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Polyphasic taxonomy of *Aspergillus* section *Aspergillus* (formerly *Eurotium*), and its occurrence in indoor environments and food

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Abstract: *Aspergillus* section *Aspergillus* (formerly the genus *Eurotium*) includes xerophilic species with uniseriate conidiophores, globose to subglobose vesicles, green conidia and yellow, thin walled eurotium-like ascomata with hyaline, lenticular ascospores. In the present study, a polyphasic approach using morphological characters, extrolites, physiological characters and phylogeny was applied to investigate the taxonomy of this section. Over 500 strains from various culture collections and new isolates obtained from indoor environments and a wide range of substrates all over the world were identified using calmodulin gene sequencing. Of these, 163 isolates were subjected to molecular phylogenetic analyses using sequences of ITS rDNA, partial β-tubulin (*BenA*), calmodulin (*CaM*) and RNA polymerase II second largest subunit (*RPB2*) genes. Colony characteristics were documented on eight cultivation media, growth parameters at three incubation temperatures were recorded and micromorphology was examined using light microscopy as well as scanning electron microscopy to illustrate and characterize each species. Many specific extrolites were extracted and identified from cultures, including echinulins, epiheveadrides, auroglaucins and anthraquinone bisanthrons, and to be consistent in strains of nearly all species. Other extrolites are species-specific, and thus valuable for identification. Several extrolites show antioxidant effects, which may be nutritionally beneficial in food and beverages. Important mycotoxins in the strict sense, such as sterigmatocystin, aflatoxins, ochratoxins, citrinin were not detected despite previous reports on their production in this section. Adopting a polyphasic approach, 31 species are recognized, including nine new species. ITS is highly conserved in this section and does not distinguish species. All species can be differentiated using *CaM* or *RPB2* sequences. For *BenA*, *Aspergillus brunneus* and *A. niveoglaucus* share identical sequences. Ascospores and conidia morphology, growth rates at different temperatures are most useful characters for phenotypic species identification.

Key words: *Ascomycota*, *Eurotiales*, *Aspergillaceae*, Multi-gene phylogeny, Extrolites, *Aspergillus proliferans*, *Eurotium amstelodami*.

Taxonomic novelties: *Aspergillus aerius* A.J. Chen, Frisvad & Samson, *A. aurantiacoflavus* Hubka, A.J. Chen, Jurjević & Samson, *A. caperatus* A.J. Chen, Frisvad & Samson, *A. endophyticus* Hubka, A.J. Chen, & Samson, *A. levisporus* Hubka, A.J. Chen, Jurjević & Samson, *A. porosus* A.J. Chen, Frisvad & Samson, *A. tamarindosoli* A.J. Chen, Frisvad & Samson, *A. teporis* A.J. Chen, Frisvad & Samson, *A. zutongqii* A.J. Chen, Frisvad & Samson.

INTRODUCTION

Aspergillus subgenus *Aspergillus*, typified with *A. glaucus* (L.) Link, was introduced to include *Aspergillus* species with uniseriate conidiophore heads with hyaline, brownish or greenish stipes, and slightly inflated to subglobose vesicles and green conidia in mass (Gams *et al.* 1985). The subgenus contains two sections, namely sections *Aspergillus* (*Aspergillus glaucus* group Thom & Raper 1941, 1945, Raper & Fennell 1965) and *Restricti* (*Aspergillus restrictus* group Raper & Fennell 1965). The main difference of these two sections is that species in sect. *Aspergillus* readily produce a sexual state in culture (homothallic) and this sexual morph was, in the dual name nomenclature system, classified in the genus *Eurotium* (Malloch & Cain 1972, Pitt 1985). While the majority of species in sect. *Restricti* are asexually reproducing, one exception is *A. halophilicus*, which produces a eurotium-like sexual state (Christensen *et al.* 1959, Peterson *et al.* 2008). Peterson (2008) examined *Aspergillus* phylogenetically using β-tubulin (*BenA*), calmodulin (*CaM*), *ID* region of rDNA (ITS and partial LSU) and RNA polymerase II second largest subunit (*RPB2*), and showed that sections *Aspergillus* and *Restricti* formed a monophyletic subgenus *Aspergillus*. The monophyly of both sections was recently confirmed using a larger data set by Sklenář *et al.* (2017). Houbraken & Samson (2011) assessed relationships in the *Trichocomaceae* using a multigene phylogeny (*RPB1*, *RPB2*, *Tsr1* and *Cct8*) and showed that *Aspergillus* and its sexual states formed a monophyletic clade closely related to *Penicillium*. This was again confirmed using a 25-gene phylogeny (Houbraken *et al.* 2014). Pitt & Taylor (2014) on the other hand, re-examined and analysed data from Houbraken and Samson (2011), and claimed that *Penicillium* could be included in a very broad concept of *Aspergillus*, which would only be monophyletic if *Penicillium* was included. This was partly caused by *Aspergillus paradoxus*, *A. malodoratus* and *A. crystallinus*, which were at that time still classified in *Aspergillus*, but currently in

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Penicillium. Similarly, *Penicillium inflatum* was combined in *Aspergillus* as *Aspergillus inflatus* (Visagie *et al.* 2014b, Samson *et al.* 2014). Furthermore, Pitt and Taylor (2014, 2016) proposed to maintain the genus *Eurotium* for subgenus *Aspergillus* and subdivided *Aspergillus* into several smaller genera based on the corresponding sexual names. Most recently, Kocsubé *et al.* (2016) brought strong evidence that *Aspergillus* and *Penicillium* are monophyletic based on a robust multiple gene phylogenetic analyses and extrolite profiles. These findings rejected the hypothesis of *Aspergillus* being a paraphyletic genus (Pitt & Taylor 2014, 2016), and were in agreement with the previous studies of Houbraken & Samson (2011) and Houbraken *et al.* (2014).

To avoid instability and nomenclatural confusion, the broad concept of *Aspergillus* was chosen by a majority of the International Commission of *Penicillium* and *Aspergillus* (ICPA) on April 11, 2012. Consequently, Hubka *et al.* (2013a) transferred all *Eurotium* taxa to *Aspergillus*. This treatment is widely accepted. Subsequently five species producing a eurotium-like sexual state, namely *A. cumulatus*, *A. mallochii*, *A. megasporus*, *A. osmophilus* and *A. sloanii* were introduced in sect. *Aspergillus* and *Aspergillus* names preferred over *Eurotium* by most authors (Asgari *et al.* 2014, Kim *et al.* 2014, Visagie *et al.* 2014a, 2017). Before sequence data became widely available, the taxonomy of sect. *Aspergillus* was based on morphological characters. Ascospore pattern, shape and size were considered the most important characters distinguishing species, whereas the conidial apparatus and mycelial pigmentation provide valuable additional information (Thom & Raper 1941, 1945, Raper & Fennell 1965). Raper (1957) emphasized that in some strains the sexual state is dominating, while in others it is the asexual state, which has significant influence on the appearance of colonies. Blaser (1975) found that morphology and size of ascospores, surface ornamentation and colour of conidia are dependent on the temperature and water activity of cultivation media and thus reduced some species to synonyms. Samson (1979) compiled the sect. *Aspergillus* species published since Raper and Fennell's treatment in 1965, and synonymized six species under earlier names. Pitt (1985) reappraised the nomenclature and taxonomy of *Eurotium* (sect. *Aspergillus*), and accepted seven species based on the distinct nature of their ascospores. Kozakiewicz (1989) focused on scanning electron microscope (SEM) examinations of conidia and ascospores in her treatment of the group. Based on conidial ornamentations, four conidial morphotypes were identified, namely aculeate, tuberculate, lobate-reticulate and microtuberculate. Within each group, characters of equatorial crests, furrow and convex wall ornamentation are important diagnostic features. It was shown that some species previously considered conspecific according to light microscopy, e.g. *A. cristatus* (= *Eurotium cristatum*) and *A. intermedius* (= *E. intermedium*), show distinct conidial ornamentation in SEM and deserve to be recognized as separate species (Kozakiewicz 1989). Hubka *et al.* (2013a) studied the phylogeny of sect. *Aspergillus* based on *ID* region, *BenA*, *CaM* and *RPB2* sequences, and accepted 17 species based on Genealogical Concordance Phylogenetic Species Recognition (GCPSR) approach.

Members of sect. *Aspergillus* are generally referred to as osmo-, xero- or halotolerant. They have a world-wide distribution and are common in indoor air, house dust, cereals, food products containing high concentrations of sugar, such as syrups, jams and jellies, salted meat products, semi-dry foods, feeds, leather goods and so on (Raper & Fennell 1965, Blaser 1975, Chelkowski *et al.* 1987, Pitt & Hocking 2009, Samson *et al.* 2010, Greco *et al.* 2015). Species in this section are able to initiate growth at minimum moisture levels, thus establishing bridgeheads and facilitating the invasion of slightly less xerophilic molds (Semeniuk *et al.* 1947, Raper & Fennell 1965, Kozakiewicz 1989). Some species are involved in food manufacturing. *Aspergillus cristatus* or “Golden Flower Fungus” is used in the production of Fuzhuan brick tea in China (Wen 1990, Qi & Sun 1990, Xu *et al.* 2011); *Aspergillus pseudoglaucus* (= *Eurotium repens*) is used as a starter culture in the manufacturing of katsuobushi and fish sauce (Hayakawa *et al.* 1993, Dimici & Wada 1994); *A. pseudoglaucus*, *A. chevalieri* and *A. montevidensis* are frequently isolated from meju (dried fermented soybeans); two newly described species *A. cibarius* and *A. cumulatus* are also isolated from meju or meju fermentation related environment (Hong *et al.* 2011, 2012, Kim *et al.* 2014). *Aspergillus chevalieri*, *A. cristatus*, *A. glaucus*, *A. montevidensis*, *A. proliferans*, *A. pseudoglaucus* and *A. ruber* have been reported from feedstuffs very often (Pitt & Hocking 2009, Samson *et al.* 2010, Greco *et al.* 2015). These species have also been reported from other habitats and substrates. *Aspergillus cristatus*, *A. glaucus*, *A. pseudoglaucus* and *A. ruber* were listed as marine-derived (Li *et al.* 2004a, b, 2006, 2008a, b, 2009, 2010, Wang *et al.* 2006, 2007c, Du *et al.* 2007, 2008, 2012, 2014, Smetanina *et al.* 2007, Tao *et al.* 2009, Gomes *et al.* 2012, Yan *et al.* 2012, Sun *et al.* 2013, Tang *et al.* 2014, Meng *et al.* 2015) and *A. brunneus*, *A. chevalieri*, *A. cristatus*, *A. glaucus*, *A. intermedius*, *A. montevidensis*, *A. niveoglaucus*, *A. pseudoglaucus*, *A. ruber* and *A. xerophilus* have been reported from soil (Guarro *et al.* 2012). However, sea-water and soil are matrices rather than habitats, usually of high water activity, where these fungi cannot grow or compete with other fungi. Species in sect. *Aspergillus* are not considered as important pathogens, although *A. glaucus*, *A. chevalieri* and *A. montevidensis* (= *Eurotium amstelodami*) have been reported from cases of superficial infections and sporadic invasive infections (de Hoog *et al.* 2000, Reboux *et al.* 2001, Roussel *et al.* 2004, Summerbell *et al.* 2005, Hubka *et al.* 2012).

Species of sect. *Aspergillus* produce many extrolites such as flavoglaucin, auroglaucin, isotetrahydroauroglaucin, neoechinulins A and B, echinulin, preechinulin, neochinulin E, epiheveadride and questin (Slack *et al.* 2009, Greco *et al.* 2015). Production of the potentially toxic echinulin has been reported from various strains of *A. montevidensis* (= *E. amstelodami*) (Allen 1972, Gatti & Fuganti 1979) and *A. pseudoglaucus* (= *E. repens*) (Smetanina *et al.* 2007). Other so-called toxins such as flavoglaucin and auroglaucin co-occur in various taxa of sect. *Aspergillus*, along with isotetrahydroauroglaucin in some *A. montevidensis* (= *E. amstelodami*) and *A. ruber* (= *E. rubrum*) strains (Slack *et al.* 2009). Interestingly, none of the compounds produced by these fungi have been classified as real mycotoxins, as the definition of the word mycotoxin is secondary metabolites (or extrolites) produced by filamentous fungi that are toxic to human beings and other vertebrates when introduced in small amounts via a natural route (orally, through pulmonary tract or skin) (Bennett & Klich 2003). On the other hand, the small molecule extrolites, such as dihydroauroglaucin (DAG), tetrahydroauroglaucin (TAG), anthraquinone derivatives, etc. produced by sect. *Aspergillus* species are antioxidant, and may even be beneficial to health (Ishikawa *et al.* 1985, Li *et al.* 2004a, 2009, Miyake *et al.* 2009, Meng *et al.* 2016). Reports of sect. *Aspergillus* species producing true mycotoxins such as aflatoxins, ochratoxin A and sterigmatocystin were proved to be incorrect (Frisvad *et al.* 2007).

The aim of this study is to provide a taxonomic revision of sect. *Aspergillus* using a polyphasic approach. Phylogenetic relationships between sect. *Aspergillus* members were investigated using a combined data set (*BenA*, *CaM* and *RPB2* sequences), and comparison of single-gene phylogenies was executed to determine tentative species boundaries based on genealogical concordance principle. Furthermore, phenotypic features including macro- and micro-morphology, ecophysiology and extrolite profiles are included in the polyphasic approach. Finally, the details on the identification of world-wide indoor environment strains have been included here.

MATERIAL AND METHODS

Fungal strains

Strains used in this study were obtained from: 1) CBS, Culture Collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; 2) CGMCC, China General Microbiological Culture Collection Centre, Beijing, China; 3) NRRL, Agricultural Research Service Culture Collection, Peoria, Illinois, USA; 4) KACC, Korean Agricultural Culture Collection, Wanju, South Korea; 5) CCF, Culture Collection of Fungi, Prague, Czech Republic; 6) CCM (F-), Czech Collection of Microorganisms, Brno, Czech Republic; 7) IBT, the culture collection of Department of Biotechnology and Biomedicine, Technical University of Denmark; 8) DAOMC, Canadian Collection of Fungal Cultures, at the Ottawa Research and Development Centre – Agriculture and Agri-Food, Ottawa, Canada; and 9) BCCM/IHEM, Belgian Coordinated Collections of Microorganisms. Strains deposited in the working collection of the Applied and Industrial Mycology department (DTO) housed at the Westerdijk Fungal Biodiversity Institute, were also included in this study (Table 1).

For newly isolated strains from the indoor environments, different isolation techniques were used. House dust samples were collected as described in Amend *et al.* (2010) and isolated using a modified dilution-to-extinction method (Visagie *et al.* 2014a). Air samples were collected approximately 1 m above the ground with a viable impaction sampler (MAS 100 Merck) (Peterson & Jurjević 2013). Indoor surfaces (walls, ceilings) were sampled with the swab (Greiner Bio-One, Alphen aan de Rijn, the Netherlands). For air and swab sampling, standard microbiological techniques were used for isolation. Malt extract agar (MEA) with chloramphenicol and Dichloran 18 % glycerol agar (DG18) were used as isolation media.

DNA extraction, PCR amplification and sequencing

Strains were grown for 1 wk on M40Y prior to DNA extraction. DNA was extracted using the Ultraclean™ Microbial DNA isolation Kit (MoBio, Solana Beach, U.S.A.) or the ArchivePure DNA yeast and Gram2+ kit (5 PRIME Inc., Gaithersburg, MD) according to manufacturer instructions updated by Hubka *et al.* (2015). Target loci, i.e. ITS, *BenA*, *CaM* and *RPB2*, were amplified using primer combination listed in Table 2. PCR product purification followed the protocol described by Réblová *et al.* (2016). Automated sequencing was performed at the Macrogen Sequencing Service (Amsterdam, the Netherlands) using same primers used in PCR.

Phylogenetic analysis

Sequences were inspected and assembled in BioEdit v.7.1.8 (http://www.mbio.ncsu.edu/bioedit/bioedit.html). Sequence alignments were performed using the FFT-NSi strategy implemented in MAFFT v.7 (Katoh & Standley 2013). Alignment characteristics are listed in Table 3. Maximum likelihood (ML) trees were constructed with IQ-TREE v. 1.4.0 (Nguyen *et al.* 2015). Optimal partitioning scheme and substitution models were selected using PartitionFinder v1.1.0 (Lanfear *et al.* 2012) with setting allowing introns, exons and codon positions to be independent datasets. The Bayesian information criterion was used to determine the model that best fits the data. Proposed partitioning schemes and substitution models for each dataset are listed in Table 4. Support values at branches were obtained from 1 000 bootstrap replicates. The trees were rooted with *Hamigera avellanea* NRRL 1938. MrBayes 3.2.2 (Ronquist *et al.* 2012) was used to calculate Bayesian posterior probabilities (PP). Optimal partitioning scheme and substitution models were selected using PartitionFinder v1.1.0 as described above. The analyses ran for 10^7 generations, two parallel runs with four chains each were used, every 1 000th tree was retained, and the first 25 % of trees were discarded as burn-in. All alignments are available from the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.7hn1j.

Morphological analysis

Macroscopic characters were studied on agar media Czapek yeast autolysate agar (CYA), CYA with 20 % sucrose agar (CY20S), CYA supplemented with 5 % NaCl (CYAS), Malt extract agar (MEA; Oxoid), MEA with 40 % sucrose agar (M40Y), MEA with 60 % sucrose agar (M60Y), MEA supplemented with 10 % NaCl (MEA10S) and Dichloran 18 % glycerol agar (DG18). Trace elements (0.1 g $ZnSO_4 \cdot 7H_2O$ and 0.5 g $CuSO_4 \cdot 5H_2O$ in 100 ml distilled water) were added to all media to obtain stable pigment production and consistent conidial colours (Smith 1949, Samson *et al.* 2014). Isolates were inoculated at three points on 90 mm plates and incubated for 7 d at 25 °C in darkness. In addition, CY20S and M60Y plates were incubated at 30 °C and 37 °C, respectively. After 7 d of incubation, colony diameters were recorded. Colony texture, degree of sporulation, obverse and reverse colony colours, production of soluble pigments, exudates and ascomata were determined. Colour codes used in description refer to Rayner (1970).

Light microscope preparations were made from 1 wk old colonies grown on M40Y. Ascomata, asci and ascospores were observed after 2 or 4 wks. Lactic acid (60 %) was used as mounting fluid. Ethanol (96 %) was used to remove excess conidia and prevent air bubbles. A Zeiss Stereo Discovery V20 dissecting microscope and Zeiss AX10 Imager A2 light microscope both equipped with Nikon DS-Ri2 cameras and NIS-Elements D v 4.50 software were used to capture digital images.

Cryo Scanning Electron Microscopy (cryo-SEM) observations of ascospores were prepared based on Chen *et al.* (2016), alternatively, an osmium tetroxide method was used for fixation as described by Hubka *et al.* (2013b). To prevent conidia collapsing, agar blocks containing conidial structures were snap-frozen and observed as described in Visagie *et al.* (2013).

Table 1. Section *Aspergillus* strains used in phylogenetic analyses.

Species	Strain nr.[1]	Source	GenBank accession nr.			
			ITS	*BenA*	*CaM*	*RPB2*
Aspergillus aerius	CBS 141771^{T} = DTO 241-G7 = IBT 34446	The Netherlands, air treatment system in production plant, 2013, *J. Houbraken*	LT670916	LT670990	LT670991	LT670992
A. appendiculatus	CBS 374.75^{T} = IMI 278374 = FRR 2793 = JCM 1566 = IBT 34507	Switzerland, Stäfa, smoked sausage, 1971, *P. Blaser*	HE615132	HE801333	HE801318	HE801307
	CBS 101746 = CGMCC 3.04673 (AS 3.4673) (ex-type of *A. aridicola*)	China, Tibet, sheep dung, *H.Z. Kong* & *Z.T. Qi*	HE615133	HE801334	HE801319	HE801308
A. aurantiacoflavus	CBS 141930^{T} = EMSL No. 2903 = CCF 5393 = DTO 355-I1 = IBT 34485	USA, California, San Diego, baby carrier – backpack, 2015, *Ž. Jurjević*	LT670917	LT670993	LT670994	LT670995
	EMSL No. 2693 = CCF 5391 = DTO 355-H7	USA, IL, Chicago, rubber toy imported from China, 2015, *Ž. Jurjević*	LT670918	LT670996	LT670997	LT670998
	EMSL No. 3024 = CCF 5394 = DTO 355-H9	USA, New Jersey, Cherry Hill, cake spread, 2015, *Ž. Jurjević*	LT670919	LT670999	LT671000	LT671001
A. brunneus	CBS 112.26^{T} = CBS 524.65 = IBT 5341 = NRRL 131 = NRRL 134 = ATCC 1021 = IFO 5862 = IMI 211378 = QM 7406 = Thom 4481 = Thom 5633.4 = WB 131 = CCF 5587 (neotype of *A. echinulatus*)	USA, California, fruit (*Ficus carica*), *M.B. Church*	EF652060	EF651907	EF651998	EF651939
	DTO 357-A1 = KAS7575	Canada, house dust, 2015, *C.M. Visagie*	LT670920	LT671002	LT671003	LT671004
	NRRL 133 = CCF 5586	Unknown source, *G. Smith*	EF652061	EF651908	EF651999	EF651940
	NRRL 124 = CBS 113.27 = CCF 5585 (ex-type of *A. medius*)	Unknown source, *W. McRae*	EF652056	EF651904	EF651997	EF651938
	DTO 197-B3 = CBS 117328	Canada, Manitoba, *M. Desjardins*	LT670921	LT671005	LT671006	LT671007
A. caperatus	CBS 141774^{T} = DTO 337-E6 = IBT 34451	South Africa, Robben Island, soil, 2015, *M. Meijer*	LT670922	LT671008	LT671009	LT671010
A. chevalieri	CBS 522.65^{T} = NRRL 78 = ATCC 16443 = IMI 211382 = NRRL A-7803 = Thom 4125.3 = WB 78 = IBT 5680 (neotype of *A. equitis*)	USA, coffee beans, 1916, *C. Thom*	EF652068	EF651911	EF652002	EF651954
	NRRL 79	USA, Indiana, Indianapolis, unknown source, *Dr. Adams*	EF652069	EF651912	EF652003	EF651955
	NRRL 4755	USA, culture contamination, *D.I. Fennell*	EF652071	EF651913	EF652004	EF651956
	CCF 3291 = DTO 355-B6	Czech Republic, Brno, rice, 1999, *V. Ostrý*	FR727116	HE578085	HE578099	HE801314
	CCF 1676 = DTO 355-B7	Czech Republic, Prague, semolina, 1979, *V. Muzikář*	LT670923	LT671011	LT671012	LT671013
	CCF 4788 = KACC 47145 = DTO 355-B8	South Korea, soybeans, 2012, *D.H. Kim*	LT670924	LT671014	LT671015	LT671016
	CGMCC 3.06132 = DTO 348-G5	China, Tibet, soil, 2001	LT670925	LT671017	LT671018	LT671019
	DTO 238-E3	Unknown source, *S. Suhendriani*	LT670926	LT671020	LT671021	LT671022
	CBS 141769 = DTO 088-D7	Madagascar, soil, 2008, *J. Houbraken*	LT670927	LT671023	LT671024	LT671025
	CGMCC 3.06492 = DTO 348-H3	China, Yunnan, moldy peel, 2001	LT670928	LT671026	LT671027	LT671028
	DTO 092-D3	Madagascar, soil, 2008, *J. Houbraken*	LT670929	LT671029	LT671030	LT671031
A. cibarius	KACC 46346^{T} = DTO 197-D3 = IBT 32307 = CCF 4783	South Korea, Icheon, meju, 2011, *S.B. Hong*	JQ918177	JQ918180	JQ918183	JQ918186
	CCF 4098 = NRRL 62493 = DTO 354-I8	Czech Republic, Prague, toenail of 56-year-old woman, 2010, *P. Lysková*	FR848828	FR837968	FR837973	FR837979
	CCF 4235 = NRRL 62492 = DTO 354-I7	Czech Republic, Prague, toenail of 63-year-old man, 2012, *P. Lysková*	HE801341	HE801330	HE801324	HE801313
	CCF 4264 = DTO 354-I9	Spain, Nerja cave, near Málaga, cave sediment (entrance chambre), 2011, *A. Nováková*	HE974462	HE974436	HE806186	HE974428
	KACC 49766 = CCF 4784	The Netherlands, black bean, 2012, *M. Meijer*	LT670930	LT671032	LT671033	LT671034
	EMSL No. 1652 = CCF 5385 = DTO 355-G6	USA, Pennsylvania, child's shoes, 2012, *Ž. Jurjević*	LT670931	LT671035	LT671036	LT671037
	EMSL No. 2498 = CCF 5383 = DTO 355-G7	USA, Washington DC, chocolate glazed frosted donut, 2014, *Ž. Jurjević*	LT670932	LT671040	LT671041	LT671042
	EMSL No. 2865 = CCF 5384 = DTO 355-G8	USA, California, Danville, chocolate chip cookies, 2015, *Ž. Jurjević*	LT670933	LT671043	LT671044	LT671045

Table 1. (Continued).

