296382 |
| T. obtusus | CBS 403.99 = AHC 1000 = IFO 4587 = IMI 040217 = MUCL 29233 = NRRL 2023 = QM 1936 = IBT 18220 | AF033490 KJ834494 KJ866993 |
| T. oxalicus | CBS 118171 = IBT 23253 | GU981574 GU981647 KF296382 |
| T. penicillatus | CBS 114838 = BBA 65745 | AJ748692 KJ834500 KJ867012 |
| T. vanderhammenii | CBS 126216 = IBT 23203 | GU981574 GU981647 KF296382 |
| T. virgatum | CBS 114838 = BBA 65745 | AJ748692 KJ834500 KJ867012 |
| T. wotroi | CBS 118171 = IBT 23253 | GU981574 GU981647 KF296382 |

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and *P. rubens* were isolated from four and *P. corylophilum*, *P. glabrum* and *P. pancosmium* from three. *Penicillium chrysogenum* was isolated in high numbers from dust in Australia and the United Kingdom. *Penicillium rubens*, a close relative of *P. chrysogenum* and the correct name for Fleming’s penicillin producer (Houbraken et al. 2011a), were also abundant in Australia, New Zealand, South Africa and the United Kingdom.

*Taalaromyces allahabadensis* and *T. atroroseus* occurred in three countries, with *T. albobiverticillius*, *T. diversus* and *T. minioluteus* occurring in two.

DNA sequences generated for identified species include 568 ITS barcodes (*Aspergillus* 283, *Penicillium* 229, *Talaromyces* 56). As secondary identification markers, 391 BenA (*Aspergillus* 126, *Penicillium* 203, *Talaromyces* 26) and 507 CaM (*Aspergillus* 278, *Penicillium* 56, *Talaromyces* 26) sequences were generated. All sequences were uploaded onto the Indoor Molds Database housed at the CBS-KNAW Fungal Biodiversity Center (http://www.cbs.knaw.nl/indoor/) and representative sequences for each species have been submitted to GenBank under accession numbers KJ775068–KJ775228, KJ775248–KJ775432, KJ775451–KJ775735 and KJ866960–KJ867021. Table 2 summarises GenBank numbers of strains used for multigene phylogenies in the Taxonomy section.

### Phylogenetic analysis

#### Aspergillus phylogeny

An ITS phylogeny (Fig. 1) was used to place *Aspergillus* isolates into their respective sections. The aligned data set included 347 strains and was 622 bp long, and the analysis employed the General Time Reversible (GTR) model with Gamma distribution (+G), with a certain fraction of sites that are evolutionary...
**Aspergillus**

Fig. 1. Aspergillus phylogeny of the ITS gene region showing the placement of representative strains isolated from house dust in bold. The coloured blocks indicate the different clades referred to in the text. The tree was rooted to *Talaromyces flavus*.
Clade 3 sect. Flav

EF409240 A. paniscrotligenus CBS 121.62
EF409241 A. arachidicola CBS 117610
AF357795 A. suboliavescens CBS 501.65
KJ775529 A. pseudonidus DTO 267D6
KJ775530 A. pseudonidus DTO 267H7
AF338643 A. pseudonidus CBS 119388
AF027660 A. nomius CBS 260.88
KJ775514 A. nomius DTO 246A1
KJ775515 A. nomius DTO 246B2
AF104444 A. bombycis CBS 117187
AF049830 A. caelatus CBS 763.97
AF027863 A. flavus CBS 569.65
AF272574 A. pseudotamarii CBS 766.97
AY373859 A. parasiticus CBS 100926
AF027860 A. oryzae CBS 102.07
KJ775475 A. flavus DTO 132A4
KJ775476 A. flavus DTO 245A7
KJ775574 A. tamarii DTO 248C1
KJ775575 A. tamarii DTO 267E4
KJ775576 A. tamarii DTO 267I7
EF669586 A. terreus CBS 601.65
KJ775579 A. terreus DTO 237B7
FJ31192 A. alabamensis CBS 125693
AY922633 A. neoafricanus CBS 130.55
EF669598 A. pseudotamarii CBS 123890
FJ31192 A. hortii NRRL 274
EF669580 A. auroterreus CBS 503.65
FJ531205 A. floccosus CBS 116.37
EF669816 A. neoindicus CBS 444.75
EF669601 A. alabamensis CBS 130.55
KJ775452 A. allahabadii DTO 179G7
EF669611 A. carneus CBS 494.65
EF669615 A. niveus CBS 115.27
EF669617 A. aurufugens CBS 653.74
KJ775559 A. capensis sp. nov. CBS 138188
KJ775544 A. templicola sp. nov. CBS 138180
KJ775545 A. templicola sp. nov. CBS 138181
EF669597 A. azukiae CBS 541.69
EF669591 A. flavipes NRRL 302
KJ775546 A. micronesiensis sp. nov. CBS 138182
KJ775547 A. micronesiensis sp. nov. CBS 138187
KJ775548 A. micronesiensis sp. nov. CBS 138183
KJ775549 A. micronesiensis sp. nov. CBS 138186
EF669578 A. janus CBS 118.45
EF669582 A. brevijanus CBS 111.46
EF661194 A. ellipticus CBS 482.65
EU921305 A. heteromorphus CBS 117.55
A. carbonarius DTO 179C6
A. carbonarius DTO 179F4
FJ629321 A. brasiliensis CBS 101740
KJ775590 A. welwitschiae DTO 178C2
KJ775580 A. tubingenensis DTO 178C1
KJ775588 A. neoniger DTO 268A8
KJ775504 A. neoniger DTO 266G3
FJ491682 A. neoniger CBS 115656

Fig. 1. (Continued).
Clade 5 sect. *Nigri* clade 1

| Accession | Name | Reference |
|-----------|------|-----------|
| FJ491682 | A. neoniger CBS 115656 | |
| EU821316 | A. luchuensis CBS 112811 | |
| KJ775583 | A. tubingensis DTO 244F5 | |
| KJ775513 | A. niger DTO 267I2 | |
| KJ775507 | A. neoniger DTO 267I9 | |
| JX500081 | A. luchuensis CBS 205.80T | |
| EU821317 | A. pulverulentus CBS 558.65 | |
| EF661193 | A. tubingensis NRRL 4875 | |
| AY585549 | A. vandenbos CBS 113365 | |
| KJ775594 | A. welwitschiae DTO 266D4 | |
| KJ775592 | A. welwitschiae DTO 247F7 | |
| KJ775582 | A. tubingensis DTO 244F3 | |
| KJ775512 | A. niger DTO 266D8 | |
| KJ775506 | A. neoniger DTO 267E8 | |
| FG629340 | A. welwitschiae CBS 139.54T | |
| EF661186 | A. niger CBS 554.65 | |
| FJ491684 | A. coreanus CBS 117059 | |
| KJ775505 | A. neoglaber CBS 111574 | |
| EU482439 | A. eucalypticola CBS 122712 | |
| A. acanthosporus CBS 558.71 | |
| EF661209 | A. parvulus CBS 136.61 | |
| EF661208 | A. cervinus CBS 537.65 | |
| EF669942 | A. clavatus CBS 513.65 | |
| KJ775469 | A. clavatus DTO 134A5 | |
| EU078625 | A. acanthosporus CBS 558.71 | |
| EF669928 | A. giganteus CBS 526.65 | |
| EF669919 | A. longipes CBS 530.71 | |
| EF669986 | A. clavatonanicus CBS 474.65 | |
| EU078652 | A. rhizopus CBS 450.75 | |
| EF669997 | A. unilateralis CBS 126.56 | |
| KJ775493 | A. hiratsuka DTO 237B5 | |
| KJ775494 | A. hiratsuka DTO 237B6 | |
| FR733873 | A. hiratsuka CCF 3988 | |
| FR733872 | A. hiratsuka CCF 3544 | |
| EF669948 | A. neoglaber CBS 111.55 | |
| EF669979 | A. igneus CBS 466.65 | |
| EF669984 | A. palaeocres CBS 498.65 | |
| EF669947 | A. quadrigingens CBS 135.52 | |
| EF669994 | A. fumigatus CBS 598.74 | |
| EF669961 | A. otani NRRL 32571 | |
| EF669971 | A. duricaulis CBS 481.65 | |
| EF669954 | A. brevipes CBS 118.53 | |
| EF669943 | A. phialatus NRRL 20549 | |
| EF669946 | A. thermomutatus CBS 208.92 | |
| HE974451 | A. nishimurae CBS 117265 | |
| KJ775487 | A. fumigatus DTO 267D3 | |
| KJ775488 | A. fumigatus DTO 267H1 | |
| KJ775485 | A. fumigatus DTO 266H1 | |
| KJ775482 | A. fumigatus DTO 244G7 | |
| KJ775484 | A. fumigatus DTO 244G3 | |
| KJ775483 | A. fumigatus DTO 179G6 | |
| EF669931 | A. fumigatus CBS 133.61 | |
| EF669950 | A. auroleucites CBS 105.55 | |
| JX021685 | A. felis CBS 130245 | |
| AB250781 | A. udagawae CBS 114217 | |

Fig. 1. (Continued)
Clade 6 sect. Fumigati & Clavati & Cervini

- AB250781. A. udagawae CBS 114217
- EF669936. A. fischeri CBS 544.65
- EF669878. A. viridinutans CBS 127.56
- AB250779. A. fumisynnematus IFM 42277
- AB299413. A. laevisus CBS 117721
- EF669997. A. lentulus CBS 117885
- EF669988. A. spinosus CBS 483.65
- KJ775497. A. lentulus DTO 178A2
- KJ775498. A. lentulus DTO 178A4
- KJ775534. A. restrictus DTO 236I8
- KJ775535. A. restrictus DTO 237A2
- KJ775533. A. restrictus DTO 236I7
- EF652065. A. intermedius CBS 523.65
- KJ775503. A. montevidensis DTO 267H2
- KJ775502. A. montevidensis DTO 180B6
- KJ775468. A. chevalieri DTO 267H3
- KJ775467. A. chevalieri DTO 266F8
- HE615136. A. costiformis CBS 101749
- EF652078. A. cristatus CBS 123.53
- EF652077. A. montevidensis CBS 491.65
- EF652068. A. chevalieri CBS 522.65
- KJ775519. A. penicillioides DTO 267A4
- KJ775520. A. penicillioides DTO 267A9
- EF652087. A. leucocarpus CBS 353.68
- EF652088. A. halophilicus CBS 122.62
- KJ775536. A. ruber DTO 266G4
- KJ775537. A. ruber DTO 267H3
- EF652066. A. ruber CBS 530.65
- HE615132. A. appendiculatus CBS 374.75
- EF652050. A. pseudoglaucus CBS 123.28
- EF652052. A. glaucus CBS 516.65
- EF652058. A. neocarnoyi CBS 471.65
- EF652059. A. niveoglaucus CBS 114.27
- EF652060. A. brunneus CBS 112.26
- EF652081. A. tonophilus CBS 405.65
- JO918177. A. obovatus KACC 46346
- KJ775521. A. proliferans DTO 2446
- KJ775522. A. pseudoglaucus DTO 24401
- KJ775527. A. pseudoglaucus DTO 24407
- KJ775528. A. pseudoglaucus DTO 245A5
- KJ775543. A. sibonii sp. nov. CBS 138176
- KJ775540. A. sibonii sp. nov. CBS 138177
- KJ775541. A. sibonii sp. nov. CBS 138231
- KJ775542. A. sibonii sp. nov. CBS 138178
- EF652064. A. proliferans CBS 121.45
- KJ775543. A. sibonii sp. nov. CBS 138179

Clade 7 sect. Restricti & Aspergilloides & Eurotium spp.

- KJ775561. A. arenarioides sp. nov. CBS 138199
- KJ775562. A. arenarioides sp. nov. CBS 138200
- KJ775560. A. arenarioides sp. nov. CBS 138198
- KJ775559. A. arenarioides sp. nov. CBS 138197
- KJ775558. A. arenarioides sp. nov. CBS 138196
- KJ775557. A. arenarioides sp. nov. CBS 138195
- EU021615. A. arenarioides CBS 463.65
- HM853552. A. saccharolyticus CBS 127449
- EF166063. A. homomorphus CBS 101889

Fig. 1. (Continued).
| Clade 8 sect. Nigri | Clade 9 sect. Ustii |
|---------------------|---------------------|
| EF166063 A. *homonorphus* CBS 101889<sup>1</sup> | EF652428 A. *caepitosus* CBS 103.45<sup>1</sup> |
| EF661221 A. *aculeatus* CBS 172.66<sup>1</sup> | EF652426 A. *stellifer* CBS 598.65<sup>1</sup> |
| FJ491678 A. *violaceofuscus* CBS 123.27<sup>1</sup> | EU448277 A. *filler* CBS 11363<sup>1</sup> |
| AM745757 A. *uvum* CBS 121591<sup>1</sup> | EU448269 A. *stellar-maris* CBS 11363<sup>1</sup> |
| AJ279985 A. *japonicus* CBS 114.51<sup>1</sup> | EU448268 A. *olivicola* CBS 119.37<sup>1</sup> |
| AJ280005 A. *indologenus* CBS 114.80<sup>1</sup> | EU448275 A. *undulatus* CBS 261.88<sup>1</sup> |
| KJ775461 A. *brunneoviolaceus* DTO 131H2 | KJ775584 A. *unguis* DTO 237B4 |
| AJ280003 A. *brunneoviolaceus* CBS 621.78<sup>1</sup> | KJ775585 A. *unguis* DTO 270D7 |
| EU159211 A. *aculeatinus* CBS 121060T | EF652443 A. *unguis* CBS 132.55<sup>1</sup> |
| KJ775463 A. *brunneoviolaceus* DTO 245G8 | KJ775510 A. *nidulans* DTO 178B3 |
| KJ775460 A. *brunneoviolaceus* DTO 129F8 | KJ775511 A. *nidulans* DTO 244I3 |
| KJ775462 A. *brunneoviolaceus* DTO 132B2 | KJ775501 A. *montenegrino* DTO 269C3 |
| KJ775586 A. *ustus* DTO 268C1 | EF652483 A. *fruticans* CBS 486.65<sup>1</sup> |
| KJ775587 A. *ustus* DTO 268C3 | EF652434 A. *rugulovalvus* CBS 133.60<sup>1</sup> |
| KJ775563 A. *porphyreostipitatus* sp. nov. CBS 138203<sup>1</sup> | EF652427 A. *nidulans* CBS 589.65<sup>1</sup> |
| KJ775563 A. *porphyreostipitatus* sp. nov. CBS 138202 | EF652482 A. *recurvatus* CBS 496.65<sup>1</sup> |
| HE616558 A. *calidicoccus* CBS 121601<sup>1</sup> | EF652424 A. *navahoensis* CBS 351.81<sup>1</sup> |
| HE652455 A. *ustus* CBS 261.67<sup>1</sup> | KJ775570 A. *sydowii* DTO 246A3 |
| FJ531147 A. *selenium* CBS 123904<sup>1</sup> | KJ775571 A. *sydowii* DTO 266C6 |
| EF652498 A. *puniceus* CBS 495.65<sup>1</sup> | KJ775569 A. *sydowii* DTO 245G9 |
| KJ775531 A. *puniceus* DTO 247F4 | KJ775568 A. *sydowii* DTO 236E9 |
| KJ775491 A. *Germanicus* DTO 179B7 | KJ775566 A. *sydowii* DTO 236D4 |
| EF652507 A. *pseudodeflectus* CBS 756.74<sup>1</sup> | EF652450 A. *sydowii* CBS 593.65<sup>1</sup> |

Fig. 1. (Continued).
invariable (+I) selected. The analysis distributed the 59 Aspergillus species into 10 clades. The black Aspergillus species of section Nigri were resolved in two clades (clades 5 & 8), the first containing species closely related to A. nigri and the other relatives of A. aculeatus. The section is considered monophyletic following the three gene phylogeny of Peterson (2008) and four gene phylogeny of Houbraken & Samson (2011). For accurate identification, CaM phylogeny were prepared for each of the 10 clades and are presented in Figs 2–11.