Species	Strain nr.[1]	Source	GenBank accession nr.			
			ITS	*BenA*	*CaM*	*RPB2*
	CGMCC 3.06498 = DTO 348-H7	China, Hebei, soil, 2001	LT670934	LT671046	LT671047	LT671048
	CGMCC 3.00450 = DTO 348-B5	China, 1952	LT670935	LT671049	LT671050	LT671051
A. costiformis	CBS 101749^{T} = CGMCC 3.04664 (AS 3.4664) = DTO 348-D8 = IBT 34456 = IBT 33662	China, Hebei, moldy paper-box, 1992, *H.Z. Kong*	HE615136	HE801338	HE801320	HE801309
	CCF 4097 = NRRL 62483 = DTO 354-I3	Czech Republic, Prague, toenail of 5-year-old boy, 2010, *P. Lysková*	FR837960	FR837970	FR837974	FR837978
	DTO 326-B4	The Netherlands, cellophane, 2015, *J. Houbraken*	LT670936	LT671052	LT671053	LT671054
	CGMCC 3.06520 = DTO 348-I5	China, Hebei, moldy box, 2001	LT670937	LT671055	LT671056	LT671057
A. cristatus	CBS 123.53^{T} = NRRL 4222 = ATCC 16468 = BCRC 33090 = FRR 1167 = IBT 5355 = IHEM 5619 = IMI 172280 = JCM 1569 = MUCL 15644 = NRRL 4222 = WB 4222 = CCF 5591 (ex-type of *A. cristatellus*)	South Africa, unknown, 1953, *H.J. Swart*	EF652078	EF651914	EF652001	EF651957
	IHEM 2423 = DTO 355-B3	Zaire, Kinshasa, soil, 1984	LT670938	LT671058	LT671059	LT671060
	CCF 4701 = DTO 355-B1	China, Hunan, tea block, 2013, *Q.L. Pan & L. Wang*	KF923732	KF923737	KF923741	KF923734
	CCF 4702 = DTO 355-B2	China, Guangxi, tea block, 2013, *Q.L. Pan & L. Wang*	KF923733	KF923739	LT714711	KF923736
	CGMCC 3.06081 = DTO 348-E9	China, Hubei, soil, 2001	LT670939	LT671061	LT671062	LT671063
A. cumulatus	KACC 47316^{T} = DTO 303-D9 = IBT 34470 = IBT 33670	South Korea, Anseong, rice straw used in meju fermentation	KF928303	KF928297	KF928300	KF928294
	KACC 47513 = DTO 303-D8	South Korea, air of a meju fermentation room	KF928304	KF928298	KF928301	KF928295
	KACC 47514	South Korea, air of a meju fermentation room	KF928305	KF928299	KF928302	KF928296
	EMSL No. 2827 = CCF 5376 = DTO 355-G9	USA, New York, Bronx, bedroom ceiling, 2015, *Ž. Jurjević*	LT670940	LT671064	LT671065	LT671066
A. endophyticus	CBS 141766^{T} = DTO 354-I2 = CCF 5345 = IBT 34511	Czech Republic, Prague, Stromovka park, endophyte of *Acer pseudoplatanus*, 2013, *I. Kelnarová*	LT670941	LT671067	LT671068	LT671069
A. glaucus	CBS 516.65^{T} = NRRL 116 = ATCC 16469 = DTO 197-A1 = IBT 32295 = IMI 211383 = LCP 64.1859 = Thom 5629.C = WB 116	USA, Washington DC, unpainted board (K.B. Raper's residence), 1938, *K.B. Raper*	EF652052	EF651887	EF651989	EF651934
	NRRL 117 = DTO 355-B4 = CCF 5582 (ex-type of *A. mangini*)	USA, Washington DC, unpainted board (K.B. Raper's basement), 1938, *K.B. Raper*	EF652053	EF651888	EF651990	EF651935
	EMSL No. 2529 = CCF 5381 = DTO 355-H1	Puerto Rico, Bayamon, office, air, 2014, *Ž. Jurjević*	LT670942	LT671070	LT671071	LT671072
	NRRL 120 = 117.46 = CBS 532.65 = CCF 5583 (ex-type of *A. umbrosus*)	USA, coffee beans, 1925, *F.A. McCormick*	EF652054	EF651889	EF651991	EF651936
	NRRL 121 = DTO 355-B5 = CCF 5584	Unknown source	EF652055	EF651890	EF651992	EF651937
	EMSL No. 3317 = CCF 5382 = DTO 355-H2	USA, New York, Ulster Park, bedroom, settle plates, 2015, *Ž. Jurjević*	LT670943	LT671073	LT671074	LT671075
A. intermedius	CBS 523.65^{T} = NRRL 82 = ATCC 16444 = DSM 2830 = IBT 5677 = IMI 089278ii = IMI 89278 = LSHBBB 107 = LSHTM 107 = QM 7403 = Thom 5612.107 = WB 82 = CCF 5581	UK, cotton yarn, 1927, *G. Smith*	EF652074	EF651892	EF652012	EF651958
	NRRL 84	Unknown source	EF652070	EF651893	EF652013	EF651959
	NRRL 4817 = DTO 355-B9 = IFO 5322 = IMI 313754 = JCM 23051 = CCF 5608	Unknown country, butter	EF652072	EF651894	EF652014	EF651960
	NRRL 25823	USA, IL, Peoria, soy protein, *A.J. Moyer*	EF652073	EF651895	EF652015	EF651961
	CBS 377.75 (ex-type of *A. spiculosus*)	Spain, Badajoz, soil, *P. Blaser*	HE974459	HE974432	HE974437	HE974425
	CCF 127 = DTO 354-I5	China, industrial material, 1955, *V. Zánová*	HE578060	HE974431	HE578100	HE974426
	CCF 4681 = DTO 354-I6	Czech Republic, Prague, sputum of 55-year-old woman, 2013, *P. Lysková*	LT670944	LT671076	LT671077	LT671078

(*continued on next page*)

Table 1. (Continued).

Species	**Strain nr.**[1]	**Source**	**GenBank accession nr.**			
			ITS	***BenA***	***CaM***	***RPB2***
	CCF 5377 = DTO 355-G5	Czech Republic, Prague, air sampler, surgical operating room, 2014, *A. Ešnerová*	LT670945	LT671079	LT671080	LT671081
	CGMCC 3.03968 = DTO 348-D6	China, unknown source, 1969	LT670946	LT671082	LT671083	LT671084
	CGMCC 3.00664 = DTO 348-C1	Czech Republic, unknown source, 1956	LT670947	LT671085	LT671086	LT671087
A. leucocarpus	CBS 353.68^{T} = IBT 5350 = IMI 278375 = NRRL 3497 = QM 9365 = QM 9707 = CCF 5590	Germany, Giessen, dried sausage, *R. Hadlok*	EF652087	EF651925	EF652023	EF651972
	DTO 357-A2 = KAS7576	Canada, house dust, 2015, *C.M. Visagie*	LT670948	LT671088	LT671089	LT671090
	DTO 174-I5	Madagascar, vanilla sticks, 2012, *J. Houbraken*	LT670949	LT671091	LT671092	LT671093
A. levisporus	CBS 141767^{T} = DTO 355-G4 = EMSL No. 3211 = CCF 5378 = IBT 34512	USA, Missouri, Saint Louis, bedroom, wood base, 2015, *Ž. Jurjević*	LT670950	LT671094	LT671095	LT671096
A. mallochii	CBS 141928^{T} = DTO 357-A5 = KAS7618 = DAOMC 146054	USA, California, San Mateo, pack rat dung, *D. Malloch*	KX450907	KX450889	KX450902	KX450894
	CBS 141776 = DTO 343-G3	The Netherlands, chocolat miroir, 2015	KX450908	KX450890	KX450903	KX450895
A. megasporus	CBS 141929^{T}= DTO 356-H7 = KAS6176 = DAOMC 250799	Canada, Nova Scotia, Wolfville, house dust, 2015, *C.M. Visagie*	KX450910	KX450892	KX450905	KX450897
	CBS 141772 = DTO 048-I3	The Netherlands, Dutch chocolate butter, 2007, *M. Meijer*	KX450911	KX450893	KX450906	KX450898
	DTO 356-H1 = KAS5973 = DAOMC 250800	Canada, New Brunswick, Little Lepreau, house dust, 2015, *C.M. Visagie*	KX450909	KX450891	KX450904	KX450896
A. montevidensis	CBS 491.65^{T} = NRRL 108 = ATCC 10077 = IBT 5685 = IHEM 3337 = IMI 172290 = NRRL 109 = QM 7423 = Thom 5290 = Thom 5633.24 = WB 108	Uruguay, Montevideo, tympanic membrane of human ear, 1932, *R.V. Talice* & *J.E. MacKinnon*	EF652077	EF651898	EF652020	EF651964
	NRRL 89	Unknown source	EF652075	EF651896	EF652016	EF651962
	NRRL 90 = CBS 518.65 (ex-type of *A. hollandicus*)	USA, unknown source, ~1910	EF652076	EF651897	EF652017	EF651963
	NRRL 4716	USA, Missouri, Columbia, candied grapefruit rind, *D.I. Fennell*	EF652079	EF651899	EF652018	EF651965
	NRRL 25850	USA, IL, Peoria, refrigerated bread dough, *R. Graves*	EF652082	EF651900	EF652021	EF651966
	NRRL 35697	USA, IL, Chicago, nasal swab	EF652084	EF651902	EF652022	EF651968
	NRRL A-13891 = CBS 410.65 (ex-type of *A. heterocaryoticus*)	Mexico, *Oryza sativa* kernel, 1963, *C.R. Benjamin*	EU021619	EU021670	EU021687	EU021659
	CBS 651.74 = ATCC 24717 = IMI 174724 = VKM F-1760 (ex-type of *A. vitis*)	Kazakhstan, Alma-Ata, ex grapes, 1968, *L.A. Beljakova*	HE974460	HE974433	HE974441	HE974424
	CCF 3998	Czech Republic, Prague, neck skin of 78-year-old woman, 2008, *M. Skořepová*	FR727117	HE974434	FR751447	HE974418
	CCF 4069	Czech Republic, heel skin of 32-year-old man, Prague, 2007, *M. Skořepová*	FR839679	FR775356	HE974440	HE974419
	CCF 4070	Czech Republic, fingernail of 32-year-old woman, Prague, 2007, *M. Skořepová*	FR848825	FR775335	FR751442	HE974420
	CCF 4071	Czech Republic, Prague, thigh and neck skin of 42-year-old woman, 2010, *P. Lysková*	FR839680	HE974435	FR751449	HE974421
	CCF 4248	Czech Republic, Skrbeň, window sill, 1997, *A. Kubátová*	HE974461	HE801339	HE974442	HE974422
	EMSL No. 2934 = CCF 5379 = DTO 355-H3	USA, PA, Mahanoy City, bedroom, settle plates, 2015, *Ž. Jurjević*	LT670951	LT671097	LT671098	LT671099
	CBS 111.52 = DTO 351-C9	Suriname, plywood, *M.B. Schol-Schwarz*	LT670952	LT671100	LT671101	LT671102
	DTO 147-I4	Hungary, indoor air, 2014, *M. Meijer*	LT670953	LT671103	LT671104	LT671105
	CGMCC 3.03888 = DTO 348-D3	China, mite, 1969	LT670954	LT671106	LT671107	LT671108
A. neocarnoyi	CBS 471.65^{T} = NRRL 126 = ATCC 16924 = IBT 6016 = IMI 172279 = LSHTM A32 = QM 7402 = Thom 5612.A32 = WB 126 = DTO 196-H6 = CCF 5588	Unknown source, *P. Biourge*	EF652057	EF651903	EF651985	EF651942

Table 1. (Continued).

Species	Strain nr.[1]	Source	GenBank accession nr.			
			ITS	*BenA*	*CaM*	*RPB2*
	EXF-10029 = DTO 357-E2	Slovenia, Ljubljana, Slovene Ethnographic museum, air at the sampling of shaman statue originating from Mali, 2016, *P. Zalar*	LT670955	LT671109	LT671110	LT671111
A. niveoglaucus	CBS 114.27^{T} = CBS 517.65 = NRRL 127 = ATCC 10075 = BCRC 33096 = CGMCC 3.04374 = FRR 927 = IBT 5356 = IMI 32050 = JCM 1578 = LSHBA 16 = NRRL 129 = NRRL 130 = QM 1977 = Thom 5612.A16 = Thom 5633 = Thom 5633.7 = Thom 7053.2 = UAMH 6591 = WB 127 = WB 130 = CCF 5589 (lectotype of *A. glauconiveus*)	Unknown source, *A. Blochwitz*	EF652058	EF651905	EF651993	EF651943
	NRRL 128	Unknown source, *G. Smith*	EF652059	EF651906	EF651994	EF651944
	NRRL 136	Unknown source, *G. Smith*	EF652062	EF651909	EF651995	EF651945
	NRRL 137	Unknown source	EF652063	EF651910	EF651996	EF651946
	CCF 4191 = DTO 355-C1	Spain, Andalusia, Málaga, Cueva del Tesoro, cave sediment from the cave wall, 2010, *A. Nováková*	HE801344	HE801332	HE974438	HE974427
	CCM F-530 = CCF 4038	Czech Republic, garlic, *L. Marvanová*	HE578069	HE578086	HE578092	HE578114
	EMSL No. 2211 = CCF 5380 = DTO 355-H8	USA, Montana, Great Falls, air of bathroom, 2013, *Ž. Jurjević*	LT670956	LT671112	LT671113	LT671114
	IHEM 1811 = DTO 355-C3	Belgium, Namur, indoor air, 1983	LT670957	LT671115	LT671116	LT671117
	CBS 101750 = CGMCC 3.04665 (AS 3.4665) = DTO 197-B4 (ex-type of *A. parviverruculosus*)	China, Hebei, soil	HE615135	HE801331	HE801323	HE801312
	CCF 4787 = KACC 47144 = DTO 355-C4	South Korea, soybeans, 2012, *D.H. Kim*	LT670958	LT671118	LT671119	LT671120
	CCF 4790 = KACC 47147 = DTO 355-C5	South Korea, soybeans, 2012, *D.H. Kim*	LT670959	LT671121	LT671122	LT671123
	CGMCC 3.06092 = DTO 348-F3	China, Guangdong, cashew Kernel, 2001	LT670960	LT671124	LT671125	LT671126
A. osmophilus	CBS 134258^{T} = IRAN 2090C = DTO 354-C1	Iran, East Azerbaijan province, Marand, *Triticum aestivum* leaf, 2006, *B. Asgari*	KC473921	LT671127	LT671128	LT671129
A. porosus	CBS 141770^{T} = DTO 262-D7 = IBT 34443	Turkey, soil, 2013, *A. Yoltas*	LT670961	LT671130	LT671131	LT671132
	DTO 308-D1	Turkey, soil, 2014, *R. Demirel*	LT670962	LT671133	LT671134	LT671135
	CBS 375.75 = DTO 197-C4	Israel, *Arachis hypogaea* fruit, *P. Blaser*	LT670963	LT671136	LT671137	LT671138
	DTO 262-D4	Turkey, soil, 2013, *A. Yoltas*	LT670964	LT671139	LT671140	LT671141
	DTO 262-D2	Turkey, soil, 2013, *A. Yoltas*	LT670965	LT671142	LT671143	LT671144
A. proliferans	CBS 121.45^{T} = NRRL 1908 = IBT 6213 = IMI 016105ii = IMI 016105iii = IMI 16105 = LSHB BB.82 = MUCL 15625 = NCTC 6546 = QM 7462 = UC 4303 = WB 1908 = CCF 5580	UK, Manchester, cotton yarn, *G. Smith*	EF652064	EF651891	EF651988	EF651941
	DTO 322-A2	The Netherlands, egg waffles, 2014, *M. Meijer*	LT670966	LT671145	LT671146	LT671147
	CCF 4192 = DTO 355-C6	Spain, Andalusia, Aracena, Gruta de la Maravillas, cave sediment, 2010, *A. Nováková*	HE615128	HE801328	HE801316	HE801305
	NRRL 114 = DTO 355-C7 = CCF 5579	USA, Massachusetts, unknown source	EF652051	EF651886	EF651987	EF651933
	CCF 4096 = NRRL 62482 = DTO 355-C8	Czech Republic, Prague, palm skin, 28-year-old woman, 2008, *M. Skořepová*	FR848827	FR775375	HE650908	HE801303
	CCF 4115 = NRRL 62497 = DTO 355-C9	Czech Republic, Prague, toenail of 64-year-old man, 2010, *P. Lysková*	FR851850	FR851855	HE578090	HE578107
	CCF 4146 = NRRL 62494 = DTO 355-D1	Czech Republic, Prague, toenail of 48-year-old man, 2011, *P. Lysková*	HE578067	HE578076	HE650909	HE801304
	NRRL 71 = DTO 355-D2 = CCF 5578	USA, Maryland, leafhoppers, *V.K. Charles*	EF652047	EF651885	EF651986	EF651932
	CCF 4232	Czech Republic, Opava, stuffed bird, 2010, *M. Polásek*	HE615129	HE801329	HE801317	HE801306
	EMSL No. 2207 = CCF 5395 = DTO 355-H5	USA, Pennsylvania, Yardley, air of living room, 2013, *Ž. Jurjević*	LT670967	LT671148	LT671149	LT671150
	EMSL No. 2791 = CCF 5392 = DTO 355-H6	USA, New York, Troy, basement, settle plates, 2015, *Ž. Jurjević*	LT670968	LT671151	LT671152	LT671153

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Table 1. (Continued).