Clade 1 consisted of species classified in section Circumdati (Fig. 2). The aligned data set was 554 bp long, with Kimura 2-parameter (K2 + G + I) the most suitable model. This group of species is generally recognised by their ochre coloured conidio- phone heads and a large number of species produce ochratoxins (Frisvad et al. 2004a, Visagie et al. 2014b). One of these ochratoxin producers is A. westerdijkiae, which was isolated in very high numbers from the South African house dust. A monographic treatment on the section is published in this issue of Studies in Mycology and includes descriptions for two new species, A. occultus and A. pulvericola isolated in this study. We note that A. elegans and A. steynii have identical CaM sequences (Fig. 2), even though ITS (Fig. 1a) and BenA distinguishes them.

Clade 2 represents section Candidi (Fig. 3). The aligned data set was 527 bp long, with K2 + G the most suitable model. Within the clade, we identified a new species with similar morphological features to A. candidus. Phylogenetically it is distinct and is described as A. subalbidus in the taxonomy section below. Two isolates identified as A. taichungensis had sequence variation compared to the ex-type strain, but morphologically they were all identical. As such, the sequence variation was considered insufficient to justify describing a new species. Sequences for A. candidus are highly variable based on Varga et al. (2007). A new species, A. pragensis, was recently described in the A. candidus complex (Hubka et al. 2014). However, a number of strains analysed in Varga et al. (2007) do not phylogenetically conform to the clades accepted by Hubka et al. (2014) as A. candidus and A. pragensis. As such, this clade needs more revision and we tentatively identify...
Fig. 2. CaM phylogeny of Aspergillus section Circumdati, showing identities of species isolated from house dust in bold.

Fig. 3. CaM phylogeny of Aspergillus section Candidi, showing identities of species isolated from house dust in bold.
**CaM**

**Clade 3**

*sect. Flavi*

| Species          | Accession   |
|------------------|-------------|
| A. flavus        | KJ775258    |
| DTO 132A4        |             |
| A. flavus        | KJ775312    |
| DTO 245A7        |             |
| A. subolivaceus  | EF661506    |
| A. oryzae CBS 102.07T |     |
| A. parvisclerotigenus | HQ340097 |
| A. arachidicola  |             |
| A. parasiticus   | EF661526    |
| A. tamarii CBS 104.13T |     |
| A. sergii CBS 130015T |    |
| A. nomius CBS 260.88T |   |
| A. pseudonomius  | EF661529    |
| A. pseudotamarii |             |
| A. bombycis CBS 117187T |   |
| A. lanosus CBS 650.74T |  |
| A. albertensis NRRL 20602T |   |
| A. alliaceus CBS 536.65T |  |
| A. coremiiformis CBS 272.89 |   |
| A. leporis CBS 151.66T |    |
| A. avenaceus CBS 109.46T |    |
| A. robustus CBS 428.77T |   |
| A. flavipes NRRL302T | |
| A. iizukae CBS541.69T | |
| A. capensis sp. nov. CBS 138188T |     |
| A. templicola sp. nov. CBS 138181T | |
| A. janus CBS118.45T |       |
| A. carnipes CBS494.65T | |
| A. niveus CBS115.27T |     |
| A. aureofulgens CBS653.74T |    |
| A. flavipes CBS601.65T |   |
| A. terreus CBS601.65T | |
| A. hispanicus CBS1256693T | |
| A. flavipes NRRL302T |   |
| A. iizukae CBS541.69T | |
| A. capensis sp. nov. CBS 138188T | |
| A. templicola sp. nov. CBS 138181T | |
| A. janus CBS118.45T |       |
| A. carnipes CBS494.65T | |
| A. niveus CBS115.27T |     |
| A. aureofulgens CBS653.74T |    |
| A. flavipes CBS601.65T |   |
| A. hispanicus CBS1256693T | |
| A. flavipes NRRL302T |   |
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| A. janus CBS118.45T |       |
| A. carnipes CBS494.65T | |
| A. niveus CBS115.27T |     |
| A. aureofulgens CBS653.74T |    |
| A. flavipes CBS601.65T |   |
| A. hispanicus CBS1256693T | |
| A. flavipes NRRL302T |   |
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| A. janus CBS118.45T |       |
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| A. flavipes CBS601.65T |   |
| A. hispanicus CBS1256693T | |
| A. flavipes NRRL302T |   |
| A. iizukae CBS541.69T | |
| A. capensis sp. nov. CBS 138188T | |
| A. templicola sp. nov. CBS 138181T | |
| A. janus CBS118.45T |       |
| A. carnipes CBS494.65T | |
| A. niveus CBS115.27T |     |
| A. aureofulgens CBS653.74T |    |
| A. flavipes CBS601.65T |   |
| A. hispanicus CBS1256693T | |
| A. flavipes NRRL302T |   |
| A. iizukae CBS541.69T | |
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| A. janus CBS118.45T |       |
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| A. aureofulgens CBS653.74T |    |
| A. flavipes CBS601.65T |   |
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| A. flavipes CBS601.65T |   |
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| A. janus CBS118.45T |       |
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| A. niveus CBS115.27T |     |
| A. aureofulgens CBS653.74T |    |
| A. flavipes CBS601.65T |   |
| A. hispanicus CBS1256693T | |
| A. flavipes NRRL302T |   |
| A. iizukae CBS541.69T | |
| A. capensis sp. nov. CBS 138188T | |
| A. templicola sp. nov. CBS 138181T | |
| A. janus CBS118.45T |       |
| A. carnipes CBS494.65T | |
| A. niveus CBS115.27T |     |
| A. aureofulgens CBS653.74T |    |
| A. flavipes CBS601.65T |   |
| A. hispanicus CBS1256693T | |
| A. flavipes NRRL302T |   |
| A. iizukae CBS541.69T | |
| A. capensis sp. nov. CBS 138188T | |
| A. templicola sp. nov. CBS 138181T | |
| A. janus CBS118.45T |       |
Aspergillus section Flavi is resolved in clade 3 (Fig. 4). The CaM alignment was 517 bp long and K2 + G model selected for ML analysis. The species isolated from dust include A. flavus, A. nomius, A. pseudomonius and A. tamarindii.

Clade 4 contains sections Terrei and Flavipes (Fig. 5). The aligned data set was 571 bp long with the K2 + G model selected for ML analysis. In section Terrei, we isolated A. terreus and A. allahabadii. In section Flavipes, the three isolated species are considered new and described as A. capensis, A. micronesiensis and A. tempicola in the taxonomy section.

Clade 5, labelled section Nigri (Fig. 6), contains the black Aspergilli closely related to A. niger. The aligned data set was 442 bp long, with the K2 + G + I model was used for ML analysis. Five species were identified in this clade as A. carbonarius, A. neoniger, A. tubingsiensis and A. weilwitschiae.

Sections Fumigati, Clavati and Cervini all occurred in clade 6 (Fig. 7). The aligned data set was 578 bp long and the K2 + G model was selected for ML analysis. Strains were identified as A. clavatus, A. hitasukae, A. lentulus and A. fumigatus. The latter species was isolated in high numbers from five countries, namely Mexico, Micronesia, New Zealand, South Africa and Thailand.

Clade 7 resolves sections Restricti and Aspergillus in one clade (Fig. 8). The aligned data set was 610 bp long and the K2 + G + I model was used for ML analysis. Within the clade, we isolated one new species closely related to A. glaucus and A. proliferans, the latter also found in the dust samples together with A. chevalieri, A. montevdienis, A. penicillioides, A. pseudoglaucus, A. restrictus and A. ruber.

Clade 8 contains the black Aspergillus species closely related to A. aculeatus, labelled as Nigri clade 2 (Fig. 9). Even though the ITS phylogeny places A. arenarius closest to this clade, its taxonomic placement is currently uncertain and will be the focus of a future paper. The aligned data set was 470 bp long and the most suitable model was K2 + I. Two black species were identified as A. aculeatinus and A. brunneoviolaceus. A new species, closely related to A. arenarius, is described as A. arenarioides in the taxonomy section.

Clade 9 contains section Usti species (Fig. 10). The aligned data set was 510 bp long and K2 + I selected for the ML analysis. Five species were identified as A. germanicus, A. minutus, A. puniceus, A. ustus and a new species described as A. porphyroestiptalis.

Clade 10 contains sections Versicolores and Nidulantes (Fig. 11). The aligned data set was 545 bp long and K2 + G was selected as the most suitable model. Aspergillus versicolor is often isolated from indoor environments. Jurjević (2012) considered it to represent a complex and accepted nine species. We isolated and identified all of the new species they accepted, namely A. amoenus, A. austroafricanus, A. creber, A. fructus, A. jensennii, A. protuberus, A. paualausensis, A. tennessensis, and A. versicolor. Aspergillus sydowi was abundant and had a wide distribution in the house dust. In addition, we introduce a new species in the section as A. griseosartantius. In section Nidulantes, we identified strains as A. unguis, A. montenegroi and A. nidulans.

**Penicillium phylogeny**

An ITS phylogeny was used to place Penicillium house dust isolates in their respective sections (Fig. 12). The aligned data set included 380 strains and was 585 bp long. The GTR + G + I model was the most suitable model for the ML analysis. The phylogeny resolved the 49 house dust species, distributed among 12 clades. Clades corresponded well with the sections proposed by Houbraken & Samson (2011). To obtain more accurate identifications, BenA gene trees were analysed for each ITS clade and are presented in Figs 13–24.

Clade 1 contains section Citrina (Fig. 13), a group of species of wide distribution and isolated from a wide range of sources (Houbraken et al. 2011b). The aligned data set was 448 bp long, with the K2 + G model selected for ML analysis. Species were identified as P. citrinum, P. panscosmium, P. roseopurpureum, P. sanguifluum, P. sizovae, P. steckii and P. sumatraeae. Penicillium panscosmium was abundant in samples collected from South Africa, Indonesia and Micronesia. It is also extremely common in isolations from house dust samples collected in Regina, Canada (Hirooka, Tanney & Seifert, unpubl.).

Clade 2 corresponds with the recently revised section Scolerotiora (Fig. 14) (Rivera et al. 2012, Visagie et al. 2013). The aligned data set was 374 bp long, with the K2 + G model selected for ML analysis. Penicillium brocae was the only species isolated from house dust that belongs to the section.

Clade 3 includes section Ramigena (Fig. 15). The aligned data set was 402 bp long and K2 + I was the most suitable model for ML analysis. Two species, P. hispanicum and P. ramusculum, were identified from house dust. BenA also shows that P. cyanum, P. dierckii and P. sublateritum are synonyms, with P. cyanum (Bainier & Sartory) Bourrie, Cellule 33: 102. 1923 representing the oldest name.

Clade 4 includes species classified in section Cinna-mopurpurea (Fig. 16). The aligned BenA dataset was 390 bp long, with the K2 + G model selected for the ML analysis. One species was identified as P. incoloratum, while a second is described as P. infrapurpureum below.

Clade 5 contains the section Aspergilloides (Fig. 17), which is reviewed in Houbraken et al. (2014b). The alignment was 459 bp long and K2 + G was selected as the most suitable model for ML analysis. Three species were identified, including P. glabrum and two new species, P. sublecatum prov. nom. and P. longicatenatum prov. nom., described in Houbraken et al. (2014b).

Clade 6 contains section Exilicaulis (Fig. 18). The aligned data set was 448 bp long and K2 + G was selected for ML analysis. Species isolated include P. atrosanguineum, P. citreoquum, P. coryophilum, P. decumbens, P. melini, P. restrictum and P. rubefaciens. From the phylogeny, it is clear that some species need further study. The P. restrictum complex, including five species, represents one of these. This will be the focus of a future paper: We thus tentatively identify isolates in this complex as P. restrictum, mainly based on their morphological characters.

Clade 7 includes species of section Lanata-Diviricata (Fig. 19). The aligned data set was 472 bp long, with the K2 + G model selected for ML analysis. Isolates were identified as P. oxalicum and a new species is described here as P. singorensense.

Clade 8 contains species classified in section Canescentia (Fig. 20). The BenA alignment was 403 bp long, with K2 + G selected for the ML analysis. We describe one new species in this section as P. dunedinense.

Sections Brevicompacta and Ramosa are resolved in clade 9 (Fig. 21). The aligned data set was 394 bp long and K2 + G was selected for the ML analysis. One of the more common species
Fig. 6. CaM phylogeny of Aspergillus section Nigri clade 1, showing identities of species isolated from house dust in bold.

Fig. 7. CaM phylogeny of Aspergillus sections Fumigati, Clavati and Cervini, showing identities of species isolated from house dust in bold.
found in dust was *P. brevicompactum*. Our data suggest that the recently described *P. kongii* (Wang & Wang 2013) is a synonym of *P. brevicompactum*. The remaining isolates were identified as *P. buchwaldii* and *P. olsonii*. In section *Ramosa*, we isolated *P. swiecickii* and one new species closely related to *P. soppii*, described below as *P. lenticrescens*.

The species in clade 10 are classified in sections *Paradoxa* and *Turbata* (Fig. 22). The aligned data set was 394 bp long and K2 + G was selected for ML analysis. Within section *Paradoxa*, we describe two new species in the *P. atramentosum* species complex as *P. mexicanum* and *P. magnielliptisporum*. In section *Turbata*, we identified one of the species as *P. madriti*.

Clade 11 comprises the recently reviewed section *Chrysogena* (Houbraken et al. 2012) (Fig. 23). This group of species was well represented in dust samples, especially *P. rubens* and to a lesser degree *P. chrysogenum*. The aligned data set was 444 bp long and the K2 + G model selected for the ML analysis. Isolates were identified as *P. allii-sativii*, *P. chrysogenum*, *P. halotolerans*, *P. lanoosocoeruleum* and *P. rubens*. 

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Fig. 8. CaM phylogeny of Aspergillus sections *Restricti*, *Aspergillus* and *Eurotium*, showing identities of species isolated from house dust in bold.
**CaM**

**Clade 8**
sect. **Nigri** clade 2 &

A. arenarius

- EF661147 A. brunneoviolaceus CBS 621.78
- KJ775257 A. brunneoviolaceus DTO 131H2
- KJ775320 A. brunneoviolaceus DTO 245G8
- KJ775255 A. brunneoviolaceus DTO 129F8
- KJ775259 A. brunneoviolaceus DTO 132B2
- HE984434 A. trinidadensis NRRL 62479
- EU159241 A. aculeatinus CBS 121060
- KJ775256 A. arenarioides sp. nov. CBS 138195
- KJ775347 A. arenarioides sp. nov. CBS 138196
- KJ775349 A. arenarioides sp. nov. CBS 138197
- KJ775388 A. arenarioides sp. nov. CBS 138198
- KJ775389 A. arenarioides sp. nov. CBS 138199
- KJ775390 A. arenarioides sp. nov. CBS 138200

Fig. 9. CaM phylogeny of Aspergillus section Nigri clade 2 and A. arenarius, showing identities of species isolated from house dust in bold.

**CaM**

**Clade 9**
sect. **Usti**

- KJ775266 A. germanicus DTO 178B8
- KJ775276 A. germanicus DTO 179B4
- KJ775277 A. germanicus DTO 179B7
- KJ775365 A. germanicus DTO 267G4
- FJ531141 A. germanicus CBS 123887
  - HE615120 A. thesauroicus NRRL 62487
- KJ775270 A. minutus DTO 178C4
- KJ775387 A. minutus DTO 268C7
- EF652369 A. insuetus CBS 107.25
- EF652393 A. minutus NRRL 4876
- EU076365 A. keveii CBS 209.92
- EF652419 A. pseudodeflectus CBS 756.74
- HE616559 A. calidoustus CBS 121601
- KJ77531 A. puniceus DTO 247F4
- EF652410 A. puniceus CBS 495.65
- KJ775260 A. porphyreostipitatus sp. nov. CBS 138202
- KJ775338 A. porphyreostipitatus sp. nov. CBS 138203
- HE615117 A. baeticus NRRL 62501
- FJ531129 A. pseudoustus CBS 123904
- EF652367 A. ustus CBS 261.67
- KJ775383 A. ustus DTO 268C1
- KJ775384 A. ustus DTO 268C3
- EF652411 A. compatibilis CBS 488.65
- EF652355 A. unguis CBS 132.55

Fig. 10. CaM phylogeny of Aspergillus section Usti, showing identities of species isolated from house dust in bold.
Fig. 11. CaM phylogeny of Aspergillus sections Versicolores and Nidulantes, showing identities of species isolated from house dust in bold.
Fig. 12. Penicillium phylogeny of the ITS gene region showing the placement of representative strains isolated from house dust in bold. The coloured blocks indicate the different clades referred to in the text. The tree was rooted to Talaromyces flavus.
Clade 2 sect. *Sclerotiora*

| Strain | Species | Accession Code |
|--------|---------|----------------|
| JN626098 | *P. guanacastense* CCFC239912 | |
| JN696435 | *P. caele* CCFC 239914 | |
| JN666437 | *P. jacksonii* CCFC 239937 | |
| KC695696 | *P. vanrougei* CBS 134406 | |
| JN626104 | *P. mallochi* CCFC 239917 | |
| JN686447 | *P. johnkugli* CCFC 239943 | |
| JN626095 | *P. hirayamae* CBS 229.60 | |
| KCT773838 | *P. malachiteum* CBS 647.95 | |
| JN626101 | *P. herquei* CBS 336.48 | |
| KJ775608 | *P. brocae* DTO 26896 | |
| KJ775609 | *P. brocae* DTO 26987 | |

Clade 3 sect. *Ramigena*

| Strain | Species | Accession Code |
|--------|---------|----------------|
| JN686433 | *P. adametzioides* CBS 313.59 | |
| KJ775639 | *P. hispanicum* DTO 268D8 | |
| KJ775640 | *P. hispanicum* DTO 269H7 | |
| KJ775638 | *P. hispanicum* DTO 268D7 | |
| JX841247 | *P. hispanicum* CBS 691.77 | |
| AF033427 | *P. cyanescens* CBS 134559 | |
| KCT773836 | *P. jugoslavicum* CBS 192.87 | |
| JN14937 | *P. biliae* CBS 221.60 | |
| JN714929 | *P. johnkrugii* CBS 209.28 | |
| JX091443 | *P. chermesinum* CBS 134558 | |
| KJ775655 | *P. ramusculum* DTO 266G6 | |

Clade 4 sect. *Cinnamopurpurea*

| Strain | Species | Accession Code |
|--------|---------|----------------|
| KJ775632 | *P. glabrum* DTO 235F2 | |
| KJ775634 | *P. glabrum* DTO 236D3 | |
| KJ734515 | *P. palmense* CBS 336.79 | |
| AF034448 | *P. thomii* CBS 225.81 | |
| AF033406 | *P. purpurascens* CBS 366.48 | |
| KC411703 | *P. patens* CBS 251.56 | |
| JX3012224 | *P. ellipsoidesporum* CBS 112493 | |
| KJ775679 | *P. infrapurpureum* sp. nov. CBS 138219 | |
| KJ775680 | *P. infrapurpureum* sp. nov. CBS 138220 | |
| KJ775681 | *P. infrapurpureum* sp. nov. CBS 138221 | |
| KJ775682 | *P. infrapurpureum* sp. nov. CBS 138222 | |
| KJ775683 | *P. infrapurpureum* sp. nov. CBS 138223 | |

Fig. 12. (Continued).
Fig. 12. (Continued).
Fig. 12. (Continued).

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Fig. 12. (Continued).
Fig. 12. (Continued).

| Clade 11 mainly sect. Chrysogena |
|----------------------------------|
| KJ775659 P. italicum CBS 339.48 |
| KJ775641 P. italicum DTO 129A5 |
| KX411695 P. aleurites CBS 210.52 |
| AV373912 P. expurpureum CBS 325.48 |
| KC345412 P. maritimum CBS 109590 |
| AF033469 P. coprophilum CBS 110760 |
| KJ775625 P. coprophilum DTO 268E4 |
| KC411763 P. concinnatum CBS 477.757 |
| DQ221696 P. brevispiliplumum A33.8937 |
| AF033472 P. crustosum CBS 115503 |
| KJ775628 P. crustosum DTO 244E8 |
| EU427296 P. ophiostigma CBS 462.72 |
| AJ008416 P. dioscoridis CBS 474.94 |
| KJ775670 P. solitum DTO 235G1 |
| KJ775648 P. palitans DTO 235D6 |
| KJ775648 P. palitans DTO 244E7 |
| KJ775624 P. biforme DTO 268E2 |
| KJ775623 P. commune DTO 1289 |
| KJ775611 P. commune DTO 244G4 |
| KJ834514 P. palitans CBS 107.11 |
| KY373932 P. solitum CBS 424.89 |
| AV213672 P. commune CBS 311.48 |
| KC34505 P. caesinicola CBS 100540 |
| KB34504 P. caesiticrum CBS 101134 |
| AF033473 P. echinulatum CBS 317.48 |
| AB473931 P. camemberti CBS 299.48 |
| EU427296 P. aquaepluvios CBS 221.203 |
| H0424338 P. aurantiogriseum CBS 112297 |
| H0424345 P. psychrophilus CBS 128137 |
| HQ424345 P. panum CBS 101032 |
| AJ005658 P. venenatum BT 106/1 |
| AJ005684 P. alti CBS 131.89 |
| AV373938 P. vernicosum CBS 603.74 |
| AJ004810 P. alboconidioides CBS 472.84 |
| KB34513 P. notoricum ATCC 44219 |
| KB34518 P. mycicola CBS 111225 |
| AV373918 P. hisutum CBS 135.41 |
| JN9607811 P. cryptorum CBS 144.45 |
| JN9607943 P. hirsutum CBS 635.93 |
| KJ775626 P. cyclopium DTO 17068 |
| AF033475 P. polonicum DTO 222.28 |
| AF033476 P. aurantialegatum CBS 249.89 |
| JN9607943 P. hirsutum CBS 111225 |
| JN9607943 P. noroconidatum CBS 199.87 |
| AV373938 P. rubens CBS 390.48 |
| KJ775644 P. melanomousdium DTO 12802 |

Clade 12 mainly sect. Penicillium & Fasciculata
**Fig. 13.** BenA phylogeny of Penicillium section *Citrina*, showing identities of species isolated from house dust in bold.

**Fig. 14.** BenA phylogeny of Penicillium section *Sclerotiora*, showing identities of species isolated from house dust in bold.
Fig. 15. BenA phylogeny of *Penicillium* section *Ramigena*, showing identities of species isolated from house dust in bold.

Fig. 16. BenA phylogeny of *Penicillium* section *Cinnamopurpurea*, showing identities of species isolated from house dust in bold.

Fig. 17. BenA phylogeny of *Penicillium* section *Aspergilloides*, showing identities of species isolated from house dust in bold.
Fig. 18. BenA phylogeny of *Penicillium* section *Exilicaulis*, showing identities of species isolated from house dust in bold.

Fig. 19. BenA phylogeny of *Penicillium* section *Lanata-Divaricata*, showing identities of species isolated from house dust in bold.
Fig. 20. BenA phylogeny of *Penicillium* section *Canescentia*, showing identities of species isolated from house dust in bold.

Fig. 21. BenA phylogeny of *Penicillium* sections *Brevicompacta* & *Ramosa*, showing identities of species isolated from house dust in bold.

Fig. 22. BenA phylogeny of *Penicillium* sections *Paradoxa* & *Turbata*, showing identities of species isolated from house dust in bold.

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Clade 12 mostly includes species classified in sections Penicillium and Fasciculata (Fig. 24). The alignment was 322 bp long and the K2 + G model was selected for ML analysis. Isolates were identified as P. biforme, P. commune, P. coprophilum, P. crustosum, P. cyclopium, P. italicum, P. melanoconidium, P. pallans and P. solitum.

**Talaromyces phylogeny**

An ITS phylogeny was used to place Talaromyces house dust isolates into their respective sections (Fig. 25), as described by Yilmaz et al. (2014). The aligned ITS data set was 605 bp long and included 125 strains. The ML analysis was done with the GTR + G + I model selected. The phylogeny resolved house dust isolates into four sections, with BenA gene trees subsequently calculated for each section.

Clade 1 contains species classified in section Talaromyces (Fig. 26). The aligned BenA data set was 413 bp long, with the K2 + G + I model most suitable for ML analysis. Isolates were identified as the newly described T. cnidii (Sang et al. 2013) and T. amestolkiae (Yilmaz et al. 2012), the previously described T. siamensis and T. verruculosus, and two new species described here as T. sayultensis and T. uomae-annae.

Clade 2 contains species that typically produce synnemata after more than one week of growth, which are classified in section Purpurei (Fig. 27). The aligned data set was 389 bp long and K2 + G was selected for ML analysis. Talaromyces ramulosus was isolated from the South African house dust, a species originally described from soil, apples (from the Fynbos biome in South Africa) and moth-damaged grapes (Ontario, Canada) (Visagie et al. 2009).

Clade 3 contains species of section Trachyspermi (Fig. 28). The aligned data set was 373 bp long, with the K2 + G model selected for ML analysis. Isolates were identified as T. albobiverticillius, T. atroroseus, T. diversus and T. minioluteus. Frisvad et al. (2013) recently introduced T. atroroseus, a species that produces large amounts of red pigmentation. In the same paper, T. albobiverticillius was shown to have genetic and phenotypic variation, with either white or green-pigmented conidia produced. Our house dust isolates produced the green phenotype. Phylogenetic data suggest that T. minioluteus represents a species complex. The dust isolates were thus tentatively identified as T. minioluteus, with strains that will be part of a future study on this complex.

Clade 4 contains species classified in section Islandici (Fig. 29). The aligned BenA data set was 435 bp long and the K2 + G model was selected for ML analysis. Isolates were identified as T. allahabadensis, T. piceus, T. rugulosus, T. scorteus, T. tratensis, T. wortmanii and the new species described here as T. yellensis.

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**Fig. 24.** BenA phylogeny of *Penicillium* sections *Penicillium* & *Fasciculata*, showing identities of species isolated from house dust in bold.
Fig. 25. Talaromyces phylogeny of the ITS gene region showing the placement of representative strains isolated from house dust in bold. The coloured blocks indicate the different clades referred to in the text. The tree was rooted to Trichocoma paradoxa.
Fig. 25. (continued).
Fig. 26. BenA phylogeny of Talaromyces section Talaromyces, showing identities of species isolated from house dust in bold.

Fig. 27. BenA phylogeny of Talaromyces section Purpurei, showing identities of species isolated from house dust in bold.
**Fig. 28.** BenA phylogeny of Talaromyces section Trachyspermi, showing identities of species isolated from house dust in bold.

**Fig. 29.** BenA phylogeny of Talaromyces section Islandicus, showing identities of species isolated from house dust in bold.
**TAXONOMY**

The genus *Aspergillus*

*Aspergillus section Candidi*

*Aspergillus subalbidus* Visagie, Hirooka & Samson, sp. nov. MycoBank MB809190. Figs 30, 31.

*Etymology:* Latin, *subalbidus*, referring to morphological similarity to *A. candidus*.

*Diagnosis:* White sporulation dominating colony appearance, purplish black sclerotia produced by some strains, no growth on CYA at 37 °C.

*Typus:* Brazil, Instituto Biologica, 1939, isolated by Reis (holotype CBS H-21807, culture ex-type CBS 567.65 = ATCC 16871 = IMI 230752 = NRRL 312).

*Additional materials examined:* Thailand, Songkla, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138193 = DTO 129E3. Federated States of Micronesia, Malem on Kosrae Island, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138194 = DTO 266I9.

*ITS barcode:* KJ866983 (alternative markers: BenA = EU076295; CaM = EF669551)

*Colony diam,* 7 d (mm): CYA 15–18; CYA 30 °C 17–21; CYA 37 °C no growth; MEA 17–19; YES 25–30; CYAS 25–33; OA 14–17; CREA 4–9.

*Colony characters:* CYA 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas white; soluble pigment absent; exudate absent; reverse olive (3F8) to brown (5E8). MEA 25 °C, 7 d: Colony surface floccose; mycelial areas white; sporulation white, centrally brownish grey (5C2); soluble pigment absent; exudate abundant, clear; reverse brown (6E8–8E8). YES 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas white; sclerotia present in some strains, black; soluble pigment absent; exudate absent; reverse centrally light brown (5D6), fading into light yellow (4A5) near margin. DG18 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas white; soluble pigment absent; exudate absent; reverse centrally light to pale yellow (4A5–2A3), elsewhere pale. OA 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas white; sclerotia purplish black; soluble pigment absent; exudate absent; reverse white. CYAS 25 °C, 7 d: Colony surface floccose; white to pale yellow (1A2); soluble pigment absent; exudate absent; reverse beige to light yellow (4C3–B4). CREA 25 °C, 7 d: Colony surface velutinous; mycelial areas white, sporulation white; acid not produced.

*Micromorphology:* Conidial heads globose; Conidiophores biseriate, sometimes reduced Penicillium-like structures present, on DG18 much larger than on MEA; Stipes hyaline, minor proportion having a brown pigment, smooth, 30–300(–2000) on DG18 × 3–6 (MEA) or 7–16 (DG18) μm; Vesicles globose to subglobose, on MEA 6–14 μm, on DG18 10–55 μm, covering 100 % of the head; Metulae 6.5–25 × 4–8 μm; Phialides ampulliform, 6–9 × 2.5–3.5 μm; Conidia globose to subglobose, smooth, 3–4 μm (3.5 ± 0.18 × 3.5 ± 1.19, n = 56), average width/length = 0.98, n = 54; Hülle cells absent; Sclerotia purplish to black, especially on OA, 270–620 μm diam.