Species	**Strain nr.**[1]	**Source**	**GenBank accession nr.**			
			ITS	***BenA***	***CaM***	***RPB2***
	CCF 4789 = KACC 47146 = DTO 355-D3	South Korea, soybeans, 2012, *D.H. Kim*	LT670969	LT671154	LT671155	LT671156
A. pseudoglaucus	CBS 123.28^{T} = NRRL 40 = ATCC 10066 = IBT 5353 = IMI 016122 = IMI 016122ii = LSHBA 19 = MUCL 15624 = QM 7463 = Thom 5343 = WB 40 (lectotype of *A. glaucoaffinis*)	Unknown source, 1929, *A. Blochwitz*	EF652050	EF651917	EF652007	EF651952
	NRRL 13 = CBS 529.65 (ex-type of *A. reptans*)	France, *Prunus domestica*, *da Fonseca*	EF652048	EF651915	EF652005	EF651950
	NRRL 17	USA, wrist skin	EF652049	EF651916	EF652006	EF651951
	NRRL 25865	Japan, Tokyo, unknown source, *T. Ohtsuki*	EF652065	EF651918	EF652008	EF651953
	CBS 101747 = CGMCC 3.04674 (AS 3.4674) (ex-type of *A. fimicola*)	China, Tibet, animal dung	HE615130	HE801335	HE801321	HE801310
	CBS 379.75 (ex-type of *A. glaber*)	Switzerland, Zuoz, *Vaccinium myrtillus* leaf, *P. Blaser*	HE615131	HE801336	HE801322	HE801311
	CCF 3283	Czech Republic, Prague, 2002, *A. Kubátová*	FR727114	FR775360	HE974439	HE578110
	CCF 4011	Czech Republic, Prague, back skin of 39-year-old woman, 2008, *M. Skořepová*	FR839678	FR775358	FR751446	HE578111
	EMSL No. 1780 = CCF 5388 = DTO 355-I2	USA, Pennsylvania, floor swab, 2012, *Ž. Jurjević*	LT670970	LT671157	LT671158	LT671159
	EMSL No. 2779 = CCF 5389 = DTO 355-I3	USA, Florida, Melbourne, vent, settle plates, 2015, *Ž. Jurjević*	LT670971	LT671160	LT671161	LT671162
	EMSL No. 2809 = CCF 5386	USA, New York, Endicott, office, settle plates, 2015, *Ž. Jurjević*	LT670972	LT671163	LT671164	LT671165
	EMSL No. 2474 = CCF 5387 = DTO 355-I4	USA, New Jersey, Piscataway, air, basement, 2014, *Ž. Jurjević*	LT670973	LT671166	LT671167	LT671168
	EMSL No. 2853 = CCF 5390 = DTO 355-I5	USA, Missouri, St. Louis, cheddar cheese, 2015, *Ž. Jurjević*	LT670974	LT671169	LT671170	LT671171
	CBS 108961 = DTO 351-D2	The Netherlands, Woerden, parmezan cheese, *J. Houbraken*	LT670975	LT671172	LT671173	LT671174
	DTO 147-G3	Hungary, indoor air, 2010	LT670976	LT671175	LT671176	LT671177
	CGMCC 3.00460 = DTO 348-B9	China, tea, 1952	LT670977	LT671178	LT671179	LT671180
A. ruber	CBS 530.65^{T} = NRRL 52 = ATCC 16441 = IBT 5453 = IMI 211380 = JCM 22942 = QM 1973 = Thom 5599B = WB 52	Unknown source	EF652066	EF651920	EF652009	EF651947
	NRRL 76	Unknown source, *G. Smith*	EF652067	EF651921	EF652011	EF651948
	NRRL 5000 = CBS 464.65 (ex-type of *A. athecius*)	UK, coffee beans, 1965, *E. Yuill*	EF652080	EF651922	EF652010	EF651949
	CBS 101748 = CGMCC 3.04632 (AS 3.4632) (ex-type of *A. tuberculatus*)	China, Shanxi, soil	HE615134	HE801337	HE801325	HE801315
	CCF 2920	Czech Republic, Nymburk, malt dust, 1993, *A. Kubátová*	FR727112	FR775357	FR751444	HE974430
	CCF 4377	Czech Republic, Prague, toenail of 60-year-old woman, 2011, *P. Lysková*	HE578065	HE578087	HE578098	LT671190
	CBS 104.18 = DTO 351-C4	Unknown source, 1918, *O. Goethals*	LT670978	LT671181	LT671182	LT671183
	DTO 238-C4	Unknown source, *Rahmawati*	LT670979	LT671184	LT671185	LT671186
	CGMCC 3.00457 = DTO 348-B6	China, tea, 1952	LT670980	LT671187	LT671188	LT671189
A. sloanii	CBS 138177^{T} = DTO 245-A1 = IBT 34509 = CCF 4927	UK, Middlesex, house dust, 2010, *E. Whitfield & K. Mwange*	KJ775540	KJ775074	LT671038	KX463365
	CBS 138176 = DTO 244-I8 = CCF 4926	UK, Middlesex, house dust, 2010, *E. Whitfield & K. Mwange*	KJ775539	KJ775073	LT671039	KX463364
	CBS 138231 = DTO 245-A6	UK, Middlesex, house dust, 2010, *E. Whitfield & K. Mwange*	KJ775541	KJ775075	KJ775311	KX450899
	CBS 138178 = DTO 245-A8	UK, Middlesex, house dust, 2010, *E. Whitfield & K. Mwange*	KJ775542	KJ775076	KJ775313	KX450900
	CBS 138179 = DTO 245-A9	UK, Middlesex, house dust, 2010, *E. Whitfield & K. Mwange*	KJ775543	KJ775077	KJ775314	KX450901

Table 1. (Continued).

Species	Strain nr.[1]	Source	GenBank accession nr.			
			ITS	*BenA*	*CaM*	*RPB2*
A. tamarindosoli	CBS 141775^{T} = DTO 054-A8 = IBT 34432	Thailand, Hua Hin, soil under tamarind, 2007, *R.A. Samson* & *J. Houbraken*	LT670981	LT671191	LT671192	LT671193
A. teporis	CBS 141768^{T} = DTO 058-E5 = IBT 34513	The Netherlands, heat treated corn kernels, 2008, *M. Meijer*	LT670982	LT671194	LT671195	LT671196
A. tonophilus	CBS 405.65^{T} = NRRL 5124 = ATCC 16440 = ATCC 36504 = IBT 21230 = IMI 108299 = QM 8599 = WB 5124 = CCF 5592	Japan, Tokyo, binocular lens, *T. Ohtsuki*	EF652081	EF651919	EF652000	EF651969
	DTO 356-H6 = KAS6175	Canada, house dust, 2015, *C.M. Visagie*	LT670915	LT671197	LT671198	LT671199
	CCF 4785 = KACC 45365 = DTO 355-A2	South Korea, meju, 2012, *S.B. Hong*	LT670984	LT671200	LT671201	LT671202
	CCF 4786 = KACC 47150 = DTO 355-A1	South Korea, soybeans, 2012, *D.H. Kim*	LT670985	LT671203	LT671204	LT671205
A. xerophilus	CBS 938.73^{T} = NRRL 6131 = IBT 5429 = IBT 5489 = IBT 34503 = DTO 083-A2 = CCF 5593	Egypt, Western desert, desert soil, *J. Mouchacca*	EF652085	EF651923	EF651983	EF651970
	NRRL 6132 = CBS 755.74	Egypt, Western desert, desert soil, *J. Mouchacca*	EF652086	EF651924	EF651984	EF651971
A. zutongqii	CBS 141773^{T} = CGMCC 3.13917 = DTO 349-E1 = IBT 34450	China, Beijing, peanut shell, 2008, *L. Wang*	LT670986	LT671206	LT671207	LT671208
	CGMCC 3.06103 = DTO 348-F7	China, Ningxia, 2001	LT670987	LT671209	LT671210	LT671211
	CGMCC 3.03980 = DTO 348-D7	China, 1969, *Z.T. Qi*	LT670988	LT671212	LT671213	LT671214
	CGMCC 3.03961 = DTO 348-D5	China, ocular lens, 1969, *Z.T. Qi*	LT670989	LT671215	LT671216	LT671217

[1] Culture collection designations: CBS, Culture Collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC, China General Microbiological Culture Collection Centre, Beijing, China; NRRL, Agricultural Research Service Culture Collection, Peoria, Illinois, USA; KACC, Korean Agricultural Culture Collection, Wanju, South Korea; CCF, Culture Collection of Fungi, Prague, Czech Republic; CCM (F-), Czech Collection of Microorganisms, Brno, Czech Republic; IBT, culture collection of the DTU Systems Biology, Lyngby, Denmark; DAOMC, Canadian Collection of Fungal Cultures, at the Ottawa Research and Development Centre – Agriculture and Agri-Food, Ottawa, Canada; BCCM/IHEM, Belgian Coordinated Collections of Microorganisms; DTO, working collection of the Applied and Industrial Mycology department (DTO) housed at the Westerdijk Fungal Biodiversity Institute.

Table 2. Primers used in this study for amplification and sequencing.

Locus	Primer	Amplification	Annealing temp (°C)	Cycles	Orientation	Sequence (from 5′ to 3′)	References
ITS	V9G (General, Gen.)	Standard	55 (alt. 52)	35	Forward	TTACGTCCCTGCCCTTTGTA	de Hoog & Gerrits van den Ende (1998)
	LS266 (Gen.)				Reverse	GCATTCCCAAACAACTCGACTC	Masclaux *et al.* (1995)
	ITS1 (Alternative, Alt.)				Forward	TCCGTAGGTGAACCTGCGG	White *et al.* (1990)
	ITS4 (Alt.)				Reverse	TCCTCCGCTTATTGATATGC	White *et al.* (1990)
BenA	Bt2a (Gen.)	Standard	55 (alt. 52)	35	Forward	GGTAACCAAATCGGTGCTGCTTTC	Glass & Donaldson (1995)
	Bt2b (Gen.)				Reverse	ACCCTCAGTGTAGTGACCCTTGGC	Glass & Donaldson (1995)
	T10 (Alt.)				Forward	ACGATAGGTTCACCTCCAGAC	O'Donnell & Cigelnik (1997)
	Ben2F (Alt.)				Forward	TCCAGACTGGTCAGTGTGTAA	Hubka & Kolařík (2012)
CaM	CMD5 (Gen.)	Standard	55 (alt. 52)	35	Forward	CCGAGTACAAGGAGGCCTTC	Hong *et al.* (2005)
	CMD6 (Gen.)				Reverse	TTTYTGCATCATRAGYTGGAC	Hong *et al.* (2005)
	CF1L (Alt.)				Forward	GCCGACTCTTTGACYGARGAR	Peterson (2008)
	CF1M (Alt.)				Forward	AGGCCGAYTCTYTGACYGA	Peterson (2008)
	CF4 (Alt.)				Reverse	TTTYTGCATCATRAGYTGGAC	Peterson (2008)
RPB2	fRPB2-5F (Gen.)	Standard	55 (alt. 52 or 50)	35	Forward	GAYGAYMGWGATCAYTTYGG	Liu *et al.* (1999)
	fRPB2-7CR (Gen.)				Reverse	CCCATRGCTTGYTTRCCCAT	Liu *et al.* (1999)
	fRPB2ResF100 (Alt.)	Touch-up	44-46-48	5-5-30	Forward	TGAARTAYGCICTTGCYAC	Sklenář *et al.* (2017)
	fRPB2ResR950 (Alt.)				Reverse	CARTGYGTCCADGTRTGKGC	Sklenář *et al.* (2017)
	RPB2-F50-CanAre (Alt.)	Touch-down	65-64-63-62-61-60-55	1-1-1-1-1-1-38	Forward	TTGAACATTGGTGTCAAGGC	Jurjević *et al.* (2015)

Table 3. Overview of alignments characteristics used for phylogenetic analyses (excluding outgroup).

	ITS	*BenA*	*CaM*	*RPB2*	*BenA* + *CaM* + *RPB2*
Length (bp)	538	402	710	969	2 081
Variable position	76	164	284	286	734
Parsimony informative sites	52	149	251	243	643

Table 4. Partition-merging results and best substitution model for each partition according to Bayesian information criterion (BIC) as proposed by PartitionFinder v1.1.0.

Dataset	Phylogenetic method	Partitioning scheme (substitution model)
ITS	ML	ITS1 + ITS2 (HKY+G); 5.8S (JC+I)
	BI	ITS1 + ITS2 (HKY+G); 5.8S (JC+I)
BenA	ML	introns (K80+G); 1st codon positions (JC+I); 2nd codon positions (JC); 3rd codon positions (K81uf+G)
	BI	introns (K80+G); 1st codon positions (JC+I); 2nd codon positions (JC); 3rd codon positions (HKY+G)
CaM	ML	introns (HKY+I+G); 1st codon positions (TrN+I); 2nd codon positions (F81); 3rd codon positions (TrN+G)
	BI	introns (HKY+I+G); 1st codon positions (HKY+I); 2nd codon positions (F81); 3rd codon positions (GTR+G)
RPB2	ML	1st codon positions (TrN+I+G); 2nd codon positions (JC+I); 3rd codon positions (TrNef+G)
	BI	1st + 2nd codon positions (K80+I+G); 3rd codon positions (HKY+G)
BenA + *CaM* + *RPB2*	ML	*BenA* + *CaM* introns (K81uf+I+G); 1st codon positions of *BenA* + *CaM* + *RPB2* (TrN+I+G); 2nd codon positions of *BenA* + *CaM* + *RPB2* (F81+I); 3rd codon positions of *BenA* + *CaM* (GTR+G); 3rd codon positions of *RPB2* (TrNef+G)
	BI	*BenA* + *CaM* introns (HKY+I+G); 1st codon positions of *BenA* + *CaM* + *RPB2* (GTR+I+G); 2nd codon positions of *BenA* + *CaM* + *RPB2* (F81+I); 3rd codon positions of *BenA* + *CaM* (GTR+G); 3rd codon positions of *RPB2* (HKY+G)

Extrolite analysis

Strains were incubated on DG18, CY20S and YES for 7 d at 25 °C in darkness. Two agar plugs (diameter 6 mm) were subsequently cut out from each medium and placed in an Eppendorf plastic vial and extracted with ethyl acetate / isopropanol (75:25, vol/vol) with 1 % formic acid. After ultrasonication for 50 mins the extraction liquid was transferred to another Eppendorf vial and the organic solvents evaporated. The chemical content was re-dissolved in 400 µl methanol and centrifuged at 13 400 rpm for 3 min. One µl liquid was injected into a HPLC-DAD with an additional fluorescence detector as described by Nielsen *et al.* (2011). For fluorescence detection, the excitation wavelength was 230 nm and the emission wavelengths were 333 nm and 450 nm. This allowed for sensitive detection of ochratoxins, aflatoxins, citrinin and indol alkaloids. Alkylphenone retention indices were calculated according to Frisvad & Thrane (1987, 1993).

RESULTS AND DISCUSSION

Phylogeny

The phylogenetic relationships between 163 sect. *Aspergillus* strains were studied using concatenated sequence data of three loci: *BenA*, *CaM* and *RPB2*. In the 50 % majority consensus ML tree shown in Fig. 1, members of sect. *Aspergillus* are resolved in three major clades (named here the *A. ruber*, *A. glaucus* and *A. chevalieri* clades) and several, mostly basal, lineages containing one or two species. The Bayesian consensus tree was nearly identical to ML and therefore Bayesian posterior probabilities (PP) are shown on the ML tree nodes.

The ***A. ruber* clade** contains *A. appendiculatus*, *A. cumulatus*, *A. mallochii*, *A. pseudoglaucus*, *A. ruber*, *A. sloanii*, *A. tonophilus*, and a new species *A. zutongqii*, with four strains originating from China (CBS 141773, CGMCC 3.03961, CGMCC 3.03980, CGMCC 3.06103) forming a sister clade to *A. ruber*. Its placement as sister to *A. ruber* is further supported by the single-gene trees (Figs 2–4). *Aspergillus fimicola* (ex-type: CBS 101747), *Aspergillus glaber* (ex-type: CBS 379.75) and *A. reptans* (ex-type: NRRL 13) resolve in the *A. pseudoglaucus* lineage; *A. tuberculatus* (ex-type: CBS 101748) and *A. athecius* (ex-type: NRRL 5000) in the *A. ruber* lineage; and *A. aridicola* (ex-type: CBS 101746) in the *A. appendiculatus* lineage. Very similar topologies of the *A. ruber* clade was produced by phylogenetic analyses based on *BenA* (86 % BS / 0.97 PP; Fig. 2) and *RPB2* (96 % BS / 0.79 PP; Fig. 4), while these topologies were not supported by *CaM*-based phylogeny (Fig. 3). All eight lineages within the clade were strongly supported in the combined phylogenetic analyses as well as single-gene analyses (BS $\geq$ 90 %, PP $\geq$ 0.98). The exception is in the *BenA* phylogeny where nodes bearing *A. mallochii* and *A. appendiculatus* had limited support (79 % BS / 0.92 PP and 76 % BS / 0.88 PP, respectively; Fig. 2).

The ***A. glaucus* clade** contains *A. brunneus*, *A. glaucus*, *A. megasporus*, *A. niveoglaucus*, *A. neocarnoyi*, *A. proliferans* and three new species (Fig. 1). Three isolates originating from the USA (CBS 141930, CCF 5391 and CCF 5394) formed a well-supported clade (94 % BS / 1.00 PP) closely related to *A. glaucus* and *A. proliferans* (Fig. 1); this clade showed moderate to high support in *BenA* and *RPB2* phylogenies (Figs 2, 4), but weak support in the *CaM* tree (Fig. 3). The clade is introduced as a new species, *A. aurantiacoflavus*, in the taxonomy section. All three species (*A. glaucus*, *A. proliferans* and *A. aurantiacoflavus*) have fixed single-nucleotide polymorphisms at *BenA*, *CaM* and *RPB2* loci that guarantee their reliable discrimination from each other (positions in particular alignments available in Dryad Digital Repository — *BenA*: positions 53, 138, 219 and 297; *CaM*: positions 2, 131, 460, 600; *RPB2*: positions 211, 279, 666). CBS 141771 and CBS 141767 formed distinct single-isolate lineages nested in the *A. glaucus* clade but with unresolved position. They are distantly related to each other and remaining taxa in the clade based on *CaM* and *RPB2* data, and are proposed below as new species *A. aerius* and *A. levisporus*. In the *BenA* phylogeny, these two species are resolved on a

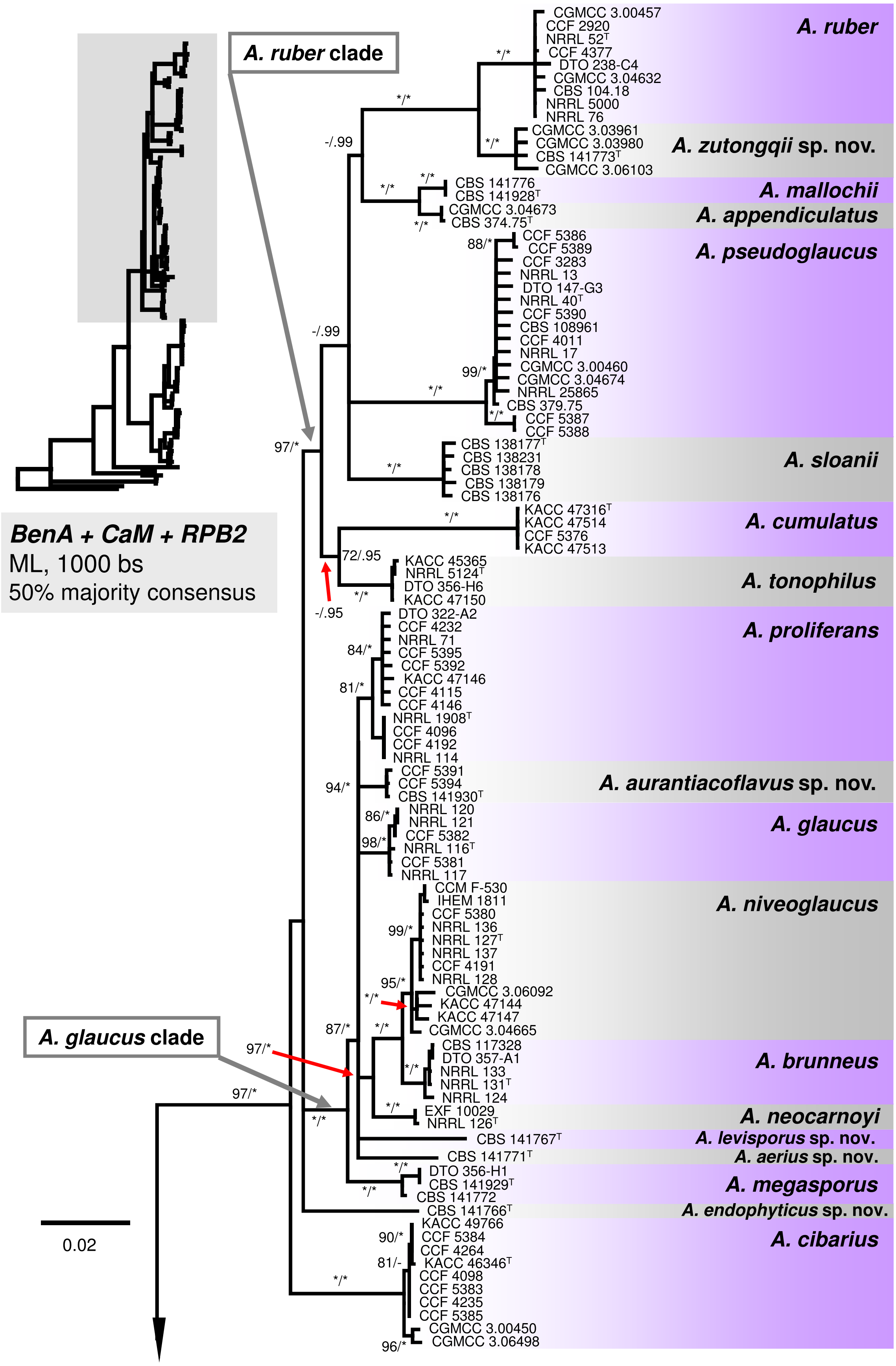


Fig. 1. A 50 % majority rule Maximum likelihood consensus tree based on combined dataset of *BenA*, *CaM* and *RPB2* sequences showing the relationship of species within *Aspergillus* sect. *Aspergillus*. Dataset contained 164 taxa, other alignment characteristics, partitioning scheme and nucleotide substitution models are listed in Tables 3–4. Maximum likelihood bootstrap proportion (bs) and Bayesian posterior probability (pp) are appended to nodes; only bs $\geq$ 70 % and pp $\geq$ 95 % are shown, lower supports are indicated with a hyphen, whereas asterisks indicate full support (100 % bs or 1.00 pp); ex-type strains are designated by a superscript T. The tree is rooted with *Hamigera avellanea* NRRL 1938^T.