*Notes:* *Aspergillus subalbidus* is morphologically almost identical to *A. candidus*. The new species also includes strains (CBS 567.65 and CBS 112449) previously identified as *A. candidus* and most recently, as *A. taichungensis* (Varga et al. 2007). Morphologically these strains lack the yellow colours observed in *A. taichungensis* and do not grow on CYA at 37 °C. Phylogenetically, the new species forms a distinct clade closely related to *A. campestris*, *A. candidus*, *A. taichungensis* and *A. tritici*. A few strains of *A. tanneri* were used as outgroup. Names in blue are new species described in this study. Model selected: K2 + G, combined alignment 1 529 bp.

**Fig. 30.** Combined phylogeny for ITS, BenA and CaM of *Aspergillus* section Candidi. *Aspergillus tanneri* was used as outgroup. Names in blue are new species described in this study. Model selected: K2 + G, combined alignment 1 529 bp.
Fig. 31. Aspergillus subalbidus. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, DG18 and obverse CREA. B. Purple to black sclerotia on OA. C–G. Conidiophores on DG18 (E. on MEA). H. Conidia. Scale bars: C, D, F–H = 10 μm; E = 50 μm.
(Fig. 30). Both A. subalbidus and A. candidus are distinguished from these species by their typical white colonies, smooth conidia and inability to grow at 37 °C. Minor differences were observed when comparing the new species with A. candidus. The new species grew slightly slower on CYA, YES and DG18. The purple to black sclerotia common in A. subalbidus when grown on OA were not observed in A. candidus, as previously reported by Varga et al. (2007). These minor differences make morphological identification very difficult. However, phylogenetically this species is distinct and these minor phenotypic differences warrant describing it as new.

**Aspergillus section Flavipes**

**Aspergillus templicola** Visagie, Hirooka & Samson, sp. nov. MycoBank MB809191. Figs 32, 33.

*Etymology:* Latin, templicola, meaning church-dweller, in reference to the ex-type strain, which was isolated from dust collected in a Mexican church.

*Diagnosis:* Colonies yellowish white to pale yellow, reverse brown to dark brown, Hülle cells absent, conidiophores biseriate with vesicles elongated, diminutive conidiophores present.

*Typus:* Mexico, Sayulita, dust from church, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21808, culture ex-type CBS 138181 = DTO 270C6).

*Additional material examined:* Thailand, Bangkok, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138180 = DTO 267H4.

*IITS barcode:* KJ775545 (alternative markers: BenA = KJ775092; CaM = KJ775394).

*Colony diam, 7 d (mm):* CYA 25–32; CYA 30 °C 35–36; CYA 37 °C 22–25; MEA 23–26; YES 32–38; DG18 28–34; OA 17–19; CREA 13–21.

*Colony characters:* Colony surface floccose; sporulation and mycelial areas yellowish white to pale yellow (4A2–3); soluble pigment brown to absent; exudate clear; reverse brown to dark brown (5F8–6F8). CYA 30 °C, 7 d: Colonies similar to CYA at 25 °C, except for yellowish colour in colonies in DTO 267H4. CYA 37 °C, 7 d: Colonies similar to CYA at 25 °C. MEA 25 °C, 7 d: Colony surface floccose; mycelial areas orange white (5A2); sporulation brownish grey (4C2); soluble pigment absent; exudate absent; reverse brown (6E8). YES 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas yellowish white to yellowish grey to greyish yellow (4A2–B2–3); soluble pigment brown; exudate absent; reverse brown (6D8–7E8). DG18 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas pale orange to greyish orange (5A3–B3); soluble pigment absent; exudate absent; reverse light yellow to greyish orange (4A4–5C5). OA 25 °C, 7 d: Colony surface velutinous to somewhat floccose; sporulation and mycelial areas pale orange (5A3); soluble pigment olive, inconspicuous; exudate absent; reverse brownish orange (5C5). CREA 25 °C, 7 d: Colony surface velutinous to somewhat floccose, orange white to pale orange (5A2–3); acid not produced.

*Micromorphology:* Conidial heads radiating, generally bigger on DG18, often diminutive on MEA and DG18; Conidiophores biseriate; Stipes hyaline to dark brown, smooth walled, some very finely rough walled, 120–1400 × 5–10 μm; Vesicles, elongate, a minor proportion more subglobose, 9–23 μm wide; Metulae 6–8 × 3–4 μm, covering 75–100 % of head; Phialides amylopalliform, 4,5–8,5 × 2,5–3,5 μm; Conidia subglobose, smooth to finely roughened, 2,5–3 × 2,5–2,5 μm (2,7 ± 0,1 × 2,5 ± 0,1; n = 50), average width/length = 0,93, n = 50; Sclerotia absent.

*Notes:* Aspergillus templicola is resolved in a clade with A. flavipes, A. iizukae and the two new species described here as A. micronesiensis and A. capensis (Fig. 32). This group of species is morphologically very similar, which makes identification based on phenotypic characters challenging. In their Fig. 32. Combined phylogeny for ITS, BenA and CaM of Aspergillus section Flavipes. Names in blue are new species described in this study. Aspergillus janus and A. brevijanus was used as outgroup. Model selected: Tamura-Nei (TN93) combined alignment 1695 bp.
Fig. 33. Aspergillus templicola. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, DG18 and obverse CREA. B–H. Conidiophores. I. Conidia. Scale bars: B = 50 μm; C–I = 10 μm.

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description of *A. flavipes*, Raper & Fennell (1965) described conidiophore vesicles as subglobose to vertically elongate. We also observed this in strains of *A. flavipes*. For *A. templicola*, vesicles were consistently elongated, whilst *A. micronesiensis* had subglobose vesicles. Compared to *A. capensis* and *A. iizukae*, strains of *A. templicola* had less intense and paler reverses. Hülle cells were observed in *A. flavipes* and *A. micronesiensis* but not in *A. iizukae*, *A. capensis* and *A. templicola*. Morphologically, *A. capensis* could not be distinguished from *A. iizukae* using phenotypic characters, although it is phylogenetically distinct. Sequence data is recommended for their identification.

**Aspergillus micronesiensis** Visagie, Hirooka & Samson, *sp. nov*. MycoBank MB809192. Figs 32, 34.

**Etymology**: Latin, *micronesiensis*, in reference to the ex-type strain, which was isolated from dust collected in Micronesia.

**Diagnosis**: Colonies yellowish white to pale yellow, reverse colour brown to dark brown, Hülle cells present, conidiophores biseriate with vesicles subglobose, diminutive conidiophores present.

**Typus**: **Federated States of Micronesia**, Yela of Kosrae Island, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21810, culture ex-type CBS 138183 = DTO 267D5).

Additional materials examined: **Haiti**, soil, 1960, isolated by J. Rabel, CBS 586.65 = NRRL 4578 = ATCC 16805 = IMI 135423. **Mexico**, Sayulita, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138182 = DTO 245D7. **Thailand**, Bangkok, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138186 = DTO 267H5.

**ITS barcode**: KJ775548 (alternative markers: *BenA* = KJ775085; *CaM* = KJ775355)

**Colony diam, 7 d (mm)**: CYA 22–28; CYA 30 °C 30–36; CYA 37 °C 17–25; MEA 20–25; YES 35–44; DG18 15–25; OA 14–24; CREA 12–17.

**Colony characters**: CYA 25 °C, 7 d: Colony surface floccose; mycelial areas white mycelial areas; sporulation yellowish white to greyish orange (5C3); soluble pigment brown; exudate clear to brown; reverse brown to dark brown (6E8–F8). CYA 30 °C, 7 d: Colonies similar to CYA at 25 °C. CYA 37 °C, 7 d: Colonies similar to CYA at 25 °C. MEA 25 °C, 7 d: Colony surface floccose; mycelial areas yellowish white to pale yellow (3A2–3); sporulation brownish orange (5C4); Hülle cells present, yellow, sexual development not observed; soluble pigment absent; exudate absent or in some strains yellow to brown; reverse brown to dark brown (6D7–7F7). YES 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas yellowish white to pale yellow (3A2–3) to brownish orange (5C4); soluble pigment orange brown; exudate absent; reverse brown (6D7–7E7). DG18 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas yellowish white to light yellow (4A2–4); soluble pigment brown; exudate absent; reverse greyish orange (6B6) to brown (7F7). OA 25 °C, 7 d: Colony surface velutinous to floccose; sporulation and mycelial areas orange white (5A3); Hülle cells yellow, sexual development not observed cells; soluble pigment brown; exudate absent; reverse light brown (6D6). CREA 25 °C, 7 d: Colony surface floccose, yellowish white to light yellow to brownish orange (4A2–4–5C4); acid not produced.

**Micromorphology**: Conidial heads radiating, generally bigger on DG18; Conidiophores biseriate; Stipes hyaline to dark brown, smooth walled, some very finely roughened, 250–1900 × 5.5–9.5 μm; Vesicles globose, minor proportion elongated, 13.5–31 μm wide; Metulae 5–13 × 3.5–6.5 μm, covering 75–100 % of head; Phialides ampulliform, 6.5–8.5 × 2.5–4 μm; Conidia globose to subglobose, smooth to finely roughened, 2.5–3.5 × 2.5–3.5 μm (2.7 ± 0.2 × 2.7 ± 0.2, n = 5), average width/length = 0.98, n = 50; Sclerotia absent.

**Notes**: See notes for *A. templicola* above.

**Aspergillus capensis** Visagie, Hirooka & Samson, *sp. nov*. MycoBank MB809193. Figs 32, 35.

**Etymology**: Latin, *capsensis*, in reference to the ex-type strain, which was isolated from dust collected in the Cape Town metropolitan area, South Africa.

**Diagnosis**: Colonies yellowish white to pale yellow, reverse dark brown, Hülle cells absent, conidiophores biseriate with vesicles subglobose, diminutive conidiophores present.

**Typus**: **South Africa**, Kuils River in the Cape Town metropolitan area, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21810, culture ex-type CBS 138188 = DTO 179E6).

**ITS barcode**: KJ775550 (alternative markers: *BenA* = KJ775072; *CaM* = KJ775279)

**Colony diam, 7 d (mm)**: CYA 28–29; CYA 30 °C 30–31; CYA 37 °C 18–19; MEA 19–20; YES 39–40; DG18 25–26; OA 12–13; CREA 16–17.

**Colony characters**: CYA 25 °C, 7 d: Colony surface floccose; mycelial areas white to yellowish white; sporulation yellowish white to white yellow (3A2–5); soluble pigment brown; exudate brown; reverse dark brown (6F5–8). CYA 30 °C, 7 d: Colonies similar to CYA at 25 °C. CYA 37 °C, 7 d: Colony surface floccose, brownish grey (6D2); soluble pigment brown; exudate absent; reverse brownish grey to dark brown (6F3–5). MEA 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas yellowish white (2A2); soluble pigment brown; exude a few brown droplets; reverse dark brown (6F8). YES 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas dull yellow to greyish yellow (3B3–4B3); soluble pigment brown; exudate absent; reverse brown to dark brown (7E8–F8). DG18 25 °C, 7 d: Colony surface velutinous; sporulation and mycelial areas yellowish white to orange white (4A2–5A2); soluble pigment yellowish brown; exudate absent; reverse greyish yellow to dark yellow (4C6–8). OA 25 °C, 7 d: Colony surface velutinous; sporulation and mycelial areas yellowish white (2A2), olive (3E5) underneath sporulating areas; soluble pigment olive; exudate absent; reverse olive yellow to olive (3D6–F6). CREA 25 °C, 7 d: Colony surface floccose, yellowish white to light yellow (3A3–5); acid not produced.
Fig. 34. *Aspergillus micronesiensis*. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, DG18 and obverse CREA. B. Hüle cells. C–H. Conidiophores. I. Conidia. Scale bars: B, D–I = 10 μm; C = 50 μm.
Fig. 35. Aspergillus capensis. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, DG18 and obverse CREA. B–F. Conidophores. G. Conidia. Scale bars: B = 50 μm; C = 20 μm; C–G = 10 μm.
**Micromorphology:** Conidial heads radiating; Conidiophores biseriate; Stipes hyaline to dark brown, smooth walled, some very finely rough walled, 235–1 400 × 6.5–11 μm; Vesicles globose to elongated, 18–35 μm wide; Metulae 5.5–10 × 3.5–5.5 μm, metulae cover 100 % of head; Phialides ampulliform, 6–8 × 2.5–4 μm; Conidia globose to subglobose, smooth and finely roughened, 2.9 ± 0.2 × 2.9 ± 0.2, n = 44), average width/length = 0.97, n = 44; Sclerotia absent.

**Notes:** See notes for *A. templicola* above.

**Aspergillus section Aspergillus**

**Aspergillus sloanii** Visagie, Hirooka & Samson, sp. nov. MycoBank MB809194. Figs 36, 37.

**Etymology:** Latin, sloanii, named in honour of Alfred P. Sloan.

**Diagnosis:** Xerophillic species that does not grow on general media, grows well on DG18 and MEA with 20 % sucrose, eurotium-like sexual state produced with ascospore having lenticular furrows, conidiophores uniseriate with very big rough walled conidia.

**Typus:** England, Middlesex, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21811, culture ex-type CBS 138177 = DTO 245A1). Additional materials examined: England, Middlesex, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138176 = DTO 245A8, CBS 138179 = DTO 245A9, CBS 138231 = DTO 245A6.

**ITS barcode:** KJ775540 (alternative markers: BenA = KJ775074; CaM = KJ775309)

**Colony diam, 7 d (mm):** CYA no growth; CYA 30 °C no growth; CYA 37 °C no growth; MEA no growth; YES 3–8; DG18 27–36; OA no growth; CREA no growth.

**Colony characters:** CYA 25 °C, 7 d: No growth. CYA 30 °C, 7 d: No growth. CYA 37 °C, 7 d: No growth. MEA 25 °C, 7 d: Microcolonies produced after 3 wk. YES 25 °C, 7 d: Microcolony surface floccose, white to greyish white; soluble pigment absent; exudate absent; reverse greyish yellow (4C5). DG18 25 °C, 7 d: Colonies surface floccose; mycelial areas white to greenish yellow (1A6) depending on ascomata produced; sporulation dull green (26D3); ascomata yellow; soluble pigment absent; exudate absent; reverse greenish white to pale green to greyish green (30A2–3–B3). OA 25 °C, 7 d: No growth. CREA 25 °C, 7 d: No growth.