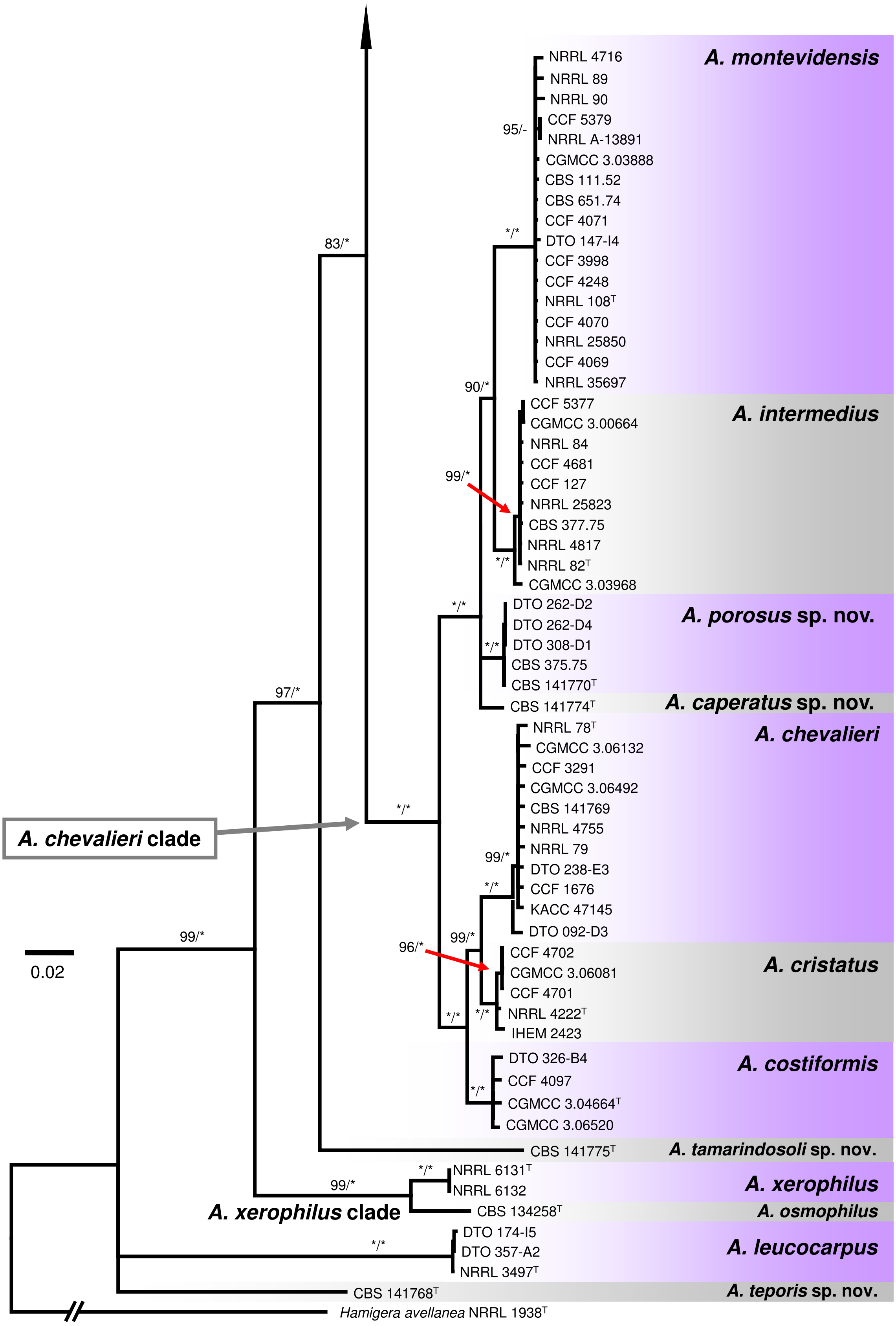


Fig. 1. (Continued).

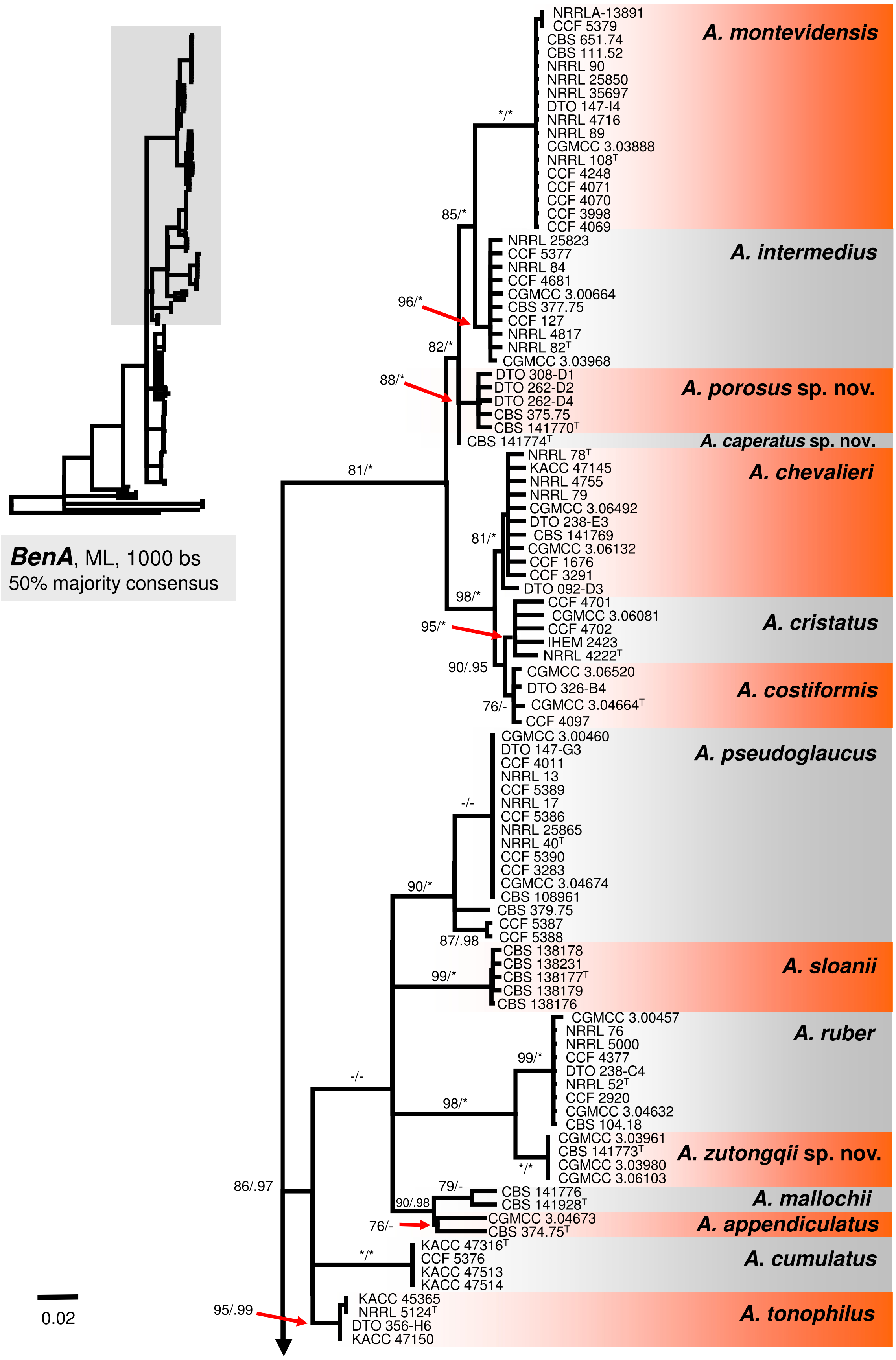


Fig. 2. A 50 % majority rule Maximum likelihood consensus tree based on partial β-tubulin (*BenA*) sequences showing the relationship of species within *Aspergillus* sect. *Aspergillus*. Maximum likelihood bootstrap proportion (bs) and Bayesian posterior probability (pp) are appended to nodes; only bs ≥ 70 % and pp ≥ 95 % are shown, lower supports are indicated with a hyphen, whereas asterisks indicate full support (100 % bs or 1.00 pp); ex-type strains are designated by a superscript T. The tree is rooted with *Hamigera avellanea* NRRL 1938T.

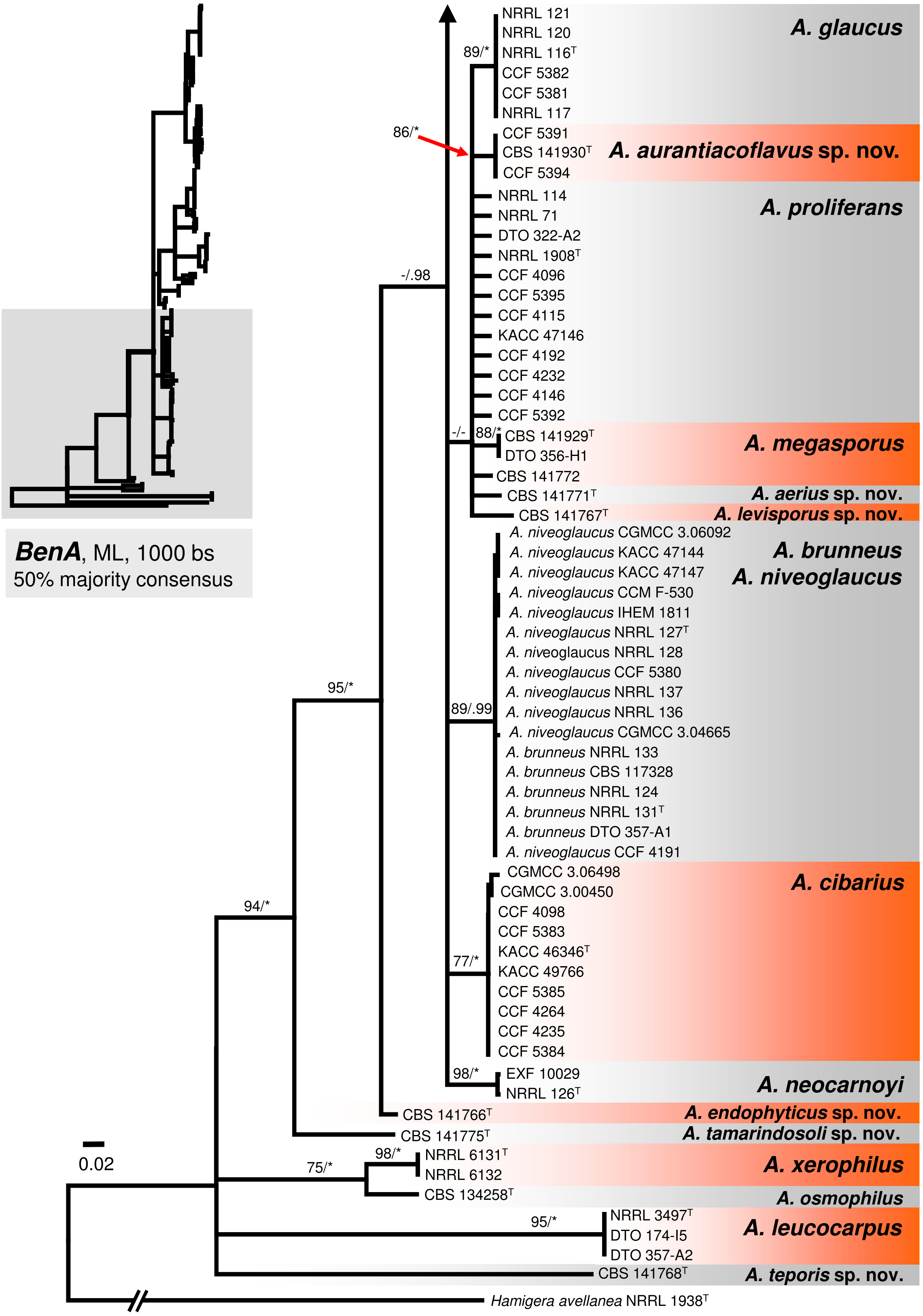


Fig. 2. (Continued).

weakly supported branch with *A. proliferans*, *A. glaucus*, *A. aurantiacoflavus* and *A. megasporus* (Fig. 2), but their sequences contain numerous substitutions sufficient for reliable identification. *Aspergillus medius* (ex-type: NRRL 124) belongs in the *A. brunneus* lineage, *A. parviverruculosus* (ex-type: CBS 101750) in the *A. niveoglaucus* lineage, and *A. manginii* (ex-type: NRRL 117) and *A. umbrosus* (ex-type: NRRL 120) in the *A. glaucus* lineage. The *A. proliferans* lineage includes a strictly anamorphic ex-type strain NRRL 1908 and numerous isolates producing eurotium-like sexual state. Tree topologies of the *A. glaucus* clade in the *CaM*, *RPB2* and combined trees are nearly identical (Figs 1, 3, 4). In contrast, the *BenA* locus has only limited discriminatory power in this clade and many species were collapsed in a polytomy (Fig. 2). But still *BenA* sequences are sufficient for identification of all species except *A. brunneus* and *A. niveoglaucus*. Species represented by at least two strains

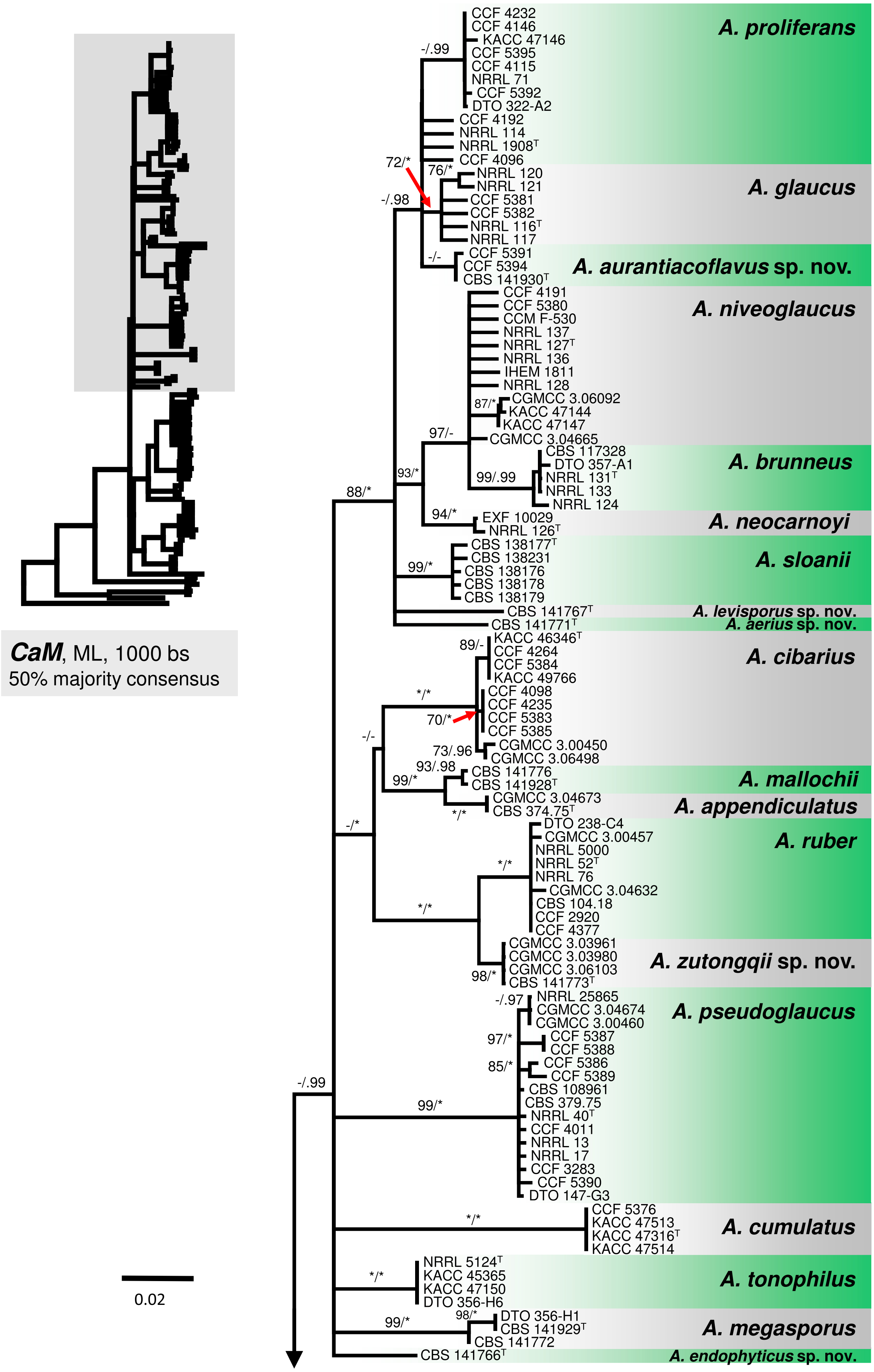


Fig. 3. A 50 % majority rule Maximum likelihood consensus tree based on partial calmodulin (*CaM*) sequences showing the relationship of species within *Aspergillus* sect. *Aspergillus*. Maximum likelihood bootstrap proportion (bs) and Bayesian posterior probability (pp) are appended to nodes; only bs $\geq$ 70 % and pp $\geq$ 95 % are shown, lower supports are indicated with a hyphen, whereas asterisks indicate full support (100 % bs or 1.00 pp); ex-type strains are designated by a superscript T. The tree is rooted with *Hamigera avellanea* NRRL 1938^{T}.

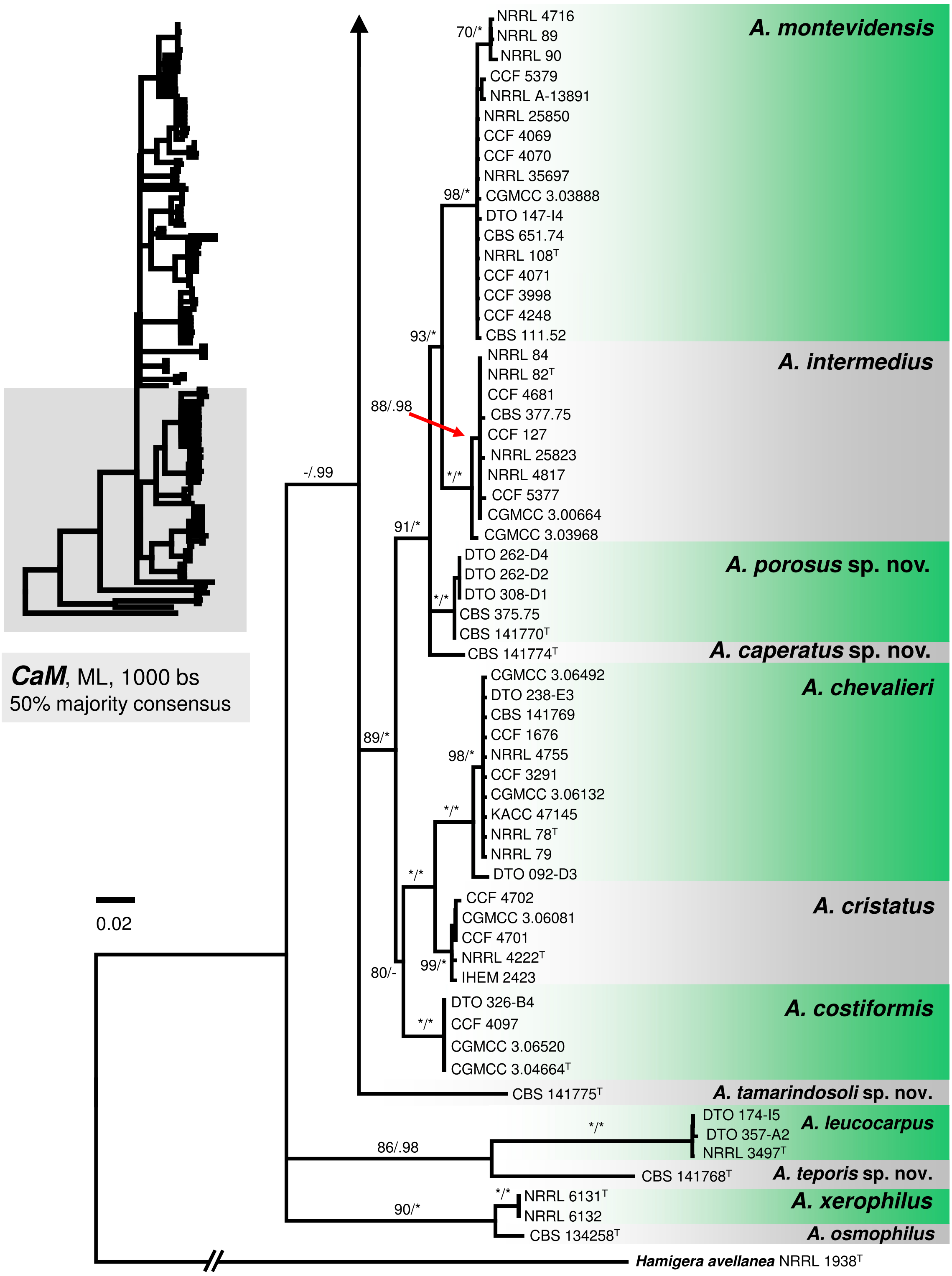


Fig. 3. (Continued).

usually gained high or moderate support in ML and BI analyses based on combined data, or *CaM* and *RPB2* genes (Figs 1, 3, 4) except *A. aurantiacoflavus*, *A. glaucus* and *A. proliferans* that were weakly supported in single-gene phylogenies. However, recognition of these species is supported by phenotype, especially by morphology of ascospores (see below). On the other hand, additional strongly supported clades delimited by same analyses (Figs 1, 3, 4) within *A. glaucus*, *A. niveoglaucus* and *A. proliferans* lineages, had no or very limited phenotypic support, which is the reason why we decided for broader species concept rather than for splitting these species.