**Micromorphology:** Conidial heads radiating, produced only on DG18; Conidiophores uniseriate; Stipes hyaline, smooth walled, 160–890 × (6.5–10–14(–16)) μm; Vesicles globose to elongated, sometimes as wide as stipe, (12.5–25–47(–61) μm. **A. niveoglaucus** CBS 114.27T

**A. niveoglaucus** NRRL 128

**A. niveoglaucus** NRRL 136

**A. niveoglaucus** NRRL 137

**A. niveoglaucus** CBS 101750

**A. brunneus** CBS 112.26T

**A. brunneus** NRRL 133

**A. proliferans** NRRL 114

**A. proliferans** CBS 121.45T

**A. proliferans** NRRL 71

**A. glaucus** NRRL 116T

**A. glaucus** NRRL 120

**A. glaucus** NRRL 121

**A. sloanii** CBS 138176

**A. sloanii** CBS 138178

**A. sloanii** CBS 138179

**A. sloanii** CBS 138177T

**A. sloanii** CBS 138231

**A. pseudoglaucus** CBS 123.28T

**A. tonophilus** CBS 405.65T

**A. ruber** CBS 530.65T

**A. xerophilus** CBS 938.73T

**Fig. 36.** Combined phylogeny for ITS, BenA and CaM of selected Aspergillus section Aspergillus. Names in blue are new species described in this study. Aspergillus xerophilus was used as outgroup. Model selected: K2 + G, combined alignment 1 695 bp.
**Fig. 37.** *Aspergillus sloanii*. A. Colonies: top row left to right, obverse CYA, DG18 of non-sexual strain, DG18 of sexual strain and OA; bottom row left to right, MEA, reverse DG18 of non-sexual strain, reverse DG18 of sexual strain and obverse CREA. B. Ascoma. C. Asci with ascospores. D–G. Conidiophores. H. Conidia. Scale bars: B = 50 μm; C–H = 10 μm.
wide; Phialides ampulliform, 9–13 × 5–7 μm, covering 100 % of head; Conidia ellipsoidal, minor proportion subglobose, spiny, up to 1.5 μm, (5.5–)7.5–9.5(–11) × 5.5–8.5 μm (8.4 ± 0.85 × 7.36 ± 0.6, n = 45), average width:length = 0.88, n = 42; Ascomata present, Eurotium-like with one layer of mycelia covering ascocarp, 80–170 μm diam; Ascii 11–22 μm diam; Ascospores lenticular, furrowed, 4.5–6.5 μm diam.

Notes: Aspergillus sloanii is a monophyletic group within a clade with Aspergillus species that produce a Eurotium-like sexual state (Fig. 36). Its closest relatives, A. glaucus and A. proliferans, grow better on media with high sugar concentrations, but can also grow on the normal CYA, MEA and OA. However, A. sloanii is unable to grow on the latter three media. Other species reported to sometimes not grow on these media include A. penicillioides and A. proliferans. Aspergillus penicillioides, however, produces smaller conidia, 3–5 μm. Aspergillus proliferans produces conidia of similar size to A. sloanii, but has globose to subglobose conidia rather than the predominant ellipsoidal conidia of A. sloanii.

**Aspergillus arenarioides clade**

**Aspergillus arenarioides** Visagie, Hirooka & Samson, sp. nov. MycoBank MB809195. Figs 38, 39.

Etymology: Latin, arenarioides, referring to the phenotypic similarity of this species to A. arenarius.

Diagnosis: Grows poorly on general media, pale yellow sclerotia produced, conidiophores often Penicillium-like, biseriate, fertile only over 25–50 % of vesicle, conidia globose, rough to echinulate.

Typus: **Federated States of Micronesia**, Malem of Kosrae Island, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21812, culture ex-type CBS 138200 = DTA 268E3).

Additional materials examined: **Federated States of Micronesia**, Malem of Kosrae Island, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138198 = DTA 268E1, CBS 138199 = DTA 268E2, CBS 138196 = DTA 267B6, CBS 138197 = DTA 267C7.

*ITS barcode:* KJ775562 (alternative markers: *BenA* = KJ775091; *CaM* = KJ775390)

**Colony diam, 7 d (mm):** CYA 9–13; CYA 30 °C 13–16; CYA 37 °C no growth; MEA 7–12; YES 10–16; DG18 12–18; CYAS 12–14; OA 7–10; CREA 3–5.

Colony characters: Colony surface velutinous when sporulating, mostly consisting of white sterile mycelia, greyish green (26D5–E5) when sporulating; sclerotia pale yellow in some isolates; soluble pigment mostly absent; some isolates conspicuously red; exudate mostly absent, clear in some isolates; reverse light yellow to olive brown (4A4–F4), brown (5E6) in isolates with soluble pigment. CYA 30 °C, 7 d: Colonies similar to CYA at 25 °C, except for more abundant sclerotia in some isolates. CYA 37 °C, 7 d: No growth. MEA 25 °C, 7 d: Colony surface velutinous when sporulating, mostly consists of white sterile mycelia, greyish green (2C4) when sporulating; sclerotia pale yellow in some isolates; soluble pigment absent; exudate clear in some isolates; reverse brownish orange to brown (5C5–F8). YES 25 °C, 7 d: Colony surface velutinous in sporulating isolates, mostly consists of white sterile mycelia, greyish green (25D5) when sporulating; soluble pigment absent; exudate absent, reverse light yellow to olive brown (4A4–D4). DG18 25 °C, 7 d: Colony surface floccose, whitish grey to grey to greyish green (30C1–C3); soluble pigment absent; exudate absent, reverse pale yellow to greyish yellow (3A3–C3) to pale orange (5A3), OA 25 °C, 7 d: Colony surface velutinous when sporulating, otherwise floccose, dull green (26D4) when sporulating; sclerotia pale yellow in some isolates; soluble pigment absent; exudate clear; reverse white. CYAS 25 °C, 7 d: Colony surface velutinous when sporulating, mostly consisting of white sterile mycelia, greyish green (26D5–E5) when sporulating; sclerotia pale yellow in some isolates; pigment absent; exudate mostly absent, clear in some isolates; reverse light yellow to olive brown (4A4–F4), brown (5E6) in isolates with soluble pigment. CREA 25 °C, 7 d: Colony surface velutinous, white to greyish green (26C3), acid not produced.

Micromorphology: Conidial heads typically Penicillium-like with some Aspergillus-like conidiophores present, on DG18 the Aspergillus-like head is prominent; Conidiophores biseriate; Stipes mostly hyaline, sometimes brown, smooth walled, 65–200 × 2.5–5.5 μm; Vesicles globose, often elongated on MEA, 5–13 μm; Metulae 5.5–8.5 × 2.5–4.5 μm, covering 25–50 % of head; Phialides ampulliform, 6.5–9.5 × 2.5–4 μm; Conidia globose to subglobose, rough to echinulate, 2.5–3.5(–5.5) μm (2.89 ± 0.2 × 2.87 ± 0.2, n = 44) average width:length = 0.98, n = 43; Hülle cells absent; Sclerotia present, 100–300 μm.

Notes: Aspergillus arenarioides is phylogenetically closely related to A. arenarius (Fig. 38). Both species grow poorly on general media, and produce pale yellow sclerotia and biseriate conidiophores that are often diminutive (Raper & Fennell 1965). Conidia are small and globose, but A. arenarius has smooth
Fig. 39. Aspergillus arenarianus. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, DG18 and obverse CREA. B. Sclerotia on CYA. C–J. Conidiophores. J. Conidia. Scale bars: B = 1000 μm; C–J = 10 μm.
walled conidia in contrast to the rough to echinulate conidia of *A. arenarioides*.

**Aspergillus section Usti**

*Aspergillus porphyreostipitatus* Visagie, Hirooka & Samson, sp. nov. MycoBank MB809196. Figs 40, 41.

**Etymology:** Latin, *porphyreostipitatus*, meaning red-brown stipe.

**Diagnosis:** Produces brownish colonies on most media, on MEA and DG18 reverse greyish green, Hülle cells produced on OA, able to grow at 37 °C, conidiophores have reddish brown stipes.

**Typus:** Mexico, Sayulita, dust from church, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21813, culture ex-type CBS 138203 = DTO 266D9).

**Additional material examined** Thailand, Songkhla, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138202 = DTO 132D1.

**ITS barcode:** KJ775564 (alternative markers: *BenA* = KJ775080; *CaM* = KJ775338)

**Colony diam, 7 d (mm):** CYA 38–41; CYA 30 °C 45–50; CYA 37 °C 5–11; MEA 28–34; YES 40–44; DG18 25–30; CYAS 12–17; OA 30–34; CREA 10–12.

**Colony characters:** CYA 25 °C, 7 d: Colony surface floccose; sporulation and mycelial areas light brown to brown (5D4–E4); soluble pigment absent; exudate redish to pink; reverse centrally dark brown to brown (6F7–7E7), elsewhere light yellow (3A5). CYA 30 °C, 7 d: Colonies similar to CYA at 25 °C. CYA 37 °C, 7 d: Colony surface floccose; mycelial areas yellowish white (2A2); soluble pigment yellow; exudate absent; reverse yellowish brown (5D8). MEA 25 °C, 7 d: Colony surface floccose; mycelial areas white; sporulation greyish turquoise to greyish green (24E4–25E4); soluble pigment absent; exudate absent; reverse brown to dark brown (6E8–F8). YES 25 °C, 7 d: Colony surface floccose; mycelial areas white; sporulation brownish grey to light brown (5D2–4); soluble pigment absent; exudate absent; reverse greyish yellow to olive brown (4B5–4D5). DG18 25 °C, 7 d: Colony surface floccose, greyish green (1D3); soluble pigment absent; exudate absent, reverse olive (1FE5–F5). OA 25 °C, 7 d: Colony surface floccose to velutinous; mycelial areas white; sporulation brownish grey (5F2); soluble pigment yellow; exudate minute, clear droplets; reverse greyish yellow (4B4–C4). CYAS 25 °C, 7 d: Colony surface colonies, brownish grey (5D2); soluble pigment absent; exudate absent; reverse olive brown (4F5). CREA 25 °C, 7 d: Colony surface velutinous, greyish brown (5D3) to greyish brown (3B5); acid not produced.

**Micromorphology:** Conidiophores biseriate, short *Penicillium*-like conidiophores present, on DG18 less dense (fewer metulae) than on MEA; Stipes reddish brown, hyaline also present, mostly smooth, some areas contain warts, (15–)30–120 × 3.5–6.5 μm; Vesicles globose, sometimes slightly elongated, 8–14 μm; Metulae 5.5–9 × 3–5 μm, covering 75 % of head; Phialides ampulliform, 6–7.5 × 2.5–3.5 μm; Conidia globose to sub-globose, often covered by a thick layer (about 0.5 μm), rough, 3–3.5 × 3–3.5 μm (3.3 ± 0.2 ± 3.1 ± 0.2, n = 40), average width/length = 0.95, n = 38; Hülle cells produced on OA; Sclerotia absent.

**Notes:** *Aspergillus porphyreostipitatus* is resolved within a larger clade with *A. baeticus, A. ustus, A. puniceus* and *A. pseudoustus* (Fig. 40). Morphologically these species are similar for producing brownish colours in colonies. The ability of the new species to grow on CYA at 37 °C easily distinguishes it from its morphologically similar relatives. Other species in other clades of section *Usti* are able to grow at 37 °C (Houbraken et al. 2007, Novakova et al. 2012). However, except for *A. compatibilis* (≡*Emericella heterothallicia*), they grow much faster than *A. porphyreostipitatus* at this temperature. *Aspergillus porphyreostipitatus* grows slower and sporulates better on MEA compared to *A. compatibilis*.

**Aspergillus section Versicolores**

*Aspergillus griseoaurantiacus* Visagie, Hirooka & Samson, sp. nov. MycoBank MB809197. Figs 42, 43.

**Etymology:** Latin, *griseoaurantiacus*, meaning greyish orange, referring to the colour of colonies on CYA and MEA.

**Diagnosis:** Colonies have a white to light orange to greyish orange colour on CYA and MEA, producing globose Hülle cells, growth on CYA at 37 °C, conidiophores present, on DG18 less dense (fewer metulae) than on MEA; Stipes reddish brown, hyaline also present, mostly smooth, some areas contain warts, (15–)30–120 × 3.5–6.5 μm; Vesicles globose, sometimes slightly elongated, 8–14 μm; Metulae 5.5–9 × 3–5 μm, covering 75 % of head; Phialides ampulliform, 6–7.5 × 2.5–3.5 μm; Conidia globose to sub-globose, often covered by a thick layer (about 0.5 μm), rough, 3–3.5 × 3–3.5 μm (3.3 ± 0.2 ± 3.1 ± 0.2, n = 40), average width/length = 0.95, n = 38; Hülle cells produced on OA; Sclerotia absent.

**Notes:** *Aspergillus griseoaurantiacus* is resolved within a larger clade with *A. baeticus, A. ustus, A. puniceus* and *A. pseudoustus* (Fig. 40). Morphologically these species are similar for producing brownish colours in colonies. The ability of the new species to grow on CYA at 37 °C easily distinguishes it from its morphologically similar relatives. Other species in other clades of section *Usti* are able to grow at 37 °C (Houbraken et al. 2007, Novakova et al. 2012). However, except for *A. compatibilis* (≡*Emericella heterothallicia*), they grow much faster than *A. porphyreostipitatus* at this temperature. *Aspergillus porphyreostipitatus* grows slower and sporulates better on MEA compared to *A. compatibilis*.
Fig. 41. Aspergillus porphyreostipitatus. A. Colonies: top row left to right, reverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, DG18 and reverse CREA. B, D–H. Conidiophores on MEA. C. Hülle cell on OA. I. Conidia. Scale bars: B = 50 \( \mu \)m; C–I = 10 \( \mu \)m.
Typus: **Federated States of Micronesia**, Yela of Kosrae Island, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21814, culture ex-type CBS 138191 = DTO 138189 = DTO 267D8).

Additional materials examined: **Thailand**, Songkhla, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138190 = DTO 267D2. **Mexico**, Sayulita, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138189 = DTO 245F5.

**ITS barcode:** KJ775553 (alternative markers: BenA = KJ775086; CaM = KJ775357)

**Colony diam, 7 d (mm):** CYA 25–28; CYA 30 °C 25–26; CYA 37 °C 3–5; MEA 18–21; YES 32–34; DG18 14–16; OA 15–20; CREA 18–20.

**Colony characters:** Colony surface floccose; mycelial areas white to light orange (5A5) to greyish orange (5B3); sporulation dull green (28D3–E3); soluble pigment brownish red; exudate minute red droplets; reverse reddish brown to dark brown (8F7–8); margin light orange (5A4). CYA 30 °C, 7 d: Colonies similar to CYA at 25 °C. CYA 37 °C, 7 d: Colony surface floccose, white; soluble pigment absent; exudate absent; reverse olive (2E5). MEA 25 °C, 7 d: Colony surface floccose; mycelial areas white to brownish orange (5C3); sporulation dull green (30D3), sometimes (26D4); soluble pigment absent; exudate minute red droplets; reverse light brown (6D6–8) centrally, sometimes greyish orange (5B6). YES 25 °C, 7 d: Colony surface floccose; mycelial areas white to light orange (5A5) to greyish orange (5B3); sporulation sparse, dull green (28D3–E3); soluble pigment absent; exudate absent; reverse deep orange to orange (5A8–B8), margin yellow to light yellow (3A6–4A5). DG18 25 °C, 7 d: Colony surface floccose; mycelial areas white to light orange (5A5) to greyish orange (5B3); sporulation dull green (28D3–E3); soluble pigment reddish brown; exudate absent; reverse deep orange to orange (6A8–B8) to brown (6D8) to olive brown (4E6). OA 25 °C, 7 d: Colony surface floccose; mycelial areas white to greyish; sporulation dull green (27E3 to 29E3) to greyish green (28C3); soluble pigment absent; exudate clear to brownish; reverse greyish yellow (3B5–C5). CREA 25 °C, 7 d: Colony surface floccose, mycelial areas white to light yellow (3A4) to greyish orange to brown (5B5–E5); acid not produced.

**Micromorphology:** Conidial heads radiating, diminutive **Penicillium**-like conidiophores typically present in aerial hyphae; Conidiophores biseriate, sometimes greenish; Stipes hyaline to brown, smooth walled, 100–500 × 3.5–8 μm; Vesicles spathulate or elongated, (3.5–)9–18(–26.5) μm wide; Metulae 4–10 × 3–5.5 μm, covering 75 % of head; Phialides ampulliform, 5.5–7 × 2.5–3.5 μm; Conidia ellipsoid, finely roughened, 2.5–4 × 2–3 μm (3 ± 0.3 × 2.5 ± 0.2, n = 53), average width/length = 0.84, n = 53; Scerotia absent.

**Notes:** **Aspergillus griseoaurantiacus** forms a coherent species within a clade closely related to A. tabacinus, A. versicolor, A. fructus, A. amoenus, A. austrocalifornicus and A. protuberus (Fig. 42). Four of these, A. griseoaurantiacus, A. amoenus, A. fructus and A. versicolor, are able to grow on CYA at 37 °C (Jurjević et al. 2012). **Aspergillus griseoaurantiacus** produces smooth walled, globose to subglobose conidia, with a small proportion ellipsoidal, whereas A. amoenus produces finely roughened ellipsoidal conidia. **Aspergillus fructus** and...
**Fig. 43.** *Aspergillus griseoaurantiacus*. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, DG18 and obverse CREA. B, C, E–H. Conidiophores. D. Hüülle cells. I. Conidia. Scale bars: B, C, E–I = 10 μm; D = 20 μm; E = 100 μm.
A. versicolor both have finely roughened conidia, but all other characters are very similar to the new species. Jurjević et al. (2012) considered phenotypic characters too similar for A. versicolor and A. fructus, and recommended the use of sequences for identification. This makes identification of our new species based on morphology similarly challenging. However, sequences easily distinguish the species.

The genus Penicillium

Penicillium alfredii Visagie, Seifert & Samson, sp. nov.

MycoBank MB809180. Figs 44, 45.

Etymology: Latin, alfredii, named in honour of Alfred P. Sloan.

Diagnosis: Growth poor on all media, colonies dense, producing monoverticillate conidiophores with short stipes, short phialides and smooth, globose conidia.

Typus: Federated States of Micronesia, Lelu of Kosrae Island, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21800, culture ex-type CBS 138224 = DTO 2698A).

ITS barcode: KJ775684 (alternative markers: BenA = KJ775177; CaM = KJ775411; RPB2 = KJ834520)

Colony diam, 7 d (mm): CYA 8–10; CYA 30 °C 5–6; CYA 37 °C no growth; MEA 9–10; YES 13–14; DG18 13–15; CYAS 5–8; OA 6–7; CREA no growth to microcolonies.

Colony characters: Colonies moderately deep, sunken at centre, plane; margins moderately deep, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green (26C4); soluble pigments absent; exudates absent; reverse dull green (27F4); soluble pigments absent; exudates absent; reverse bluish grey (20F3), some isolates less intensely coloured. MEA 25 °C, 7 d: Colonies moderately deep, sunken at centre, plane; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green (26C4); soluble pigments absent; exudates absent; reverse brownish orange (5C6) with some brown (5F4) areas. YES 25 °C, 7 d: Colonies moderately deep, sunken at centre, sulcate; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green (26C4); soluble pigments absent; exudates absent; reverse dull green (27E4); DG18 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green (26D4); soluble pigments absent; exudates absent; reverse greyish green (30B3). OA 25 °C, 7 d: Colonies low, plane; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse dark green (27F8); soluble pigments absent; exudates clear. CREA 25 °C, 7 d: Acid not produced.

Micromorphology: Conidiophores monoverticillate; Stipes smooth walled, 8–45 × 1.5–2.5 μm; Vesicles 2.5–3 μm; Phialides amphiulliform, sometimes more slender and elongated, 6–8 × 1.5–3 μm (7.1 ± 0.6 × 2.4 ± 0.2); Conidia smooth, globose to subglobose, 2–2.5 × 2–2.5 μm (2.3 ± 0.1 × 2.2 ± 0.1), average width/length = 0.94, n = 44.

Notes: This species is distinct from all Penicillium species and phylogenetically cannot be classified in any of the 25 sections proposed in Houben & Samson (2011). ITS sequences (Fig. 12) place the species closest to section Ramigena, whilst RPB2 resolves it on a long branch related to sections Torulomyces and Fracta (Fig. 44). Phenotypically, Penicillium alfredii grows poorly on all media, and colonies resemble those of species in section Torulomyces. However, the latter section includes species that were generally classified in the genus Torulomyces and produce monophaelial conidiophores. This contrasts to the monoverticillate conidiophores of P. alfredii. As such, P. alfredii probably represents a new section. However, the phylogenetic data presented is inconclusive for introducing a new section. This is mainly due to the unresolved position of P. cryptum and P. lassenii (Fig. 44) currently classified in section Torulomyces, which will be addressed in a future study.

Penicillium section Cinnamopurpurea

Penicillium infrapurpureum Visagie, Seifert & Samson, sp. nov. MycoBank MB809181. Figs 46, 47.

Etymology: Latin, infrapurpureum, meaning purple reverse, referring to the purple reverse on CYA.

Diagnosis: Dense, slow growing colonies, purpulish to bluish grey reverse on CYA, no growth on CYA at 30 °C, monoverticillate conidiophores producing smooth broadly ellipsoidal conidia.

Typus: Australia, Hobart, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21801, culture ex-type CBS 138219 = DTO 235F6).

Additional materials examined: Australia, Hobart, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138220 = DTO 235G2, CBS 138221 = DTO 235G5, CBS 138222 = DTO 235G6, CBS 138223 = DTO 235H5.

ITS barcode: KJ775679 (alternative markers: BenA = KJ775172; CaM = KJ775406)

Colony diam, 7 d (mm): CYA 14–17; CYA 30 °C no growth; CYA 37 °C no growth; MEA 14–17; YES 17–22; DG18 16–18; CYAS 16–18; OA 8–10; CREA 4–5.

Colony characters: CYA 25 °C, 7 d: Colonies moderately deep, dense, sunken at centre, sulcate; margins low, narrow, irregular; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green to dark green (25E5–F5); soluble pigments absent; exudates absent; reverse purplish to bluish grey (20F3); some isolates less intensely coloured. MEA 25 °C, 7 d: Colonies moderately dense, dense, sunken at centre, sulcate; margins low, narrow, irregular; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green to dark green (25E5–F5); soluble pigments absent; exudates absent; reverse olive brown to brown (10F8) to light brown (7D5). YES 25 °C, 7 d: Colonies deep, sulcate; margins low, narrow, irregular; mycelia white; texture velutinous; sporulation moderately dense to dense, conidia en masse greyish green to dark green (25E5–F5); soluble pigments absent; exudates absent; reverse olive brown to brown (4F5–5F5). DG18 25 °C, 7 d: Colonies low, sulcate; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense to dense,
Fig. 44. RPB2 phylogeny of the genus *Penicillium*, showing the unique position of *P. alfredii*. Names in blue are new species described in this study. *Talaromyces wortmannii* was used as outgroup. Model selected: K2 + G, combined alignment 953 bp.
**Fig. 45.** *Penicillium alfredii*. A. Colonies: top row left to right, obverse CYA, CYA 30 °C, YES and OA; bottom row left to right, reverse CYA, obverse MEA, DG18 and CREA. B–G. Conidiophores. H. Conidia. Scale bars: B–H = 10 μm.
conidia en masse dull to greyish green (26E3–4); soluble pigments absent; exudates absent; reverse greyish red (8B6–9B6) at centre, yellowish grey (3B2) near margin. OA 25 °C, 7 d: Conidiophores monoverticillate, sub-terminal branching sometimes observed; Stipes smooth walled, 20–70 × 2.5–3.5 μm; Vesicles 3.5–5.5 μm; Phialides ampulliform, sometimes more slender and elongated, 8.5–13.5 × 2.5–3.5 μm (10.8 ± 1.4 x 3.1 ± 0.3); Conidia smooth, broadly ellipsoid, 2.5–3.5 (–5.5) × 2.5–3.5 μm (3.1 ± 0.3 x 2.8 ± 0.3), average width/length = 0.9, n = 46.

Notes: Penicillium infrapurpureum is classified in section Cin
namopurpurea with other species that grow slowly on CYA and MEA (Fig. 46). The new species produces a striking purple to bluish reverse on CYA. A similar colouration was reported for P. cinnamopurpureum (Pitt 1979). Phylogenetically, P. infrapurpureum is resolved in a clade with P. idahoense and P. ellipsoideosporum. Penicillium idahoense also produces a purple reverse and smooth walled conidia (Paden 1971), but a cleistothecial morph is commonly observed, whereas P. ellipsoideosporum produces similar conidia, but lacks the colourful reverse (Wang & Kong 2000). Penicillium ellipsoideosporum also produces shorter phialides, 6.5–8.5 μm, than P. infrapurpureum and P. idahoense. Penicillium infrapurpureum does not grow on CYA at 30 °C or above, with P. idahoense sometimes growing at 37 °C. Two species described from China, P. guizhouanum and P.jiangxiense, were thought to be close relatives of P. cinnamopurpureum (Kong 2000, Kong & Liang 2003). Sequences from the ex-type strains show that this is not the case with P. guizhouanum, which has almost identical sequences to Talaromyces funiculosus. Penicillium jiangxiense is tentatively placed in section Cinnamopurpurea. Based on its ITS barcode, it does not belong in the section, but BenA and CaM is most similar to other species in the section (Fig. 46).

Penicillium section Lanata-Divaricata

Penicillium singorense Visagie, Seifert & Samson, sp. nov. MycoBank MB809182. Figs 48, 49.

Etymology: Latin, singorense, in reference to the ex-type strain, which was isolated from house dust collected in the city Singora/Songkhla, Thailand.

Diagnosis: Fast growing colonies on all media, strong growth on CYA at 30 and 37 °C, conidiophores irregular, mono- to biverticillate, producing roughened subglobose to ellipsoidal conidia.

Typus: Thailand, Songkhla, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21802, culture ex-type CBS 138214 = DTO 133C6).

Additional materials examined; Thailand, Songkhla, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138211 = DTO 129H7, CBS 138212 = DTO 129H8, DTO 131H8, CBS 138213 = DTO 131H8, DTO 132C8.

ITS barcode; KJ775674 (alternative markers: BenA = KJ775167; CaM = KJ775403)

Colony diam, 7 d (mm): CYA (35–)40–45; CYA 30 °C (35–) 40–50; CYA 37 °C 40–43; MEA (35–)45–48; YES (37–)42–45; DG18 21–26; CYAS 19–25; OA 40–45; CREA 20–25.
Fig. 47. *Penicillium infrapurpureum*. A. Colonies: top row left to right, obverse CYA, CYA 30 °C, YES and OA; bottom row left to right, reverse CYA, obverse MEA, DG18 and CREA. B–G. Conidiophores. H. Conidia. Scale bars: B–H = 10 μm.
Colony characters: CYA 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, wide, entire; mycelia white; texture floccose; sporulation sparse, conidia en masse dull green (26D3–4); soluble pigments absent; exudates absent, sometime clear; reverse greyish yellow to olive brown (4C5–D7). MEA 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, wide, entire; mycelia white; texture floccose; sporulation sparse, conidia en masse greenish grey (26C2); soluble pigments absent; exudates absent, sometimes clear; reverse light brown to brown (5D7–6D7). YES 25 °C, 7 d: Colonies low to moderately deep, sulcate; margins low, wide, entire; mycelia white; texture floccose; sporulation sparse, conidia en masse greenish grey (26B2); soluble pigments absent; exudates absent; reverse reddish to greyish yellow (4A6–B6). DG18 25 °C, 7 d: Colonies low to moderately deep, sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse, conidia en masse greyish green grey (25B2); soluble pigments absent; exudates absent; reverse yellow (2A6) at centre, greyish green (30B5) elsewhere. OA 25 °C, 7 d: Colonies low, plane; margins low, wide, entire; mycelia white; texture floccose; sporulation sparse to moderately dense, conidia in masse greyish green grey (28C3); soluble pigments absent; exudates absent. CREA 25 °C, 7 d: Acid not produced.

**Micromorphology:** Conidiophores irregular, mono- to biverticillate; stipes smooth to finely rough walled, 50–1000 × 1.5–2.5 μm; Vesicles 2–3 μm; Metulae/branches divergent, when present only two, 10–33 × 1.5–2.5 μm (20.8 ± 6.7 × 2.1 ± 0.3); Phialides ampulliform, 7–10 × 2.5–3 μm (8.4 ± 0.8 × 2.7 ± 0.2); Average length metula/phialide 2.5; Conidia finely rough to rough, sub-globose to ellipsoidal, 2.5–3 × 2–3 μm (2.7 ± 0.1 × 2.4 ± 0.1), average width/length = 0.88, n = 39.

**Notes:** *Penicillium singorense* is a close relative to *P. penarajense* and *P. vanderhammenii* (Fig. 48). The latter species do not grow on CYA at 37 °C, in contrast to the fast growing colonies of *P. singorense*. In addition, yellow cleistothecia were reported for *P. vanderhammenii* (Houbraken et al. 2010). This was not observed in *P. singorense*.

**Penicillium section Canescentia**

*Penicillium dunedinense* Visagie, Seifert & Samson, sp. nov. MycoBank MB809183. Figs 50, 51.

**Etymology:** Latin, *dunedinense*, in reference to the ex-type strain, which was isolated from dust collected in Dunedin, New Zealand.

**Diagnosis:** Fast growing colonies on MEA, brownish grey reverse on CYA, greyish orange colonies on YES, conidiophores with smooth walled stipes and rough walled conidia.

**Typus:** New Zealand. Dunedin, house dust, 2010, isolated by Ed Whitfield & Kalima Mwang (holotype CBS H-21803, culture ex-type CBS 138218 = DTO 244G1).

**ITS barcode:** KJ775678 (alternative markers: *BenA* = KJ775171; *CaM* = KJ775405)

**Colony diam., 7 d (mm):** CYA 29–31; CYA 30 °C 19–20; CYA 37 °C no growth; MEA 35–36; YES 38–40; DG18 31–32; CYAS 23–25; OA 21–22; CREA 14–15.