The ***A. chevalieri* clade** includes *A. chevalieri*, *A. costiformis*, *A. cristatus*, *A. intermedius*, *A. montevidensis* and two new species *A. caperatus* and *A. porosus*. *Aspergillus caperatus* is represented by CBS 141774 from South Africa. *Aspergillus porosus* is represented by five strains originating from Turkey and Israel (CBS 141770, CBS 375.75, DTO 308-D1, DTO 262-D2, DTO 262-D4), they formed a clade with full support that is related to *A. caperatus*, *A. intermedius* and *A. montevidensis* (Fig. 1). The topology of this subclade is identical in single-gene phylogenies and all lineages are strongly supported (Figs 2–4). The rest three species in the

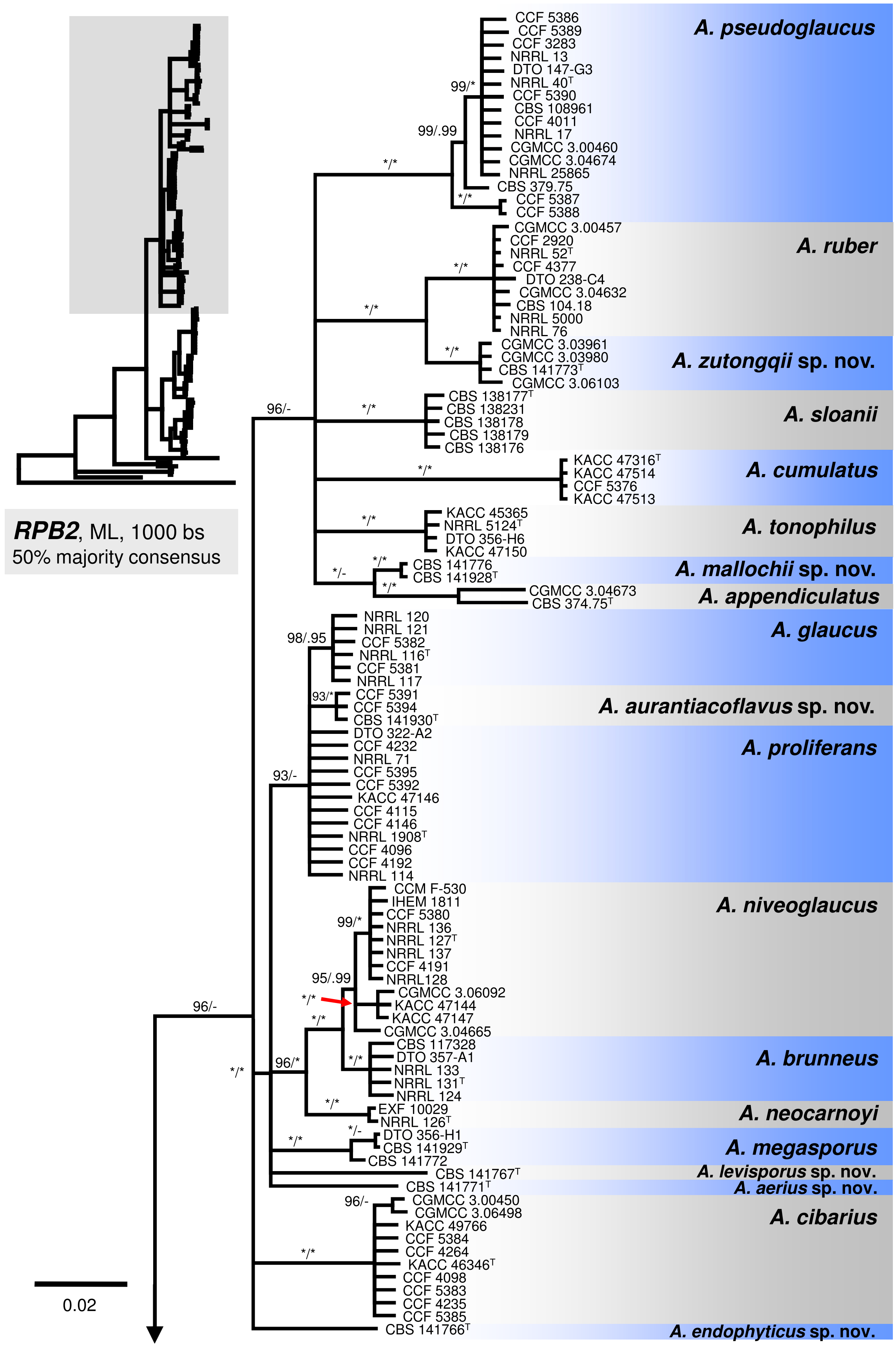


Fig. 4. A 50 % majority rule Maximum likelihood consensus tree based on partial RNA polymerase II second largest subunit (*RPB2*) sequences showing the relationship of species within *Aspergillus* sect. *Aspergillus*. Maximum likelihood bootstrap proportion (bs) and Bayesian posterior probability (pp) are appended to nodes; only bs ≥ 70 % and pp ≥ 95 % are shown, lower supports are indicated with a hyphen, whereas asterisks indicate full support (100 % bs or 1.00 pp); ex-type strains are designated by a superscript T. The tree is rooted with *Hamigera avellanea* NRRL 1938^{T}.

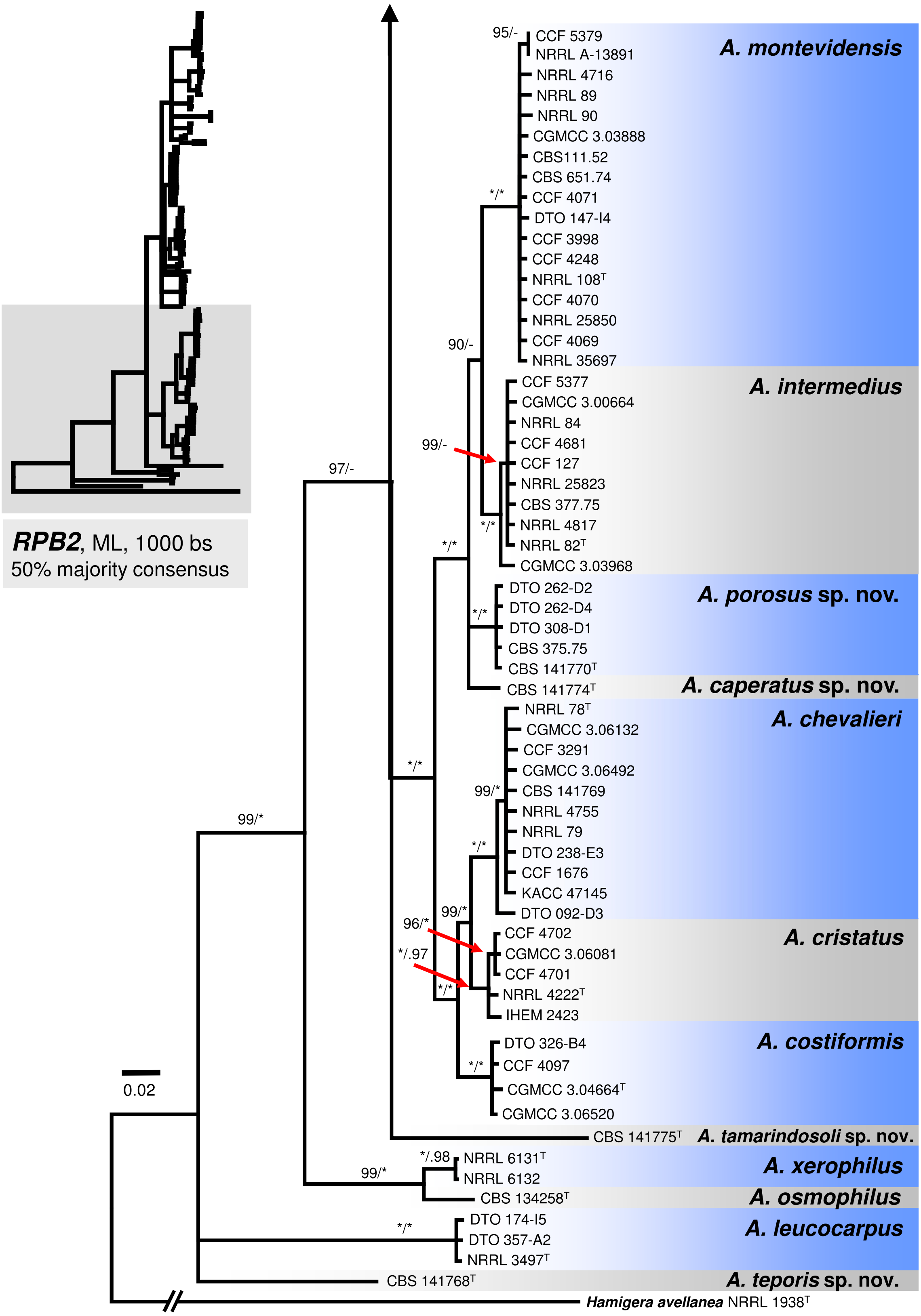


Fig. 4. (Continued).

A. chevalieri clade cluster together and form another strongly supported subclade (Fig. 1) with highly congruent topology shown in single-gene phylogenies (Figs 2–4). *Aspergillus spiculosus* (ex-type: CBS 377.75) is included in the *A. intermedius* lineage; *A. hollandicus* (ex-type: CBS 518.65), *A. heterocaryoticus* (ex-type: CBS 410.65) and *A. vitis* (ex-type: CBS 651.74) in the *A. montevidensis* lineage.

The remaining taxa belonging to sect. *Aspergillus* were distantly related to species from these three main clades and formed remote lineages with not fully resolved or basal position in the trees. *Aspergillus cibarius* and strain CBS 141766 (described below as *A. endophyticus*) were resolved in a basal position adjacent to *A. ruber* and *A. glaucus* clades (Fig. 1); their position varies between single-gene trees (Figs 2–4).

Aspergillus xerophilus and closely related *A. osmophilus* form *A. xerophilus* clade, *A. leucocarpus*, *A. tamarindosoli* and *A. teporis* formed basal lineages distantly related to core species of sect. *Aspergillus* (Figs 1–4).

ITS sequences do not contain sufficient variation for distinguishing among sect. *Aspergillus* species (Fig. 5), and therefore this locus was excluded from the combined phylogenetic analysis. Only five species had unique ITS sequences (*A. tamarindosoli*, *A. xerophilus*, *A. osmophiluc*, *A. leucocarpus* and *A. teporis*; Fig. 5); identical sequence is shared for species from the *A. chevalieri* clade (n = 7); *A. appendiculatus* and *A. mallochii*; and *A. ruber* and *A. zutongqii*. All remaining species (n = 15) are indistinguishable by ITS sequences. Intraspecific single-nucleotide polymorphisms were observed in sequences of *A. proliferans*, *A. tonophilus*, *A. intermedius*, *A. costiformis* and *A. chevalieri*.

Peterson (2008) accepted 15 species in sect. *Aspergillus* based on congruence analysis of *BenA*, *CaM*, ID and *RPB2*. Fourteen sexual species were placed under the *Eurotium* name, the only anamorphic species *A. proliferans* formed a monophylic group with two ascomata producing strains identified as "*Eurotium rubrum*" and "*E. mangini*" (NRRL 71 and NRRL 114). The phylogenetic identity of anamorphic ex-type strain NRRL 1908 and other ascosporic strains was additionally supported by Hubka *et al.* (2012) and Asgari *et al.* (2014). Hubka *et al.* (2013a) applied the GCPSR criteria in sect. *Aspergillus* based on the same four loci and adopted *Aspergillus* names for *Eurotium* species. In their study, 17 species were accepted, all of which can be distinguished by *CaM* or *RPB2* loci, and the concept of *A. proliferans* was extended by a description of its sexual state. In this study, 31 well-supported phylogenetic lineages representing species are recognized. This conclusion is based on phylogenetic analysis of concatenated and partitioned sequence data, comparison of topologies of single-gene phylogenetic trees and reflection of phenotypic data (see below). All species can be distinguished by *CaM* or *RPB2* sequences, while *BenA* can be used to identify 29 species, with *A. brunneus* and *A. niveoglaucus* sharing identical *BenA* sequences.

Morphology and physiology

Members of sect. *Aspergillus* are generally characterized by yellow cleistothecia (the only exception is *A. leucocarpus*, which produces white cleistothecia), lenticular, hyaline ascospores, uniseriate conidiophore heads and globose, subglobose or ellipsoidal conidia. In the past, colony appearance, ascospore and conidial morphology were emphasized to differentiate species in this section (Thom & Raper 1941, 1945, Raper & Fennell 1965, Blaser 1975, Kozakiewicz 1989, Sun & Qi 1994, Guarro *et al.* 2012). This led to many species recognized which do not necessarily correspond to species based on recent phylogenetic data.

Macromorphology

The colony appearance is highly variable within a species. The ratio of asexual and sexual structures can greatly influence the colony appearance (Thom & Raper 1941, 1945, Raper, 1957, Raper & Fennell 1965). Some strains of *A. brunneus*, *A. sloanii* and *A. proliferans* do not produce sexual structures. On the contrary, anamorphic structures are absent in some strains of *A. costiformis* and *A. cristatus*. Hubka *et al.* (2013a) reported that the anamorph of these species can be induced by decreasing the water activity of the medium and simultaneously raising the incubation temperature. Red-pigmented mycelium was used to distinguish *A. ruber* from other related species (Raper & Fennell 1965, Pitt 1985, Klich 2002), but can also occur after two weeks in some isolates of *A. brunneus*, *A. cibarius*, *A. glaucus*, *A. niveoglaucus*, *A. proliferans* and *A. zutongqii* (Figs 13–17). Therefore, it cannot be used as a distinguishing character for these species. White conidial heads were used for distinguishing *A. niveoglaucus* and *A. glaucus* (Thom & Raper 1941, 1945, Raper & Fennell 1965), however, green spored *A. niveoglaucus* strains were reported by Hubka *et al.* (2013a) and are also confirmed in this study. Other examples include *A. montevidensis* CBS 410.65 (ex-type of *A. heterocaryoticus*) and *A. ruber* CBS 464.65 (ex-type of *A. athecius*) which produce white or vinaceous buff conidial head, respectively (Fig. 12). Based on these examples, the conidial head colour should not be used as a single distinguishing character either.

Physiology

Growth rates at higher temperatures show certain correlation with phylogenetic topologies, most species in the *A. chevalieri* clade (except *A. costiformis* and *A. caperatus*) grow on CY20S at 37 °C, while all species in the *A. ruber* and *A. glaucus* clades do not grow under this condition. Growth profiles on M60Y at 37 °C show a similar pattern with CY20S 37 °C. The only difference is that several species from the *A. chevalieri* and *A. ruber* clades including *A. caperatus*, *A. costiformis*, *A. pseudoglaucus*, *A. ruber*, *A. tonophilus* and *A. zutongqii* grow on M60Y at 37 °C, but show no growth on CY20S at 37 °C (Table 5). The growth ability on CY20S and M60Y at 37 °C together with the size and surface morphology of ascospores were found to correlate mostly with the phylogenetic species concept in this section (Hubka *et al.* 2013a). This conclusion is confirmed in this study using a world-wide section *Aspergillus* strains, and we found the growth ability on CY20S and M60Y at 37 °C a reliable feature for distinguishing morphologically similar species. For example, *A. proliferans* and *A. ruber* share similar smooth or slightly rough, furrowed ascospores and tuberculate conidia, among them *A. proliferans* cannot grow on M60Y at 37 °C, while *A. ruber* grows well on M60Y at 37 °C. The growth ability on media with high water activity (CYA, MEA) is also useful diagnostic features for certain species. Most species in sect. *Aspergillus* grow restrictedly on these two media, some species like *A. appendiculatus*, *A. neocarnoyi*, *A. osmophilus*, *A. tonophilus* and *A. xerophilus* show more xerophilic abilities compare to others and do not grow on CYA and MEA at all.

Micromorphology

Compared to colony appearance, micro-morphological characters within a species are relatively stable and informative (Table 6). The size and ornamentation of ascospores are generally the most informative phenotypic characters for species recognition (Figs 6–8). Large ascospores (spore bodies average > 6.5 μm) are produced by *A. aerius*, *A. brunneus*, *A. costiformis*, *A. glaucus*, *A. neocarnoyi*, *A. niveoglaucus*, *A. osmophilus* and *A. zutongqii*; small ascospores (spore bodies < 5 μm) are produced by *A. caperatus*, *A. intermedius*, *A. levisporus* and *A. tamarindosoli*, while remaining species produce intermediate ascospores. Convex sides of ascospores can be smooth, verruculose or rugulose, and these ornamentations are generally

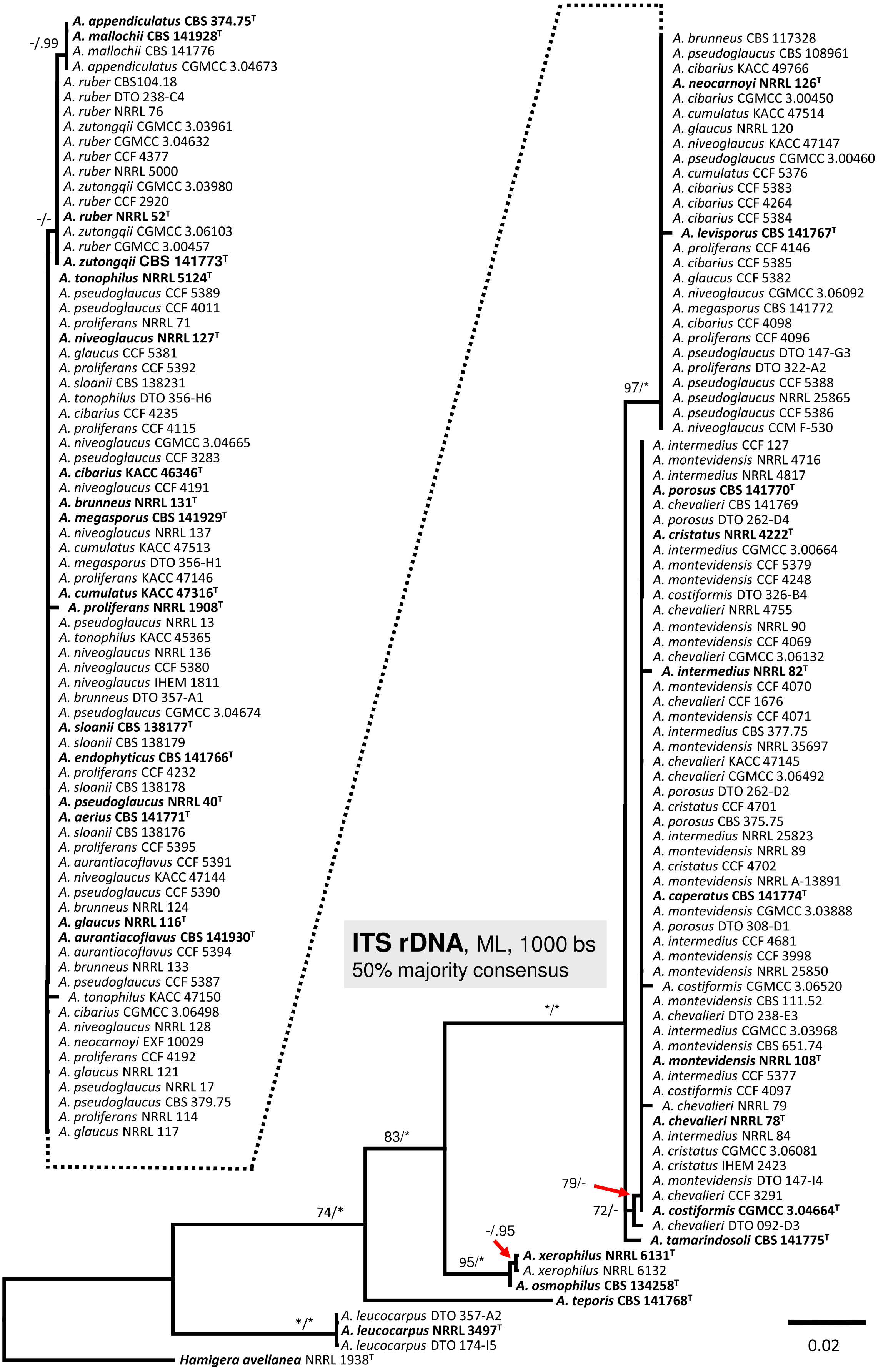
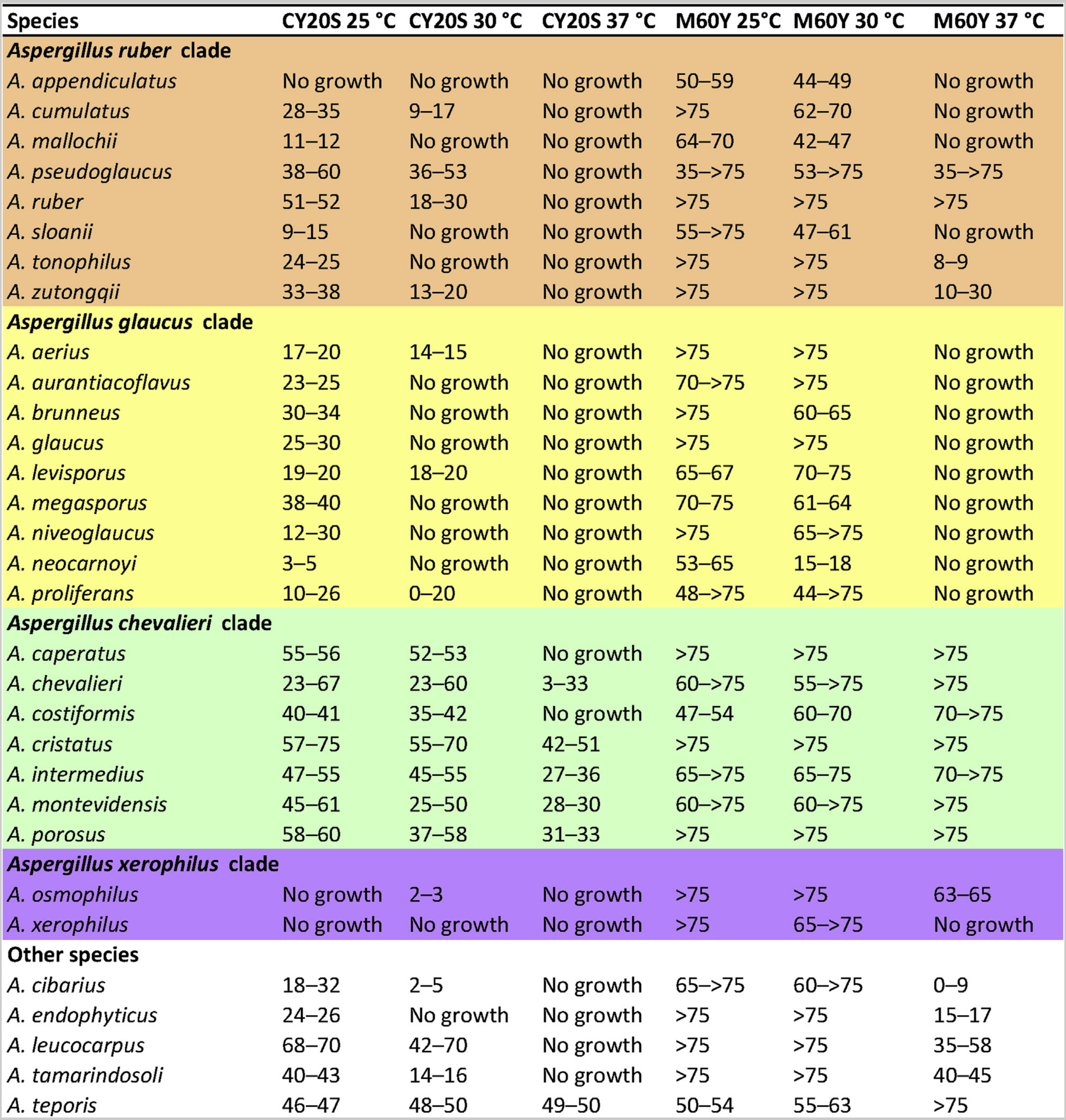


Fig. 5. A 50 % majority rule Maximum likelihood consensus tree based on ITS sequences. Maximum likelihood bootstrap proportion (bs) and Bayesian posterior probability (pp) are appended to nodes; only bs $\geq$ 70 % and pp $\geq$ 95 % are shown, lower supports are indicated with a hyphen, whereas asterisks indicate full support (100 % bs or 1.00 pp); ex-type strains are designated by a superscript T. The tree is rooted with *Hamigera avellanea* NRRL 1938^{T}.