**Colony characters:** CYA 25 °C, 7 d: Colonies moderately deep, sulcate, having an inconspicuous orange colour in non-sporulating areas; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse, conidia en masse greyish green to greenish grey (25C3–26C2); soluble pigments absent; exudates abundant, clear; reverse brownish grey (7F2). MEA 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation moderately dense, conidia en masse greyish green (25C4); soluble pigments absent; exudates orange to clear; reverse brown to
Fig. 49. *Penicillium singorense*. A. Colonies: top row left to right, obverse CYA, CYA 30 °C, YES and OA; bottom row left to right, reverse CYA, obverse MEA, DG18 and CREA. B–G. Conidiophores. H. Conidia. Scale bars: B–H = 10 μm.
dark brown (7E7–F7). YES 25 °C, 7 d: Colonies moderately deep, sulcate, having a greyish orange (6B3) colour; margins low, narrow, entire; mycelia white to greyish orange (6B3); texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse brown to dark brown (7E7–F7). DG18 25 °C, 7 d: Colonies low to moderately deep, sulcate; margins low, wide, entire; mycelia white; texture floccose; sporulation moderately dense, conidia en masse dull green (29D3) near centre, greyish green (25D3) elsewhere; soluble pigments absent; exudates clear. CREA 25 °C, 7 d: Acid not produced.

**Penicillium section Ramsa**

*Penicillium lenticrescens* Visagie, Seifert & Samson, sp. nov. MycoBank MB809184. Figs 52, 53.

**Etymology**: Latin, *lenticrescens*, meaning slow growing, referring to the restricted growth of the species on all media.

**Diagnosis**: Slow growth on general media, no growth at 30 °C, conidiophores biverticillate, producing smooth walled stipes and smooth walled subglobose conidia.

**Typus**: New Zealand, Dunedin, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21804, culture ex-type CBS 138215 = DTO 129A8).

**ITS barcode**: KJ775675 (alternative markers: *BenA* = KJ775168; *CaM* = KJ775404).

**Colony diam, 7 d (mm)**: CYA 12–14; CYA 30 °C no growth; CYAS 37 °C no growth; MEA 10–11; YES 17–18; DG18 17–18; CYAS 19–20; OA 6–8; CREA 4–5.
Fig. 51. *Penicillium dunedinense*. A. Colonies: top row left to right, obverse CYA, CYA 30 °C, YES and OA; bottom row left to right, reverse CYA, obverse MEA, DG18 and CREA. B–I. Conidiophores. J. Conidia. Scale bars: B–J = 10 μm.
Colony characters: CYA 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation moderate, conidia en masse greyish green (25B4–C4); soluble pigments absent; exudates minute droplets, clear; reverse greyish green (30C4) centrally, fading to pale yellow (25B4) near margin. MEA 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, narrow, entire; mycelia white and inconspicuously yellow; texture floccose; sporulation moderately dense, conidia en masse greyish green (25B4–C4); soluble pigments absent; exudates minute, clear droplets; reverse brownish orange (5C6). YES 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, narrow, entire; mycelia white and yellow; texture floccose; sporulation sparse to moderate, conidia en masse greyish green (26E5); soluble pigments absent; exudates absent; reverse pale to light yellow (4A3–5). DG18 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation moderately dense, conidia en masse dull green (25D4); soluble pigments absent; exudates absent; reverse pale green (30A3). OA 25 °C, 7 d: Colonies moderately deep, plane; margins low, narrow, entire; mycelia white; texture floccose; sporulation moderately dense, conidia en masse greyish green (25B4–C4); soluble pigments absent; exudates absent. CREA 25 °C, 7 d: Acid not produced.

Micromorphology: Conidiophores biverticillate; Stipes smooth walled, 150–415 × 3–4 μm; Metulae divergent, swollen at apex up to 7.5 μm, 9.5–15 × 3–4.5 μm (11.9 ± 1.4 × 3.89 ± 0.4); Phialides ampulliform, 7.5–10.5 × 2.5–3.5 μm (8.8 ± 0.6 × 2.9 ± 0.2); Average length metula/phialide 1.35; Conidia smooth, subglobose, with a minor proportion ellipsoidal, 8.8 ± 0.6 × 2.9 ± 0.2 μm (2.9 ± 0.15 × 2.6 ± 0.2), average width/length = 0.90, n = 37.

Notes: Penicillium lenticrescens forms a monophyletic clade in section Ramosa closely related to P. soppii (Fig. 52). Both species sporulate rather sparsely after 7 d of growth. However, generally P. soppii grows faster and produces abundant sclerotia, features not observed in P. lenticrescens. Conidiophores of the two species are similar.

Penicillium section Paradoxa

Penicillium mexicanum Visagie, Seifert & Samson, sp. nov. MycoBank MB809185. Figs 54, 55.

Etymology: Latin, mexicanum, in reference to the ex-type strain, which was isolated from Mexico.

Diagnosis: Slow growth on general media, on CYA at 30 °C colonies 19–21 mm, conidiophores with smooth walled stipes, smooth walled, broadly ellipsoidal to ellipsoidal conidia (3–4 × 3–3.5 μm).

Typus: Mexico, Sayulita, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21805, culture ex-type CBS 138227 = DTO 270F1).

ITS barcode: KJ775685 (alternative markers: BenA = KJ775178; CaM = KJ775412)

Colony diam, 7 d (mm): CYA 20–22; CYA 15C 18–20; CYA 30 °C 19–21; CYA 37 °C no growth; MEA 12–14; YES 25–28; DG18 23–26; CYAS 21–24; OA 21–25; CREA 5–8.

Colony characters: CYA 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, narrow, in some isolates irregular; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green (26E6); soluble pigments absent; exudates abundant, clear to purplish; reverse centrally brown (6D5–6), elsewhere orange white (5A2). MEA 25 °C, 7 d: Colonies low, radially sulcate, raised at centre; margins low, narrow, irregular; mycelia white; texture velutinous; sporulation dense, conidia en masse greyish green (26E5); soluble pigments absent; exudates absent; reverse yellowish brown (5E8) at centre, margin brown (5E8) at margin YES 25 °C, 7 d: Colonies moderately deep, randomly sulcate, raised at centre; margins low, narrow, irregular;
Fig. 53. *Penicillium lenticrescens*. A. Colonies: top row left to right, obverse CYA, CYA 30 °C, YES and OA; bottom row left to right, reverse CYA, obverse MEA, DG18 and CREA. B–G. Conidiophores. H. Conidia. Scale bars: B = 100 μm; C–H = 10 μm.
The absence of growth at 30 °C is diagnostic for the smooth walled globose conidia, good growth on CREA and Frisvad & Samson (2004) represent a species complex. In our studies, 0 strains previously assigned to P. atramentosum grew 19–21 mm and 9–10 mm respectively at 30 °C. In addition, conidia of the two new species were consistently larger than those of P. atramentosum (≤3 μm). Except for the faster growth of P. mexicanum at 30 °C, its growth is more restricted on most media than P. magnielliptisporum. In addition, P. magnielliptisporum produces much bigger conidia than P. mexicanum.

**Penicillium magnielliptisporum** Visagie, Seifert & Samson, sp. nov. MycoBank MB809186. Figs 54, 56.

*Etymology:* Latin, *magnielliptisporum,* meaning large ellipsoidal conidia, in reference to the conidia of this species, which are larger than those of its closest relatives.

*Diagnosis:* Good growth on general media, also on CREA, restricted growth on CYA at 30 °C, conidiophores with smooth walled stipes, large, smooth broadly ellipsoidal to ellipsoid conidia, 3.5–5 × 3–4 μm.

**Type:** New Zealand, Dunedin, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange (holotype CBS H-21806, culture ex-type CBS 138225 = DTO 128H8).

*Additional material examined:* New Zealand, Dunedin, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138226 = DTO 128I1.

*ITS barcode:* KJ775686 (alternative markers: BenA = KJ775179; CaM = KJ775413)

**Colony diam., 7 d (mm):** CYA 35–38; CYA 15C 26–29; CYA 30 °C 9–10; CYA 37 °C no growth; MEA 21–23; YES 31–35; DG18 22–25; CYAS 19–20; OA 31–34; CREA 8–15.

**Colony characters:** CYA 25 °C, 7 d: Colonies moderately deep, sulcate; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green (26E6); soluble pigments absent; exudates abundant, clear; reverse yellowish grey (2B3–C3). MEA 25 °C, 7 d: Colonies low, radially sulcate, slightly raised at centre; margins low, narrow, irregular; mycelia white; texture velutinous; sporulation dense, conidia en masse greyish green (26D5–E5); soluble pigments absent; exudates minute, clear droplets;
Fig. 55. *Penicillium mexicanum*. A. Colonies: top row left to right, obverse CYA, CYA 30 °C, YES and OA; bottom row left to right, reverse CYA, obverse MEA, DG18 and CREA. B–G. Conidiophores. H. Conidia. Scale bars: B–H = 10 μm.
Fig. 56. *Penicillium magnielliptisporum*. A. Colonies: top row left to right, obverse CYA, CYA 30 °C, YES and OA; bottom row left to right, reverse CYA, obverse MEA, DG18 and CREA. B–G. Conidiophores. H. Conidia. Scale bars: B–H = 10 μm.
reverse yellowish brown (5E8) at centre, margin brown (5E8). YES 25 °C, 7 d: Colonies moderately deep, randomly sulcate, raised at centre; margins low, narrow, irregular; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish to dull green (25D4–5); soluble pigments absent; exudates absent; reverse dull yellow (3B3), olive (3D5–E5). DG18 25 °C, 7 d: Colonies low, very lightly radially sulcate; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense, conidia en masse greyish green (25C5–E5); soluble pigments absent; exudates absent; reverse greenish grey (29B2–C2). OA 25 °C, 7 d: Colonies low, plane; margins low, wide, entire; mycelia white; texture velutinous; sporulation dense, conidia en masse greyish green (25F8–26F8); soluble pigments absent; exudates abundant clear. CREA 25 °C, 7 d: Acid not produced.

Micromorphology: Conidiophores terverticillate, sometimes quarterverticillate; Stipes smooth walled, 80–280 × 3–4.5 μm; Branches/rami 1–4 per stipe, 12–20 × 3–4.5 μm; Metulae appressed, 9–14 × 3–4.5 μm (11.8 ± 1.3 × 3.5 ± 0.3); Phialides ampulliform, 7.5–10 × 2.5–3.5 μm (8.7 ± 0.6 × 2.7 ± 0.2); Average length metula/phialide 1.36; Conidia smooth, broadly ellipsoidal to ellipsoidal, 3.5–5 × 3–4 μm (4.3 ± 0.3 × 3.4 ± 0.2), average width/length = 0.79, n = 33.

Notes: See notes for P. mexicanum above.

The genus Talaromyces

Talaromyces section Talaromyces

Talaromyces oumae-annae Visagie, Yilmaz, Seifert & Samson, sp. nov. MycoBank MB809187. Figs 57, 58.

Etymology: Latin, oumae-annae, named in honour of “Ouma Anna”, grandmother of Visagie, this species was isolated from dust collected in her house in Kuils River, Cape Town.

Diagnosis: Growing restrictedly on CYA and DG18, grows well on other media, conidiophores biverticillate with some subterminal branches formed, stipes smooth walled, conidia rough walled and ellipsoidal.

Typus: South Africa, Kuils River in the Cape Town metropolitan area, house dust, 2010, isolated by Ed Whitfield & Kalima T. cnidii DTO 270A8 T. cnidii DTO 270B7 T. cnidii DTO 269I6 T. cnidii DTO 269H8 T. cnidii DTO 269I2 T. cnidii KACC 46617T T. cnidii DTO 270A4 T. siamensis CBS 475.88T T. siamensis DTO 269I3 T. flavovires CBS 102801T T. aculeatus CBS 289.48T T. apiculatus CBS 312.59T T. angelicus KACC 46611T T. liani CBS 225.66T T. pinophilus CBS 631.66T T. sayulitensis CBS 138204T T. sayulitensis CBS 138205 T. sayulitensis CBS 138206 T. viridulus CBS 252.87T T. oumae-annae CBS 138207 T. oumae-annae CBS 138208T T. verruculosus CBS 388.48T T. verruculosus DTO 129H4 T. verruculosus DTO 129H5 T. dendriticus CBS 660.80T

Fig. 57. Combined phylogeny for ITS, BenA and CaM of Talaromyces section. Talaromyces species closely related to the new species from house dust. The tree was rooted to T. dendriticus. Model selected: K2 + G, combined alignment 1 452 bp.

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Fig. 58. Talaromyces oumae-annae. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, obverse YES and CREA. B–H. Conidiophores. I. Conidia. Scale bars: B–I = 10 μm.
Mwange (holotype CBS H-21797, culture ex-type CBS 138208 = DTO 269E8).

Additional materials examined: South Africa, Kuits River, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138207 = DTO 180B4.

ITS barcode: KJ775720 (alternative markers: BenA = KJ775213; CaM = KJ775425)

Colonial diam, 7 d (mm): CYA 16–18; CYA 30 °C 16–17; CYA 37 °C 10–11; MEA 29–30; YES 20–23; DG18 14–17; CYAS No growth; OA 30–35; CREA 5–6.

Colonial characters: CYA 25 °C, 7 d: Colonies low, slightly raised at centre, plane; margins low, narrow, entire; mycelia white; texture floccose and velutinous; sporulation moderately dense to dense, conidia in masse dull green (25D4–E4); soluble pigments yellow; exudates absent; reverse greyish green (29B6–C6); MEA 25 °C, 7 d: Colonies low, plane; margins low, narrow, entire; mycelia white and pastel yellow; texture velutinous, centrally floccose with sterile aerial mycelia; sporulation dense, conidia en masse greyish green (27D5–E5); soluble pigments absent; exudates absent; reverse light brown (7D6) in the centre fading into brownish orange (6C6). YES 25 °C, 7 d: Colonies low, raised at centre, lightly sulcate; margins low, narrow, entire; mycelia white to yellow; texture velutinous to floccose; sporulation dense, conidia en masse dull green (25D4–E4); soluble pigments yellow; exudates absent; reverse centre light yellow to greyish yellow (2A5–B5), at margins greyish green (27E5). DG18 25 °C, 7 d: Colonies moderately deep, lightly sulcate; margins low, narrow, entire; mycelia white to yellow; texture floccose; sporulation dense, conidia en masse greyish green (26E5–27E5); soluble pigments absent; exudates absent; reverse light orange (6A4–5). OA 25 °C, 7 d: Colonies low, plane; margins low, narrow, entire; mycelia white; texture velutinous; sporulation dense, conidia en masse greyish green to dark green (28E5–F5); soluble pigments absent; exudates absent. CREA 25 °C, 7 d: Acid not produced.

Micromorphology: Conidiophores biverticillate, subterminal branches sometimes present; Stipes smooth walled, 85–240 × 2.5–3.5 μm; Branches up to 30 μm long; Metulae appressed, 8–11 (12.5) × 2.5–3.5 μm (10.6 ± 1.0 × 3 ± 0.2); Phialides acerose, 9–11.5 × 2–3 μm (10.6 ± 0.8 × 2.7 ± 0.3); Average length metula/phialide 1.01; Conidia rough, ellipsoidal, 3.5–3.5 × 2.5–3 μm (3.2 ± 0.2 × 2.6 ± 0.2), average width/length = 0.83, n = 38.