Table 5. Temperature growth profiles (mm) of section *Aspergillus* species.



Species	CY20S 25 °C	CY20S 30 °C	CY20S 37 °C	M60Y 25°C	M60Y 30 °C	M60Y 37 °C
***Aspergillus ruber* clade**						
A. appendiculatus	No growth	No growth	No growth	50–59	44–49	No growth
A. cumulatus	28–35	9–17	No growth	>75	62–70	No growth
A. mallochii	11–12	No growth	No growth	64–70	42–47	No growth
A. pseudoglaucus	38–60	36–53	No growth	35–>75	53–>75	35–>75
A. ruber	51–52	18–30	No growth	>75	>75	>75
A. sloanii	9–15	No growth	No growth	55–>75	47–61	No growth
A. tonophilus	24–25	No growth	No growth	>75	>75	8–9
A. zutongqii	33–38	13–20	No growth	>75	>75	10–30
***Aspergillus glaucus* clade**						
A. aerius	17–20	14–15	No growth	>75	>75	No growth
A. aurantiacoflavus	23–25	No growth	No growth	70–>75	>75	No growth
A. brunneus	30–34	No growth	No growth	>75	60–65	No growth
A. glaucus	25–30	No growth	No growth	>75	>75	No growth
A. levisporus	19–20	18–20	No growth	65–67	70–75	No growth
A. megasporus	38–40	No growth	No growth	70–75	61–64	No growth
A. niveoglaucus	12–30	No growth	No growth	>75	65–>75	No growth
A. neocarnoyi	3–5	No growth	No growth	53–65	15–18	No growth
A. proliferans	10–26	0–20	No growth	48–>75	44–>75	No growth
***Aspergillus chevalieri* clade**						
A. caperatus	55–56	52–53	No growth	>75	>75	>75
A. chevalieri	23–67	23–60	3–33	60–>75	55–>75	>75
A. costiformis	40–41	35–42	No growth	47–54	60–70	70–>75
A. cristatus	57–75	55–70	42–51	>75	>75	>75
A. intermedius	47–55	45–55	27–36	65–>75	65–75	70–>75
A. montevidensis	45–61	25–50	28–30	60–>75	60–>75	>75
A. porosus	58–60	37–58	31–33	>75	>75	>75
***Aspergillus xerophilus* clade**						
A. osmophilus	No growth	2–3	No growth	>75	>75	63–65
A. xerophilus	No growth	No growth	No growth	>75	65–>75	No growth
Other species						
A. cibarius	18–32	2–5	No growth	65–>75	60–>75	0–9
A. endophyticus	24–26	No growth	No growth	>75	>75	15–17
A. leucocarpus	68–70	42–70	No growth	>75	>75	35–58
A. tamarindosoli	40–43	14–16	No growth	>75	>75	40–45
A. teporis	46–47	48–50	49–50	50–54	55–63	>75

Colour codes: yellow = *A. glaucus* clade, orange = *A. ruber* clade, green = *A. chevalieri* clade, purple = *A. xerophilus* clade.

stable with only minor intraspecific variability. However, in some rare cases, the ascospore morphology differs within a species. For example, most *A. ruber* strains produce smooth ascospores with minute rough ornamentations along equatorial ridges, but CBS 101748, previously described as *A. tuberculatus* (Sun & Qi 1994), has tuberculate ascospores (Fig. 8). Variations were also found in *A. montevidensis*, strain CCF 4248 has similar ascospores with *A. tuberculatus*, but shows identical sequences, growth parameters and colony phenotype with *A. montevidensis* (Hubka *et al.* 2013a), and another atypical strain CCF 4070 has smooth or slightly rough ascospores. It is noteworthy that ascospore ornamentation is related to the stage of development, and fine structures and ornamentation can be overlooked when observed using a light microscope (Blaser 1975, Kozakiewicz 1989, Guarro *et al.* 2012, Hubka *et al.* 2013a). In addition, some species are morphologically slightly different even when observed under SEM, and therefore careful comparison with experience is needed for morphological identification. *Aspergillus parviverruculosus* was introduced based on CGMCC 3.04665 producing verruculose ascospores (Kong & Qi 1995), Hubka *et al.* (2013a) considered it synonymous with *A. niveoglaucus* based on phylogenetic analysis and they observed appendaged ascospores. We confirmed the appendages in immature ascospores of the ex-type of *A. parviverruculosus* (CGMCC 3.04665). Filiform appendages were also observed in immature ascospores of *A. appendiculatus* (Kozakiewicz 1989, Hubka *et al.* 2013a) and these appendages can merge with ascospore body and form petaliform crests. Appendaged ascospores are also presented in *A. filifer* and *A. qinqixianii* in *Aspergillus* subgenus *Nidulantes*; however, these appendages are consistently

Table 6. Most important micromorphological characters for section *Aspergillus* species (μm).

Species	**Teleomorphic characters**					**Anamorphic characters**			
	Ascomata	**Spore bodies**	**Ornamentation of convex surface**	**Furrow**	**Crests**	**Conidiophores**	**Vesicles**	**Phialides**	**Conidia**
Aspergillus aerius	190–275	6.5–8 × 4.5–6	Smooth, rough along equatorial ridges	Present	Absent	500–1 000 × 7–15.5	26–41	7.5–12.5 × 5–8	Tuberculate, (5–)10–13 × 6–10
A. appendiculatus	100–225	5–7.5 × 4–5.5	Slightly rough	Absent or showing as a trace	Filiform appendages or petaliform, petals 1–1.5 μm at high parts	800–2 000 × 7–12(–14.5)	30–64	8–16 × 4.5–7.5	Tuberculate, 5–10(–12) × 5–7(–8.5)
A. aurantiacoflavus	110–250	4–5.5 × 3–5	Verruculose	Present	Irregular, <0.5	250–800 × 7.5–12	30–45	6–11 × 3.5–6.5	Tuberculate, 5–9 × 4–7
A. brunneus	110–240	7–10 × 6–8	Rough along equatorial ridges	Present	Irregular, <0.5	700–1 200 × 7–18	32–58	10–18.5 × 7–12.5	Tuberculate, 8–15 × 8–13
A. caperatus	130–220	3.5–4.5 × 2.5–4	Verruculose to rugulose	Pronounced	0.5–1	250–500 × 6.5–9(–12)	26–45	7.5–12 × 4–7.5	Lobate-reticulate, 3.5–5.5 × 3.5–4.5
A. chevalieri	100–250	3.5–5.5 × 3–4	Smooth to slightly verruculose	Present	0.5–1	200–1 000 × 6–12	23–47	5.5–7.5(–10) × 3–5	Tuberculate to lobate-reticulate, 3–4(–6) × 2.5–3.5(–5)
A. cibarius	100–200	4–5.5 × 3–5	Rough along equatorial ridges	Present	Irregular, <0.5	500–700 × 8–14	32–58	6–11 × 3–5.5	Tuberculate, 4–7 × 3.5–5.5
A. costiformis	100–255	5.5–7 × 5–6.5	Rugulose	Pronounced	0.5	500–800 × 7–13	20–45(–60)	6–9.5 × 3–4.5(–5.5)	Microtuberculate, 4–5.5(–6.5) × 3–4.5(–5.5)
A. cristatus	100–200	4.5–6 × 4–6	Verruculose to rugulose	Present	1.2–1.5	300–500 × (6–)8–12	(26–)35–51	5.5–9 × 3.5–6	Tuberculate, 4–6.5 × 3.5–5
A. cumulatus	100–200	4–6 × 3.5–5	Slightly rough	Pronounced	Irregular, <0.5	500–1 300 × 7–15	32–57	7–12 × 4.5–7.5	Tuberculate, 5–8 × 4–7.5
A. endophyticus	120–200	4–5.5 × 3–4.5	Verruculose to rugulose	Pronounced	0.5–1	350–800 × 9.5–14	32–52	6–10 × 3.5–5.5	Tuberculate to lobate-reticulate, 5.5–8 × 4.5–6
A. glaucus	120–250	5.5–7.5 × 3.5–6	Smooth, minute rough along equatorial ridges	Pronounced	Irregular, 0.5–1	150–500 × 10–21(–30)	30–60	(8–)12–20 × (4–)5–8.5	Tuberculate, 6–12.5 × 5.5–9
A. intermedius	100–250	3.5–5 × 3–4.5	Verruculose to rugulose	Present	0.5	250–600 × 7.5–13	(26–)40–60	5.5–7.5(–9) × 3–5.5	Microtuberculate, 3–4(–6) × 3–4.5
A. leucocarpus	80–140	4.5–5.5 × 3.5–5	Verruculose	Present	0.8–1.5	800–1 400 × 7.5–12	35–60	8–11.5 × 3.5–6.5	Tuberculate, 5.5–9 × 5–8
A. levisporus	70–130	3–4.5 × 2.5–4	Smooth	Present	Absent	400–600 × 10–14	30–44	6–8.5 × 3.5–6	Tuberculate to lobate-reticulate, 3.5–4.5 × 2.5–4
A. mallochii	130–220	4–6 × 3–5	Smooth, minute rough along equatorial ridges	Absent or showing as a trace	Petaliform, 1–2 at high parts	600–1 500 × 6–9.5 (–12)	27–43	6.5–9 × 3–5	Tuberculate, 4.5–7 × 4–5.5
A. megasporus	110–300	4–6.5 × 3.5–5.5	Smooth, rough along equatorial ridges	Present	Absent or indefinite	1 000–1 500 × 6.5–12(–21.5)	30–54	7.5–14 × 4–7.5	Tuberculate, 7–14 × 5–8.5
A. montevidensis	80–250	4–6 × 3–4.5	Generally rugulose, smooth or slightly rough in atypical strain CCF 4070, tuberculate in atypical strain CCF 4248	Pronounced	0.5	250–500 × 6–13.5	25–35(–50)	5–8.5(–11) × 3–6	Lobate-reticulate, 4–6.5 × 3.5–5

Table 6. (Continued).

Species	Teleomorphic characters					Anamorphic characters			
	Ascomata	Spore bodies	Ornamentation of convex surface	Furrow	Crests	Conidiophores	Vesicles	Phialides	Conidia
A. neocarnoyi	120–230	6.5–9 × 4.5–7	Verruculose to rugulose	Present	Absent or indefinite	1 000–2 000 × (9–) 12–23	(32–)50–92	12–21 × 6–9	Tuberculate, 8–15.5 × 6–10
A. niveoglaucus	90–240	(4.5–)5.5–7.5 × (3–)5–6	Rough along equatorial ridges or verruculose to rugulose	Present	Irregular, <0.5	1 000–1 500 × (7.5–) 10–23	(31–)55–85	8–14(–20) × 4–7 (–11)	Tuberculate, (6–)8–13.5 × 4–9
A. osmophilus	100–350	7–9 × 6–7.5	Verruculose	Pronounced	0.5	300–1 000 × 7.5–12	28–46	9–12 × 4.5–7	Microtuberculate to tuberculate, 6–8.5 × 5.5–7.5
A. porosus	80–230	3.5–5.5 × 3–4.5	Rugulose, pitted	Pronounced	0.5	250–600 × 5–12.5	24–58	5–10 × 2.5–5	Lobate-reticulate, 3.5–5.5 × 2.5–4.5
A. proliferans	100–240	4–6 × 3–5	Smooth or slightly verruculose or rough along equatorial ridges	Present or pronounced	Absent	250–1 000 × 8–16.5	20–50	6–12 × 3–5.5	Tuberculate, 5–7.5(–10) × 4–6(–7)
A. pseudoglaucus	75–200	4–6.5 × 3–4.5	Smooth or slightly rough	Absent or showing as a trace	Absent	500–1 000 × (7–)11–22	(26–)37–65	6–11 × 4–6.5	Tuberculate; microtuberculate in atypical strain CBS 379.75, (3.5–)6–9 × (3–) 5.5–7.5
A. ruber	50–175	4–6 × 3.5–5	Generally smooth or minute rough along equatorial ridges, tuberculate in atypical strain CBS 101748	Present or pronounced	Absent	500–750 × 7–13.5	25–48	7–9(–12) × 3.5–6	Tuberculate, (4.5–) 7–9(–12) × 4–6(–8)
A. sloanii	60–205	4–6 × 3–4.5	Smooth, minute rough along equatorial ridges	Present	Absent	160–900 × 7.5–16	(10–)34–53	(7.5–) 9–13.5(–18) × (5–) 7–9.5	Tuberculate, 5.5–9.5 × 5.5–9
A. tamarindosoli	130–240	3.5–5 × 3–4	Verruculose	Present	Irregular, 0.5–1.5	700–1 000 × 10–15	40–72	6.5–12 × 4–5.5	Lobate-reticulate, 4–7 × 3–4.5
A. teporis	120–180	5–6.5 × 4–5.5	Slightly verruculose	Pronounced	0.5	800–1 200 × 8–19	33–53	7–12 × 3.5–5	Lobate-reticulate, 3.5–6 × 3–4.5
A. tonophilus	100–235	4–6 × 3–4.5	Verruculose	Present	Absent	120–500 × 7–12.5	25–44	6–11 × 3–5	Tuberculate to lobate-reticulate, 5–7.5 × 3.5–6
A. xerophilus	165–330	4.5–6.5 × 3.5–5	Verruculose	Present	Irregular, <0.5	50–200 × 6.5–9.5(–12)	40–66	6–9 × 3.5–6	Microtuberculate, 3.5–5.5 × 3–4.5
A. zutongqii	110–220	6–7.5 × 4.5–6	Verruculose	Pronounced	Absent	150–500 × 7.5–13	25–40	8–12 × 4–6.5	Tuberculate, 5.5–10 × 4–7

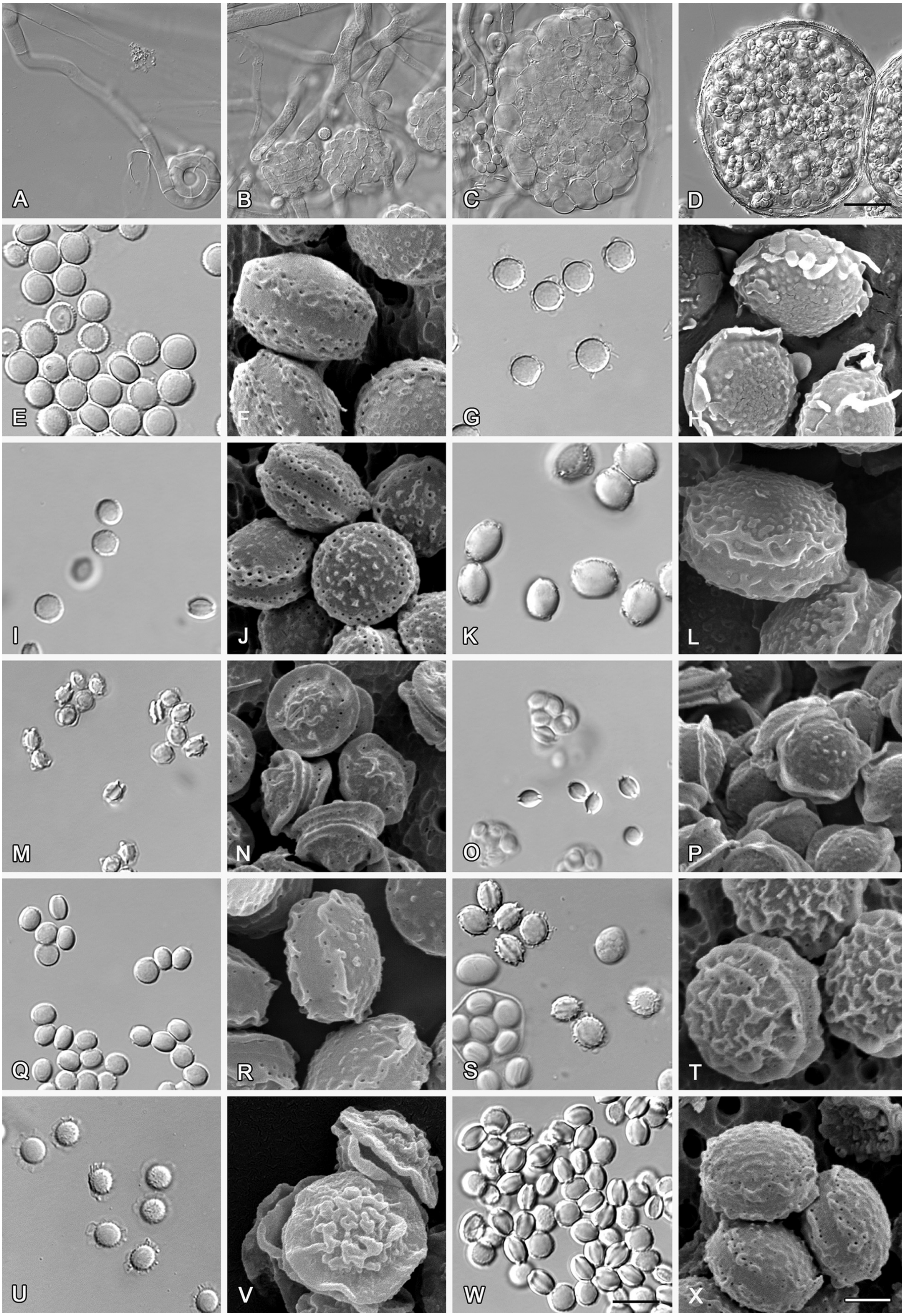


Fig. 6. Formation of ascomata and range of ascospore phenotypes. **A–D.** Initials and ascomata. **E, F.** *Aspergillus aerius CBS* 141771^{T}. **G, H.** *A. appendiculatus* CBS 374.75^{T}. **I, J.** *A. aurantiacoflavus* CBS 141930^{T}. **K, L.** *A. brunneus* CBS 112.26^{T}. **M, N.** *A. caperatus* CBS 141774^{T}. **O, P.** *A. chevalieri* CBS 522.65^{T}. **Q, R.** *A. cibarius* KACC 46346^{T}. **S, T.** *A. costiformis* CBS 101749^{T}. **U, V.** *A. cristatus* CBS 123.53^{T}. **W, X.** *A. cumulatus* KACC 47316^{T}. Scale bars: D = 20 µm, applies to A–C; W = 10 µm, applies to E, G, I, K, M, O, Q, S, U; X = 2 µm, applies to F, H, J, L, N, P, R, T, V.

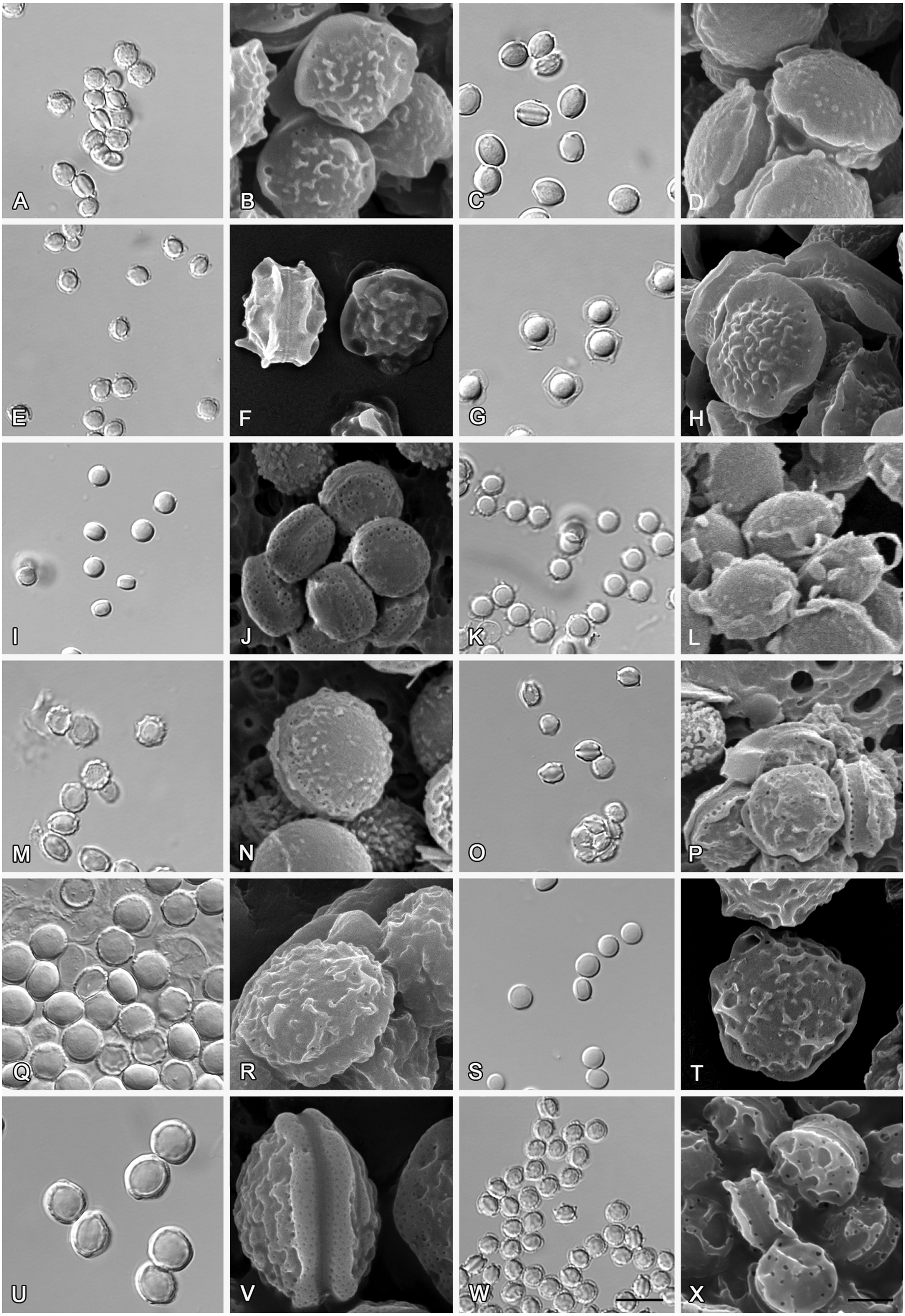


Fig. 7. Range of ascospore phenotypes. **A, B.** *Aspergillus endophyticus* CBS 141766^T. **C, D.** *A. glaucus* CBS 516.65^T. **E, F.** *A. intermedius* CBS 523.65^T. **G, H.** *A. leucocarpus* CBS 353.68^T. **I, J.** *A. levisporus* CBS 141767^T. **K, L.** *A. mallochii* CBS 141928^T. **M, N.** *A. megasporus* CBS 141929^T. **O, P.** *A. montevidensis* CBS 491.65^T. **Q, R.** *A. neocarnoyi* CBS 471.65^T. **S, T.** *A. niveoglaucus* CBS 114.27^T. **U, V.** *A. osmophilus* CBS 134258^T. **W, X.** *A. porosus* CBS 141770^T. Scale bars: W = 10 µm, applies to A, C, E, G, I, K, M, O, Q, S, U; X = 2 µm, applies to B, D, F, H, J, L, N, P, R, T, V.

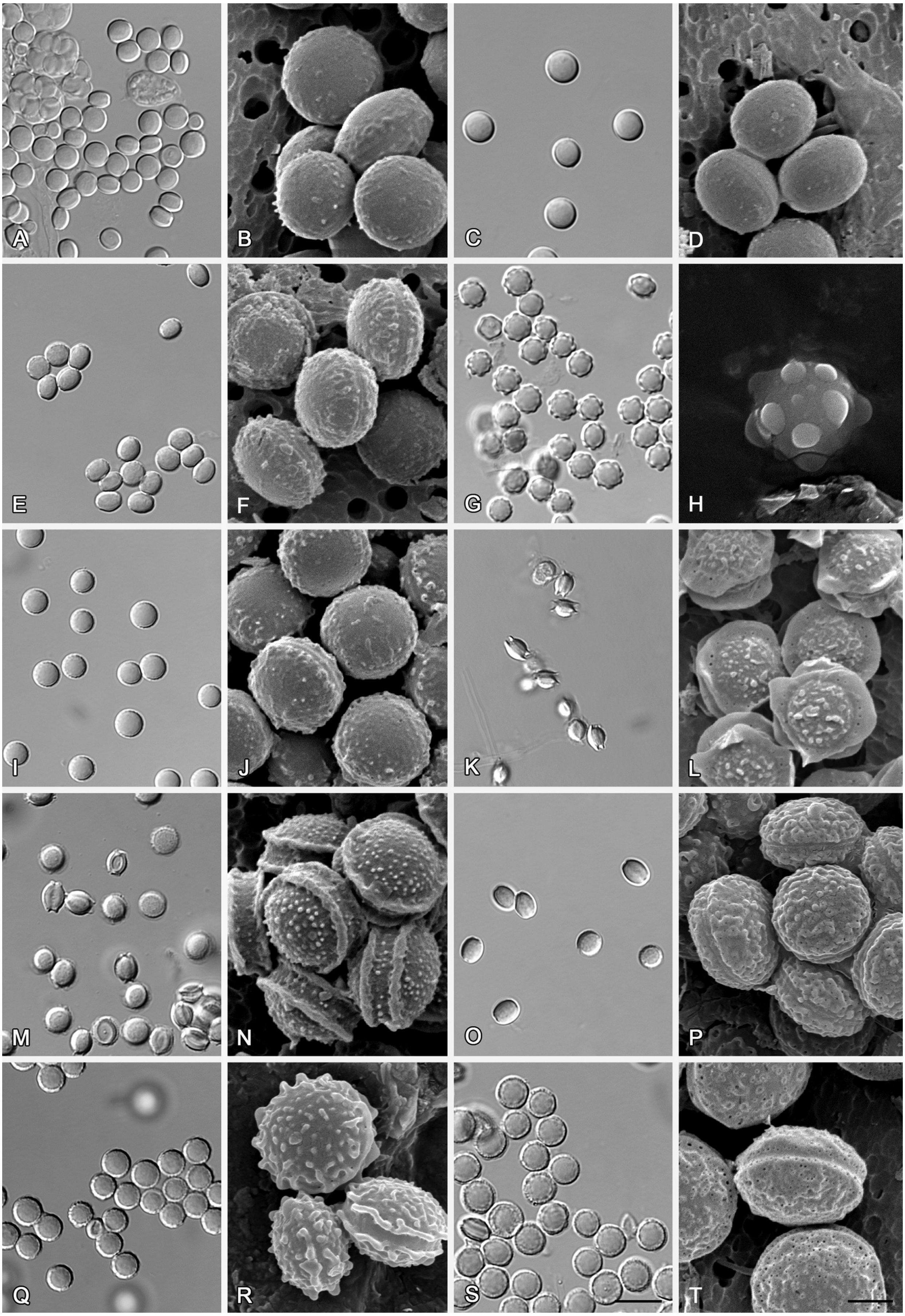


Fig. 8. Range of ascospore phenotypes. **A, B.** *Aspergillus proliferans* DTO 322-A2. **C, D.** *A. pseudoglaucus* CBS 101747 (ex-type of *A. fimicola*). **E, F.** *A. ruber* CBS 530.65^T. **G, H.** *A. ruber* CBS 101748 (ex-type of *A. tuberculatus*). **I, J.** *A. sloanii* CBS 138177^T. **K, L.** *A. tamarindosoli* CBS 141775^T. **M, N.** *A. teporis* CBS 141768^T. **O, P.** *A. tonophilus* KACC 47150. **Q, R.** *A. xerophilus* CBS 938.73^T. **S, T.** *A. zutongqii* CBS 141773^T. Scale bars: S = 10 µm, applies to A, C, E, G, I, K, M, O, Q; T = 2 µm, applies to B, D, F, H, J, L, N, P, R.

presented in mature ascospores (Horie *et al.* 2000, Zalar *et al.* 2008, Chen *et al.* 2016).

The diameter and shape of conidia are highly variable within species and generally not useful for species differentiation. However, conidial ornamentation is useful for differentiating phylogenetically related species or species with similar ascospore morphology (Figs 9–11). For example, *A. intermedius* is phylogenetically related to *A. montevidensis*. Both produce verruculose ascospores with 0.5 μm crests, however, the microtuberculate conidia of *A. intermedius* can easily distinguish it from *A. montevidensis*. Most species produce consistent conidial ornamentations, except in *A. pseudoglaucus* where most strains produce tuberculate conidia, but CBS 379.75, previously described as *A. glaber* (Blaser 1975), produces microtuberculate conidia. Kozakiewicz (1989) assigned the conidial ornamentation into four categories, ranging from microtuberculate, aculeate, tuberculate to lobate-reticulate. Based on our observations, aculeate and tuberculate ornamentations may occur in same species, and can be affected by the fixation methods or age of conidia. We therefore, combined these two types of ornamentation within the tuberculate category. The three categories of conidial ornamentation described here include microtuberculate, tuberculate or lobate-reticulate.

Extrolites

Species in sect. *Aspergillus* produce some main biosynthetic families of secondary metabolites. All species of sect. *Aspergillus* produce echinulins and derived isoechinulins and neoechinulins. *Aspergillus sloanii* is the only species that does not convert echinulins to isoechinulins and neoechinulins (Tables 7, 8). Furthermore, the echinulin related molecules arestrictin A & B and cristatin A are produced by *A. restrictus* and *A. penicillioides* in sect. *Restricti* (Itabashi *et al.* 2006). Certain polyketides are also commonly detected in sect. *Aspergillus*, including octaketide anthraquinones, such as emodin and physcion. Other compounds commonly detected include anthraquinones, and the related asperflavin. They are absent from *A. montevidensis*, which explain the bright yellow colour of its ascomata. Species that have orange-red or red mycelium covering the ascomata, such as *A. ruber*, produce additional red anthraquinones, including erythroglaucin and catenarin. Emodin and physcion and their bisanthrons are found to be common. These compounds were detected in the closely related species in sect. *Cremei*, for example in *A. wentii* (Wells *et al.* 1975, Assante *et al.* 1980, Rabie *et al.* 1986). Also, *A. stromatioides* in sect. *Cremei* produces emodin and ω-hydroxyemodin, which is shared with sect. *Aspergillus* (González-Andrade *et al.* 2013). Another octaketide, sulochrin is only recovered from *A. xerophilus*. Sulochrin and similar compounds, i.e., 3-O-methylsulochrin and 3-O-demethylsulochrin have also been recovered from *A. wentii* and *A. europaeus* in sect. *Cremei* (Rabie *et al.* 1986, Hubka *et al.* 2016). The octaketide asperentin was reported first from *A. flavus* (Grove 1972a), but the fungus was misidentified and was actually *A. pseudoglaucus*. *Aspergillus brunneus* and *A. neocarnoyi* can also produce asperentins.

Nearly all species in sect. *Aspergillus* produce auroglaucins (Table 8). These heptaketides contribute to the yellow colour of the ascomata in this group. *Aspergillus leucocarpus* does not produce auroglaucins, partly explaining its cream to white coloured ascomata. *Aspergillus teporis* also does not produce auroglaucins, and this species produces less bright creamish yellow ascomata, albeit not creamish white. *Aspergillus xerophilus* produces a small amount of dihydroauroglaucin, but not auroglaucin, flavoglaucin and tetrahydroauroglaucin. The hexaketide siderin is recovered from one strain of *A. niveoglaucus*, but this kind of compound related to orlandin and kotanins is more commonly produced in sections *Nigri* and *Clavati* (Varga *et al.* 2007, Nielsen *et al.* 2009). *Aspergillus pseudoglaucus* is an efficient producer of the meroterpenoid mycophenolic acid and was already reported to produce the tetraketide precursor 5,7-dihydroxy-4-methylphthalide by Grove (1972a), albeit misidentified as a strain of *A. flavus*. Mycophenolic acid and its precursors have also been reported from sect. *Aspergillus* (as *Eurotium* spp.) by Burkin & Kononenko (2010), Gao *et al.* (2011, 2012a, b) and Séguin *et al.* (2014). Epiheveadrides are detected in many species (Table 8). These nonadrides are biosynthesized from a polyketide and components from the citric acid cycle (Williams *et al.* 2016). They are unique to this group of Aspergilli.

Even though some extrolites from sect. *Aspergillus* have been claimed to be toxic (Bachmann *et al.* 1979, 1982, Blaser *et al.* 1980), these metabolites do not follow the definition of a mycotoxin. However, in higher amounts echinulins may be toxic when ingested as feed. The toxicity of echinulins and other secondary metabolites from *Aspergillus* sect. *Aspergillus* may need a re-evaluation as potential mycotoxins. The possible human toxicity of these compounds also needs to be re-evaluated. The real mycotoxins aflatoxin, sterigmatocystin, gliotoxin, citrinin, ochratoxin A could not be recovered from any of the species in sect. *Aspergillus* (Tables 7, 8). In fact, the species in this group may contribute to the healthiness of fermented products such as golden tea and katsuobushi via their strong antioxidant properties of their extrolites (Ishikawa *et al.* 1985, Li *et al.* 2004a, Miyake *et al.* 2009, Li *et al.* 2009, Meng *et al.* 2016).

Occurrence of *Aspergillus* section *Aspergillus* species in indoor environment

Isolations from indoor environments including air, air treatment systems, dust resulted in 96 *Aspergillus* sect. *Aspergillus* strains originating from fifteen countries including Belgium, Canada, Czech Republic, France, Germany, Hungary, Mexico, Puerto Rico, South Africa, Thailand, the Netherlands, Trinidad & Tobago, Turkey, UK and USA. Strains were identified using *CaM* sequences, with respective GenBank numbers shown in Table 9. Fourty-three (45 %) strains were identified as *A. pseudoglaucus*, 20 (21 %) as *A. montevidensis*, and 12 (13 %) as *A. chevalieri*. The remaining strains were identified as *A. appendiculatus*, *A. cibarius*, *A. glaucus*, *A. intermedius*, *A. leucocarpus*, *A. niveoglaucus*, *A. proliferans*, *A. ruber* and a new species *A. aerius*.

Members of sect. *Aspergillus* are able to grow on all types of organic materials at low moisture levels, therefore this group of fungi is frequently reported from the indoor environment (Samson *et al.* 2010, Šimonovičová *et al.* 2015, Thrasher 2016, Visagie *et al.* 2014a, Visagie *et al.* 2017). Since their wide distribution and environmental adaptation, sect. *Aspergillus* species were used as biosensor fungi to assess indoor climate and predict hidden moisture damage in homes (Abe *et al.* 1996, Baudisch *et al.* 2009). Samson *et al.* (2010) listed four common sect. *Aspergillus* species in indoor environment including *A. montevidensis* (= *E. amstelodami*), *A. chevalieri* (= *E.*

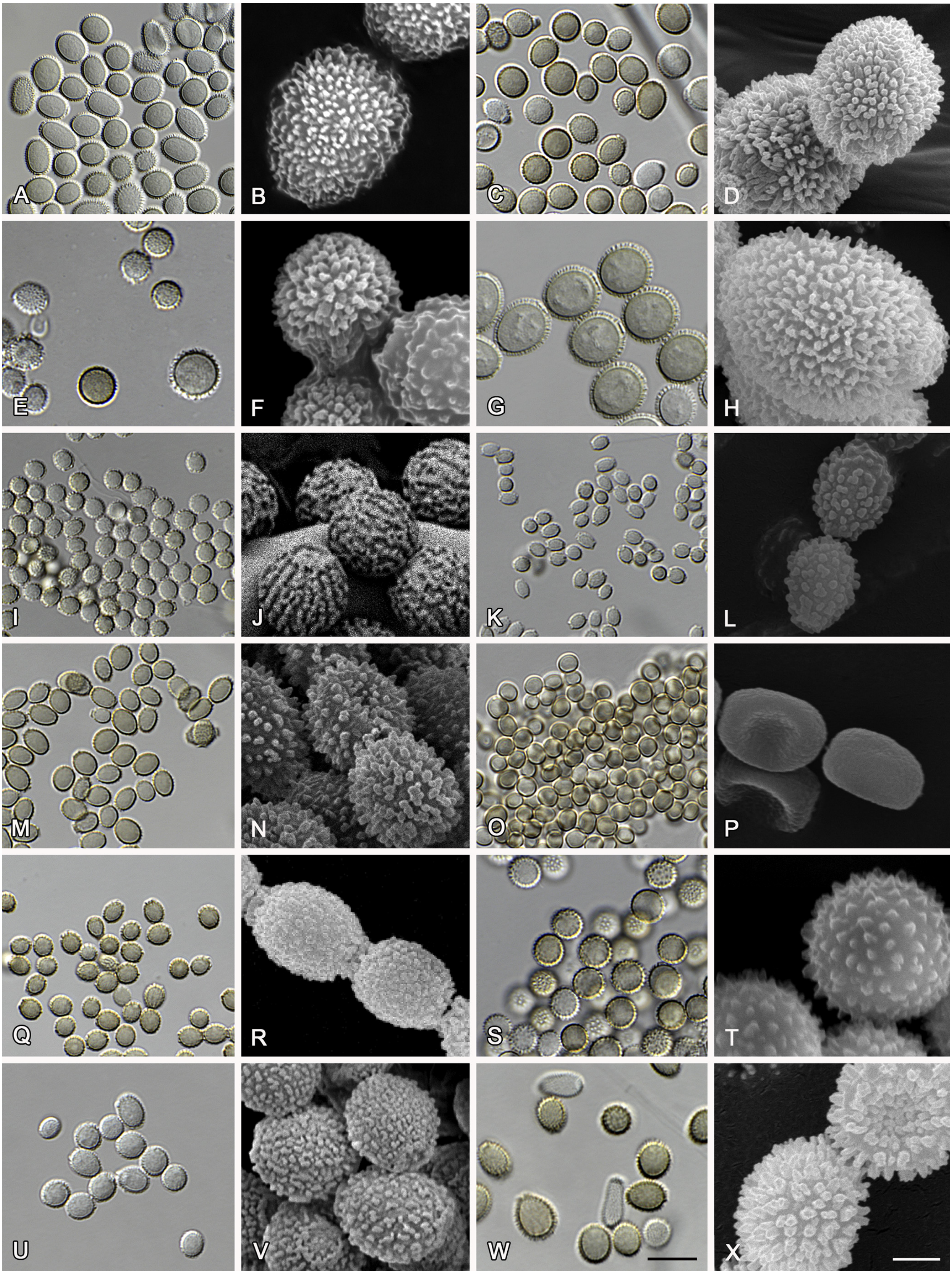


Fig. 9. Range of conidia phenotypes. **A, B.** *Aspergillus aerius* CBS 141771^T. **C, D.** *A. appendiculatus* CBS 374.75^T. **E, F.** *A. aurantiacoflavus* CBS 141930^T. **G, H.** *A. brunneus* CBS 112.26^T. **I, J.** *A. caperatus* CBS 141774^T. **K, L.** *A. chevalieri* CBS 522.65^T. **M, N.** *A. cibarius* KACC 46346^T. **O, P.** *A. costiformis* CBS 101749^T. **Q, R.** *A. cristatus* CBS 123.53^T. **S, T.** *A. cumulatus* KACC 47316^T. **U, V.** *A. endophyticus* CBS 141766^T. **W, X.** *A. glaucus* CBS 516.65^T. Scale bars: W = 10 µm, applies to A, C, E, G, I, K, M, O, Q, S, U; X = 2 µm, applies to B, D, F, H, J, L, N, P, R, T, V.

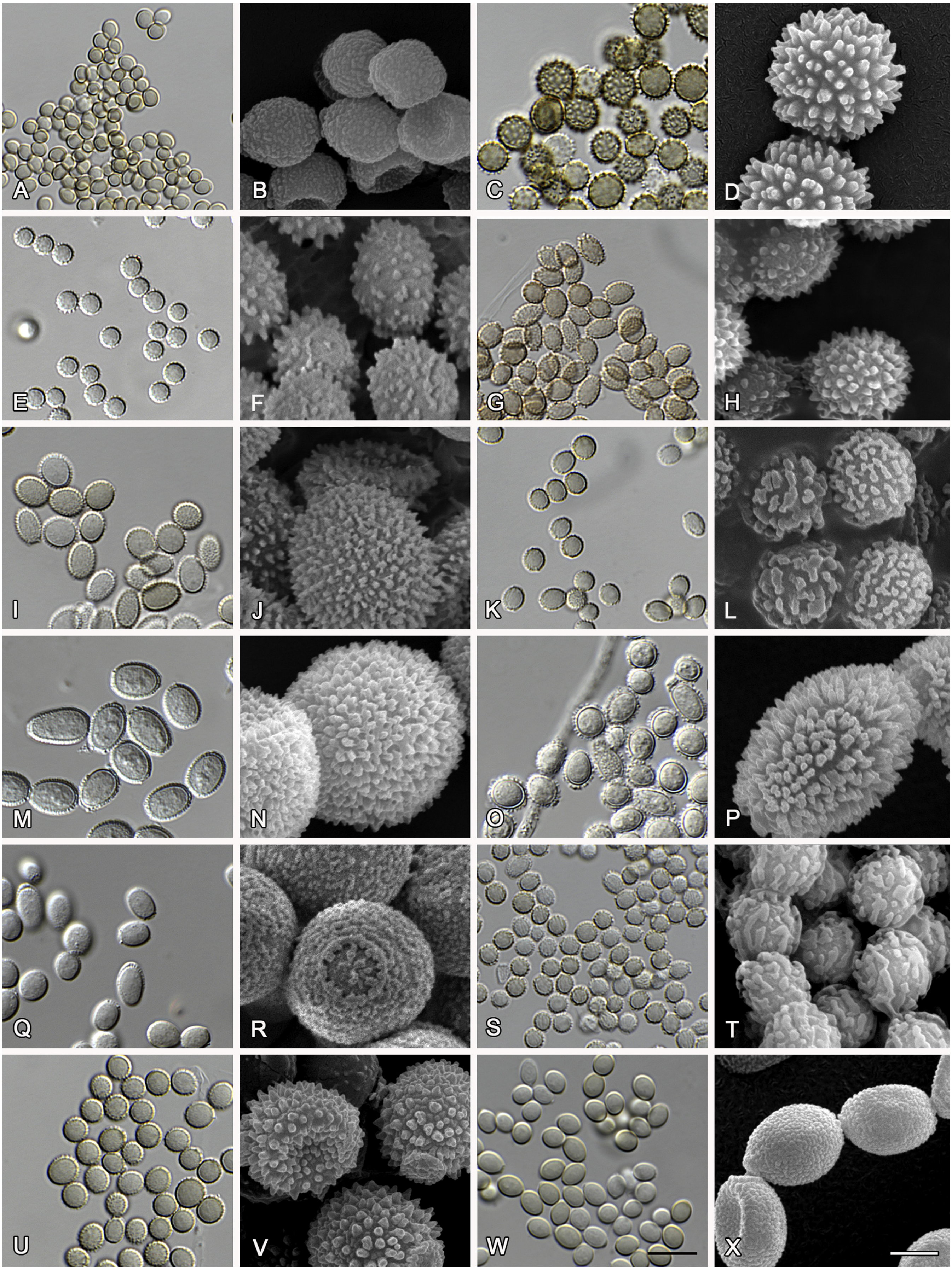


Fig. 10. Range of conidia phenotypes. **A, B.** *Aspergillus intermedius* CBS 523.65^T. **C, D.** *A. leucocarpus* CBS 353.68^T. **E, F.** *A. levisporus* CBS 141767^T. **G, H.** *A. mallochii* CBS 141928^T. **I, J.** *A. megasporus* CBS 141929^T. **K, L.** *A. montevidensis* CBS 491.65^T. **M, N.** *A. neocarnoyi* CBS 471.65^T. **O, P.** *A. niveoglaucus* CBS 114.27^T. **Q, R.** *A. osmophilus* CBS 134258^T. **S, T.** *A. porosus* CBS 141770^T. **U, V.** *A. pseudoglaucus* CBS 101747 (ex-type of *A. fimicola*). **W, X.** *A. pseudoglaucus* CBS 379.75 (ex-type of *A. glaber*). Scale bars: W = 10 µm, applies to A, C, E, G, I, K, M, O, Q, S, U; X = 2 µm, applies to B, D, F, H, J, L, N, P, R, T, V.