Notes: Talaromyces oumae-annae is phylogenetically closely related to T. verruculosus and T. viridulus (Fig. 57). However, T. oumae-annae produces ellipsoidal conidia compared to the globose conidia of T. verruculosus. The latter species also grows much faster on CYA at all temperatures (CYA 32–35; CYA 30 °C 37–38; CYA 37 °C 25–26). Talaromyces viridulus, originally described as Geosmithia viridis, produces rod-shaped conidia, in contrast to the ellipsoidal conidia of T. oumae-annae.

Talaromyces sayulitensis Visagie, Yilmaz, Seifert & Samson, sp. nov. MycoBank MB809188. Figs 57, 59.

Etymology: Latin, sayulitensis, in reference to the ex-type strain, which was isolated from dust collected in Sayulita.

Diagnosis: Yellow mycelia dominate colony appearance, good growth on CYA at 37 °C, acid produced on CREA, conidiophores biverticillate, stipes smooth walled, conidia smooth and subglobose to broadly ellipsoidal.

Typus: Mexico, Sayulita, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138204 = DTO 245H1.

Additional materials examined: Mexico, Sayulita, house dust, 2010, isolated by Ed Whitfield & Kalima Mwange, CBS 138205 = DTO 245H2, CBS 138206 = DTO 245H3.

ITS barcode: KJ775713 (alternative markers: BenA = KJ775206; CaM = KJ775422)

Colonial diam, 7 d (mm): CYA 24–29; CYA 30 °C 35–43; CYA 37 °C 32–40; MEA 37–40; YES 37–40; DG18 18–22; CYAS 5–8; OA 40–42; CREA 15–18.

Colonial characters: CYA 25 °C, 7 d: Colonies low, raised at centre, slightly sulcate; margins low, narrow, entire; mycelia white to yellow to red; texture floccose; sporulation absent; soluble pigments absent; exudates absent to clear in some isolates; reverse brown (6E6) centrally, fading into brownish orange (6C7) and light yellow (4A5). MEA 25 °C, 7 d: Colonies low, slightly raised at centre, plane; margins low, narrow, entire; mycelia white, pastel yellow and pastel red; texture loosely funiculose to floccose; sporulation sparse, conidia en masse greyish green (27D5–E5); soluble pigments absent; exudates absent; reverse brownish orange (6C6–7). YES 25 °C, 7 d: Colonies low, raised at centre, sulphate; margins low, narrow, entire; mycelia white to yellow; texture loosely funiculose to floccose; sporulation sparse to moderately dense, conidia en masse greyish green (27D5–E5); soluble pigments absent; exudates absent; reverse brownish orange (6C6–7). DG18 25 °C, 7 d: Colonies low, plane; margins low, narrow, entire; mycelia white to yellow; texture floccose; sporulation moderately dense, conidia en masse greyish green (26D5–E5); soluble pigments absent; exudates absent; reverse light yellow (3A5–4A5). OA 25 °C, 7 d: Colonies low, slightly raised at centre, plane; margins low, wide, entire; mycelia white to yellow; texture loosely funiculose and floccose, especially in the centre sterile aerial hyphae; sporulation dense, conidia en masse greyish green (27C5–D5); soluble pigments absent; exudates absent. CREA 25 °C, 7 d: Acid strongly produced.

Micromorphology: Conidiophores biverticillate, subterminal branches sometimes present; Stipes smooth walled, (40–) 85–300 × 2–3.5 μm; Branches up to 40 μm long; Metulae appressed, 8–11.5 (14) × 2.5–3 μm (10.2 ± 1.3 × 2.8 ± 0.2); Phialides acerose, 8–11 × 2.5–3 μm (9.4 ± 0.6 × 2.6 ± 0.2); Average length metula/phialide 1.09; Conidia smooth, sub-globose to broadly ellipsoidal, 2.5–3 × 2–2.5 μm (2.6 ± 0.1 ± 2.2 ± 0.1), average width/length = 0.87, n = 37.

Notes: Phylogenetically, T. sayulitensis forms a coherent clade closely related to T. pinophilus and T. liani (≡ P. liani). Talaromyces liani lacks the acid production characteristic of T. sayulitensis, produces larger conidia 2.5–4 μm, and typically produces asexual state. Talaromyces pinophilus also produces acid on CREA and also lacks a sexual state and other colony characters are very similar to T. sayulitensis, although some minor differences are observed in colony growth rates. This does
Fig. 59. Talaromyces sayulitensis. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, obverse YES and CREA. B–H. Conidiophores. I. Conidia. Scale bars: B–I = 10 μm.
not allow unequivocal morphological identification of the new species. Phylogenetically it is distinct and this justifies introducing it as a new species.

**Talaromyces section Islandici**

*Talaromyces yelensis* Visagie, Yilmaz, Seifert & Samson, sp. nov. MycoBank MB809189. Figs 60, 61.

**Etymology:** Latin, *yelensis*, in reference to the ex-type strain, which was isolated from dust collected in Yela, Micronesia.

**Diagnosis:** Very dense, deep and yellow colonies produced on general media, conidiophores biverticillate, ampulliform phialides end in fine apical pores, roughened subglobose to broadly ellipsoidal conidia.

**Typus:** Federated States of Micronesia, Yela of Kosrae Island, house dust, 2010, isolated by Ed Whitten & Kalima Mwange (holotype CBS H-21799, culture ex-type: CBS 138209 = DTO 268E5).

**Additional material examined:** Federated States of Micronesia, Yela of Kosrae Island, house dust, 2010, isolated by Ed Whitten & Kalima Mwange, CBS 138210 = DTO 268E7.

**ITS barcode:** KJ775717 (alternative markers: BenA = KJ775210)

**Colonies diam, 7 d (mm):** CYA 20–22; CYA 30 °C 25–26; CYA 37 °C 14–16; MEA 15–16; YES 20–21; DG18 16–17; CYAS 13–14; OA 18–20; CREA 9–10.

**Colony characters:** CYA 25 °C, 7 d: Colonies moderately deep; margins low, narrow, entire; mycelia white to yellowish to orange; texture floccose; sporulation absent; soluble pigments absent; exudates clear and sticky; reverse yellowish white (2A2) to light yellow (3A5) to brown (5F6). MEA 25 °C, 7 d: Colonies very deep, plane; margins deep, narrow, entire; mycelia white to yellow to orange; texture floccose; sporulation absent; soluble pigments absent; exudates yellow; reverse brownish yellow to yellowish brown to brown (5C8–E8). YES 25 °C, 7 d: Colonies very deep, plane; margins low, narrow, entire; mycelia white to yellow to orange; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse yellowish white (4A2) to greyish orange (5B5). DG18 25 °C, 7 d: Colonies deep, plane; margins low, narrow, entire; mycelia white to yellow; texture floccose; sporulation sparse, conidia en masse greyish green (26C3); soluble pigments absent; exudates yellow and sticky; reverse yellowish white to yellow (3A2–6). OA 25 °C, 7 d: Colonies moderately deep, plane; margins low, narrow, entire; mycelia white to yellow; texture floccose; sporulation moderately dense, conidia en masse dark green (26F6); soluble pigments absent; exudates clear and sticky. CREA 25 °C, 7 d: Acid not produced.

**Micromorphology:** Conidiophores biverticillate, subterminal branches sometimes present; stipes smooth walled, 60–190 × 2.5–3.5 μm; branches up to 30 μm long; metulae appressed, 8–11 × 2.5–3.5 μm (9.7 ± 0.7 × 2.9 ± 0.3); phialides ampulliform, ending in a fine apical pore, 8–10 × 2.5–3 μm (9.1 ± 0.8 × 2.7 ± 0.1); average length metula/phialide 1.06; conidia rough, subglobose to broadly ellipsoidal, 2.5–3.5 × 2.5–3 μm (2.96 ± 0.1 × 2.64 ± 0.2), average width/length = 0.89, n = 43.

**Notes:** *Talaromyces yelensis* is closely related to *T. tratensis* in section *Islandici* (Fig. 60). The latter species typically produces a sexual state with roughened ascospores and ellipsoidal smooth walled conidia. *Talaromyces yelensis* produces subglobose to broadly ellipsoidal conidia that have rough walls and lacks a sexual state.

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Fig. 60. Combined phylogeny for ITS and BenA of Talaromyces section Islandici. Names in blue are new species described in this study. The tree was rooted to *T. piceus*. Model selected: K2 + G, combined alignment 738 bp.
Fig. 61. Talaromyces yelesis. A. Colonies: top row left to right, obverse CYA, MEA, DG18 and OA; bottom row left to right, reverse CYA, MEA, obverse YES and CREA. B–G. Conidiophores. H. Conidia. Scale bars: B–H = 10 μm.
DISCUSSION

Phylogenetic species recognition

ITS is the most commonly sequenced gene for fungi and was recently accepted as the official DNA barcode (Schöch et al. 2012). Curated reference data sets are currently limited, with several publications addressing the issue (Köljalg et al. 2005, Santamaria et al. 2012, Köljalg et al. 2013, Schöch et al. 2014). With regards to Aspergillus, Penicillium and Talaromyces, the accepted species list endorsed by ICPA provides accession numbers of ITS barcodes to all ex-type strains. Although ITS does not distinguish among all species, with some species sharing identical sequences (Skouboe et al. 1999, Peterson 2000a,b, Samson et al. 2011), it does provide valuable information on sectional classification and often provides enough information for making a species identification. In order to compensate for the lack of variability in ITS, the ICPA list also include accession numbers for BenA and CaM sequences, meant to serve as secondary identification markers.

Our data shows that BenA works well for Penicillium and Talaromyces identifications, whereas CaM performs well in Aspergillus. However, some problems were experienced. Aspergillus steynii and A. elegans share identical CaM sequences (Fig. 2), something very uncommon in Aspergillus. In this case, these two species have unique ITS and BenA sequences.

In Penicillium, BenA has limitations in the P. chrysogenum (Fig. 23) and P. camemberti (Fig. 24) species complexes. Houbraken et al. (2012) reviewed section Chrysogena and distinguished several phylogenetically closely related species, and showed that different genes suggest different phylogenies. For example, although P. chrysogenum has unique BenA sequences, variation among strains makes distinguishing it from P. allii-sativi complicated. On the other hand, CaM does not distinguish well between P. chrysogenum and P. rubens (Houbraken et al. 2012), but BenA easily distinguishes the two. As such, a combination of the two genes is often required for identifying isolates within the clade. Another difficult clade is the P. camemberti complex. The ex-type cultures for P. commune, P. camemberti and P. caseifolum have identical ITS, BenA and CaM sequences, as also reported by Giraud et al. (2009) for elongation factor-1α. The importance and different roles of these species in the cheese industry makes it unsatisfactory to synonymise them, and as a result the white sporulating P. camemberti are considered a domesticated form of P. commune or P. caseifolum (green sporulating). A similar situation exists in Aspergillus, where A. oryzae is considered a domestic form of A. flavus (Varga et al. 2011). None of these problems were experienced for Talaromyces, where BenA worked very well for identifications.

In some cases, an ex-type sequence alone is insufficient reference data for making a conclusive identification, a reflection of intraspecific variation, for example in P. italicum (Fig. 24), P. sumatraense (Fig. 13) (Houbraken et al. 2011b) and in Talaromyces section Trachyspermi (Fig. 28) (Frisvad et al. 2013). As such, a verified reference data set that includes non-ex-type strains representing the sequence diversity within phylogenetically delineated species is the next crucial step for sequence-based identifications in these genera.

Fungi in house dust

Samson et al. (2010) and Flannigan et al. (2011) listed 100 fungal species common in indoor environments. From this list, we also found A. fumigatus, A. sydowii, P. brevicompactum and P. citrinum to be common in the collected house dust. Of significance is the effect of taxonomic revisions on this type of information. For example, A. versicolor used to be considered very common in indoor environments. However, it was recently shown to represent a species complex, with nine new species introduced (Jurjević et al. 2012). From our data, A. versicolor was still isolated from four different countries and A. creber was isolated in higher numbers from three countries. From unpublished data, we are also noting that most of the “A. versicolor” strains collected from indoor environments over many years in the DTO collection housed at CBS should now be identified as A. creber. Another example is Aspergillus section Circumdati. The ochratoxin producer A. westerdijkiae is reported to have a wide distribution indoors. From dust, we could only recover this species from Mexico and South Africa, whereas A. subramanianii was found in high numbers from four countries. Penicillium chrysogenum is also considered to have a worldwide distribution from indoor environments. However, after Houbraken et al. (2011a) reintroduced P. rubens as the name for the commercial penicillin producing strain closely related to P. chrysogenum, we are finding P. rubens to be very common indoors and not P. chrysogenum.

The origin of common indoor species is difficult to determine. Aspergillus sydowii is a good example. We found A. sydowii to be one of the most common species in collected dust samples and the species is generally considered as widespread. The species is often isolated from soil (Domsch et al. 1980), is very common on mouldy gypsum wallboard, dust, paint and various foods (Gorbushina et al. 2007, Samson et al. 2010, Flannigan et al. 2011) and is commonly found in marine environments where it acts as an opportunistic pathogen of sea corals (Roth et al. 1964, Smith et al. 1996, Geiser et al. 1998, Toledo-Hernández et al. 2008, Rypien et al. 2008, Rypien 2008, Kirkwood et al. 2009). The source or origin of this species is still unknown, even though most studies suggest it being a terrestrial soil-borne fungus. The suggestion thus is that A. sydowii, along with a number of other soil-borne fungi, gets carried into indoor environments. Its ability to grow in such a wide range of niches is intriguing and needs further studies.

Recent studies suggested that the indoor fungal communities as observed with metagenomics analyses exploiting next generation sequencing are mostly determined by the outdoor fungal communities (Adams et al. 2013a,b). In our study, the highest diversity was observed in countries that are also listed as biodiversity hotspots of the world (Myers et al. 2000). This might suggest that at least a considerable proportion of these species isolated from house dust originated from outdoors. However, the prevalence of specific species commonly isolated from indoor surveys suggests that the indoor environments do select for the growth of specific species. In addition, much of the metagenomics diversity may come from transient, dormant or dead spores.

From various indoor culture-independent surveys, it is apparent that the ITS database is not yet sufficient for identification of Aspergillus, Penicillium and Talaromyces (Amend
et al. 2010, Adams et al. 2013a,b). These studies often cite Aspergillus sp. and Penicillium sp. as the most abundant. It would be valuable, even if species identification were not feasible, to identify to which clade or taxonomic section or series the sequences belong. The Last Common Ancestor (LCA) analysis commonly employed for identifying OTUs in metagenomic studies employ the GenBank taxonomic hierarchy to assign query sequences to taxonomic nodes. This hierarchy generally lacks ranks between genus and species, which means that the analysis suffers from a regrettable lack of precision for large genera, such as those studied here. In order to at least partially alleviate this kind of issue, our ITS barcodes of ex-type sequences and reference barcodes created from dust isolates will be uploaded into the UNITE database as part of a planned curated set on indoor moulds. As part of a future study, these reference sequences will be used for comparing d2e and 454-pyrosequencing data (Amend et al. 2010) in order to better understand the communities of Aspergillus, Penicillium and Talaromyces in indoor environments.

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