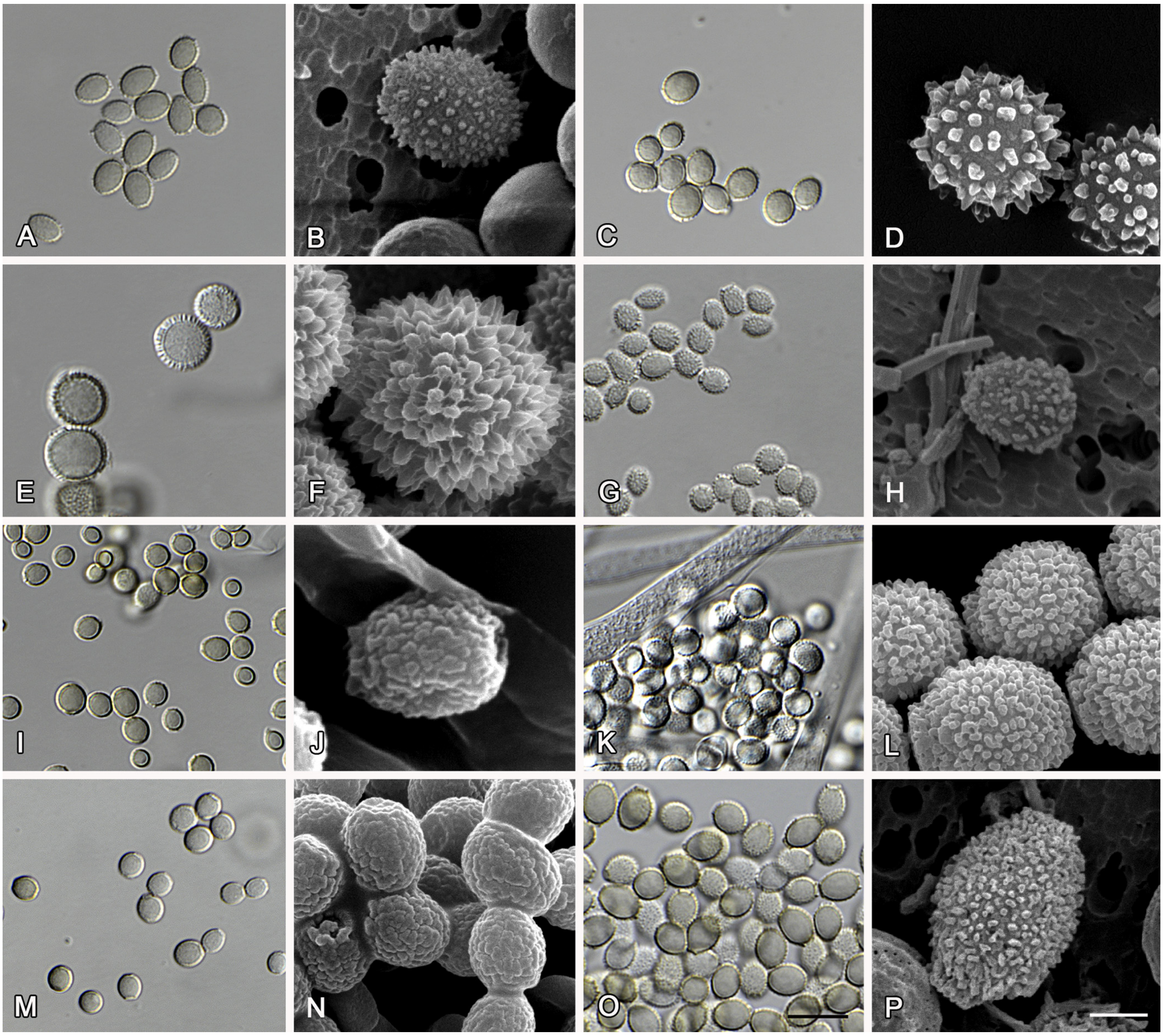


Fig. 11. Range of conidia phenotypes. **A, B.** *Aspergillus proliferans* DTO 322-A2. **C, D.** *A. ruber* CBS 530.65^{T}. **E, F.** *A. sloanii* CBS 138177^{T}. **G, H.** *A. tamarindosoli* CBS 141775^{T}. **I, J.** *A. teporis* CBS 141768^{T}. **K, L.** *A. tonophilus* KACC 47150. **M, N.** *A. xerophilus* CBS 938.73^{T}. **O, P.** *A. zutongqii* CBS 141773^{T}. Scale bars: O = 10 µm, applies to A, C, E, G, I, K, M; P = 2 µm, applies to B, D, F, H, J, L, N.

chevalieri), *A. ruber* (= *E. rubrum*) and *A. glaucus* (= *E. herbariorum*). Visagie *et al.* (2014a) reported six species including *A. ruber*, *A. proliferans*, *A. montevidensis*, *A. pseudoglaucus*, *A. sloanii* and *A. chevalieri* from house dust samples, and more recently, Visagie *et al.* (2017) reported another nine species from Canadian and Hawaiian dust. In the current study *A. pseudoglaucus*, *A. montevidensis* and *A. chevalieri* represented 78 % of all isolates. Phenotypically, these indoor species are very similar. *Aspergillus pseudoglaucus* is similar to *A. proliferans* and *A. ruber*, while *A. montevidensis* and *A. chevalieri* only bear small differences in ascospore ornamentation, and can be confused with others in the *A. chevalieri* clade (such as *A. intermedius* and *A. caperatus*). Thus molecular identification especially *CaM* instead of ITS is recommended for accurate identification. *Eurotium amstelodami* and *E. repens* are two of the most encountered names in indoor sect. *Aspergillus* species (Samson *et al.* 2010, Šimonovičová *et al.* 2015, Thrasher 2016). The names *A. montevidensis* (= *E. amstelodami*) and *A. pseudoglaucus* (= *E. repens*), respectively, were chosen based on priority and new nomenclature rules (McNeill *et al.* 2012, Hubka *et al.* 2013a). To keep the consistent species concepts which facilitate comparable research, this treatment is followed in this study.

Key to the most common section *Aspergillus* species from the indoor environments

1a) Ascospores with high crests (0.5–1 µm)	2
1b) Ascospores with low crests (< 0.5 µm) or crests lacking	4
2a) Ascospores with smooth or faintly roughened convex surface	3
2b) Ascospores with rugulose convex surface	*A. montevidensis*
3a) Ascospores small, with spore bodies measuring 3.5–5.5 × 3–4 µm	*A. chevalieri*
3b) Ascospores large, with spore bodies measuring 5.5–7.5 × 3.5–6 µm	*A. glaucus*
4a) Ascospores with low crests (< 0.5 µm)	5

4b) Ascospores lack crests	6
5a) Conidia small, 4–7 × 3.5–5.5 µm	*A. cibarius*
5b) Conidia large, (6–)8–13.5 × 4–9 µm	*A. niveoglaucus*
6a) Ascospores with furrow present or pronounced	7
6b) Ascospores with furrow absent or showing as a trace	*A. pseudoglaucus*
7a) Grows well on M60Y at 37 °C	*A. ruber*
7b) Does not grow on M60Y at 37 °C	*A. proliferans*

TAXONOMY

Aspergillus section Aspergillus

Synonyms: *Eurotium* Link, Mag. Ges. Naturf. Freunde Berlin 3: 31, t. 2:44. 1809.
Pyrobolus Kuntze, Revis. Gen. Pl. 2: 868. 1891. *fide* Kuntze 1891, Dict. Fungi 10th ed.
Edyuillia Subram., Curr. Sci. 41: 756. 1972, *fide* Samson 1979.
Gymnoeurotium Malloch & Cain, Canad. J. Bot. 50: 2619. 1972, *fide* Samson 1979, Benny & Kimbrough 1980.

Conidiophores with smooth stipes, hyaline or light brown. Vesicles globose to subglobose, uniseriate, fertile over two thirds to entire surface. Phialides flask-shaped. Conidia globose, subglobose to ellipsoidal, microtuberculate, tuberculate to lobate-reticulate. Ascomata eurotium-like, cleistothecial, superficial, yellow or rarely white to cream yellow, globose to subglobose. Asci 8-spored, globose to subglobose. Ascospores one-celled, hyaline, lenticular, in surface view globose to subglobose, generally showing an equatorial furrow with or without crests, spore bodies smooth or with different degree of rough ornamentation. Xerophilic and osmophilic, growing optimally on substrates containing high concentrations of sugar or salt.

Typus: *Aspergillus glaucus* (L.) Link, Mag. Ges. Naturf. Freunde Berlin 3: 16. 1809.

Notes: The genus *Pyrobolus* was considered as synonym of *Eurotium* (Kuntze 1891). The genera *Edyuillia* and *Gymnoeurotium* were both based on *Aspergillus athecius* Raper & Fennell, Samson (1979) suspected the type culture (CBS 464.65) of *A. athecius* had lost its ability to produce ascomata and represented an atypical form of *Eurotium*, thus regarded these two genera as synonymous with *Eurotium*. This was

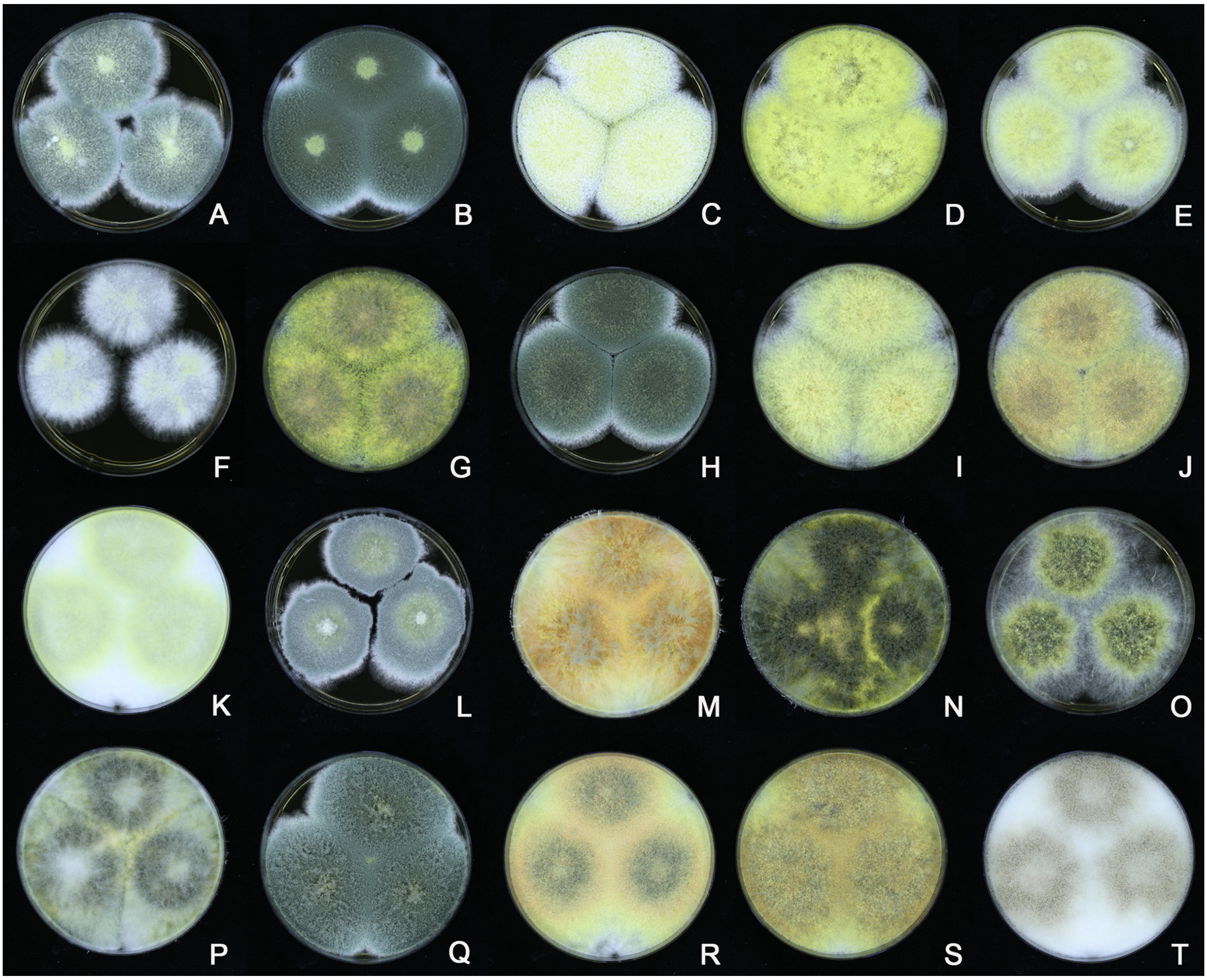


Fig. 12. Diversity of macromorphology (colonies on M40Y, 25 °C, 7 d) within *Aspergillus* sect. *Aspergillus* species. **A–E.** *A. montevidensis*. From left to right: CBS 491.65^T, CBS 651.74 (ex-type of *A. vitis*), CBS 410.65, CBS 518.65 (ex-type of *A. hollandicus*), CBS 111.52. **F–J.** *A. proliferans*. From left to right: CBS 121.45^T, DTO 322-A2, CCF 4096, CCF 5395, CCF 5392. **K–O.** *A. pseudoglaucus*. From left to right: CBS 123.28^T, CBS 101747 (ex-type of *A. fimicola*), CBS 379.75 (ex-type of *A. glaber*), DTO 147-G3, CGMCC 3.00460. **P–T.** *A. ruber*. From left to right: CBS 530.65^T, DTO 238-C4, CBS 101748 (ex-type of *A. tuberculatus*), CBS 104.18, CBS 464.65 (ex-type of *A. athecius*).

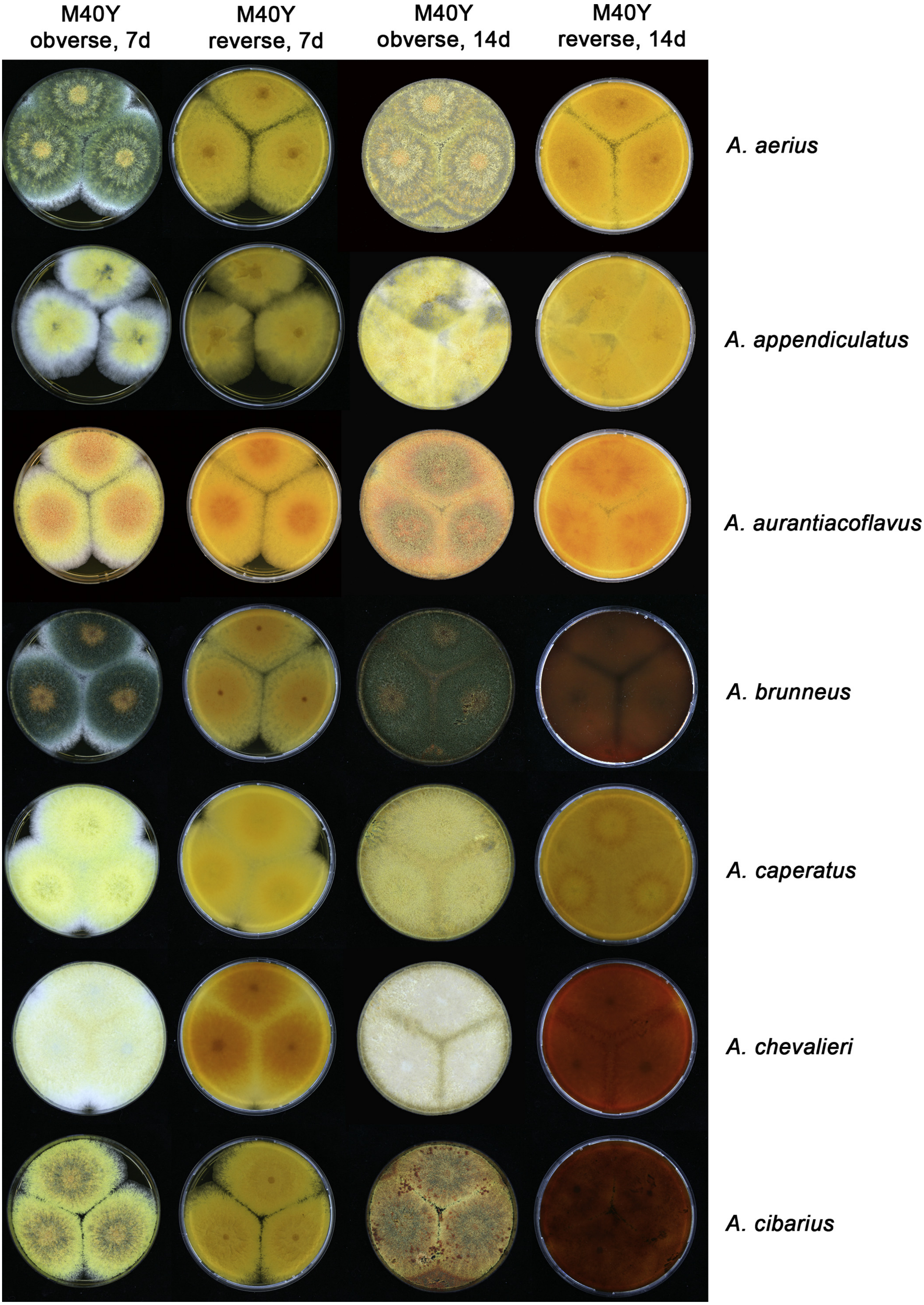


Fig. 13. Growth comparison of *Aspergillus* sect. *Aspergillus* species on M40Y for 7 d and 14 d at 25 °C.

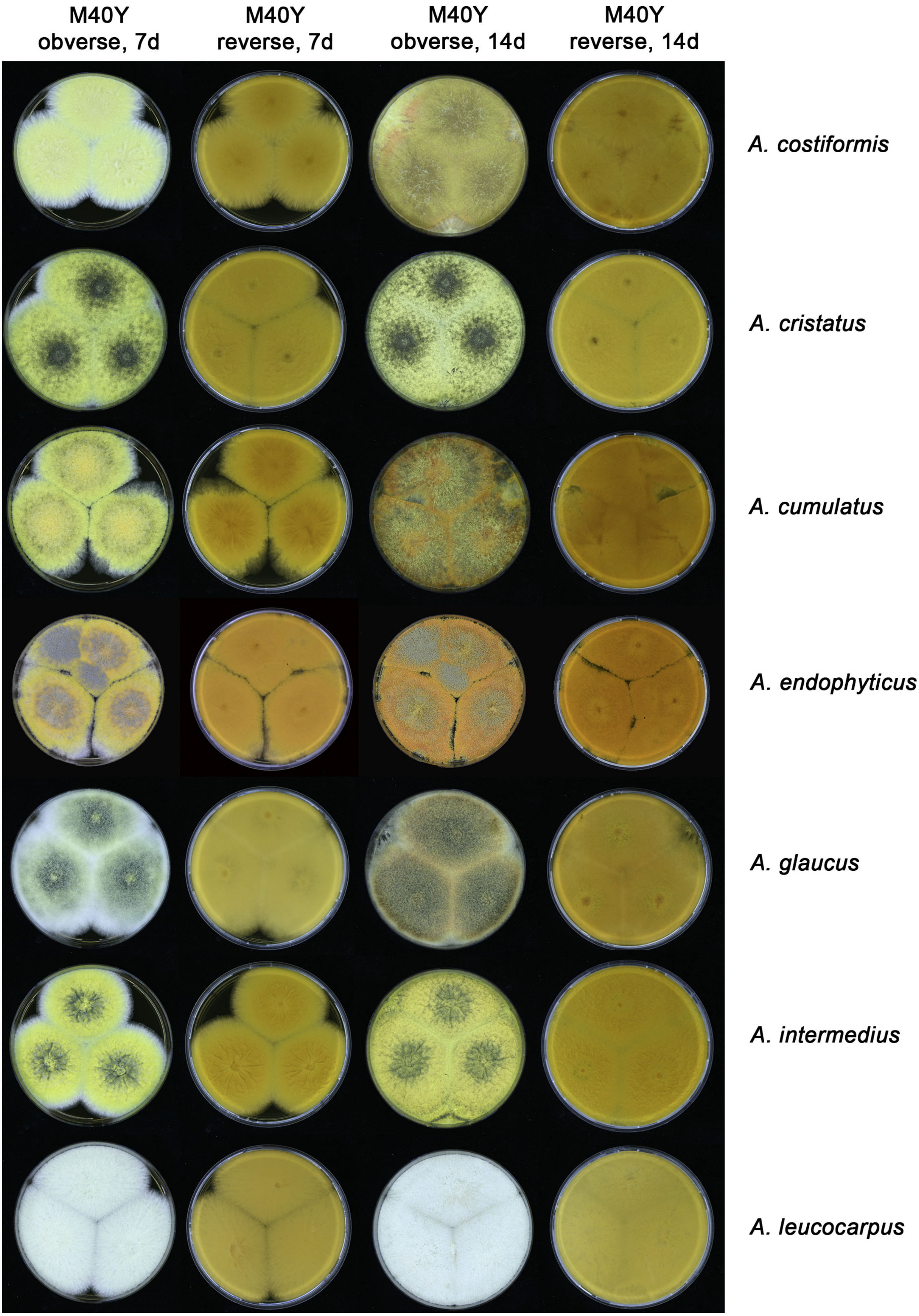


Fig. 14. Growth comparison of *Aspergillus* sect. *Aspergillus* species on M40Y for 7 d and 14 d at 25 °C.

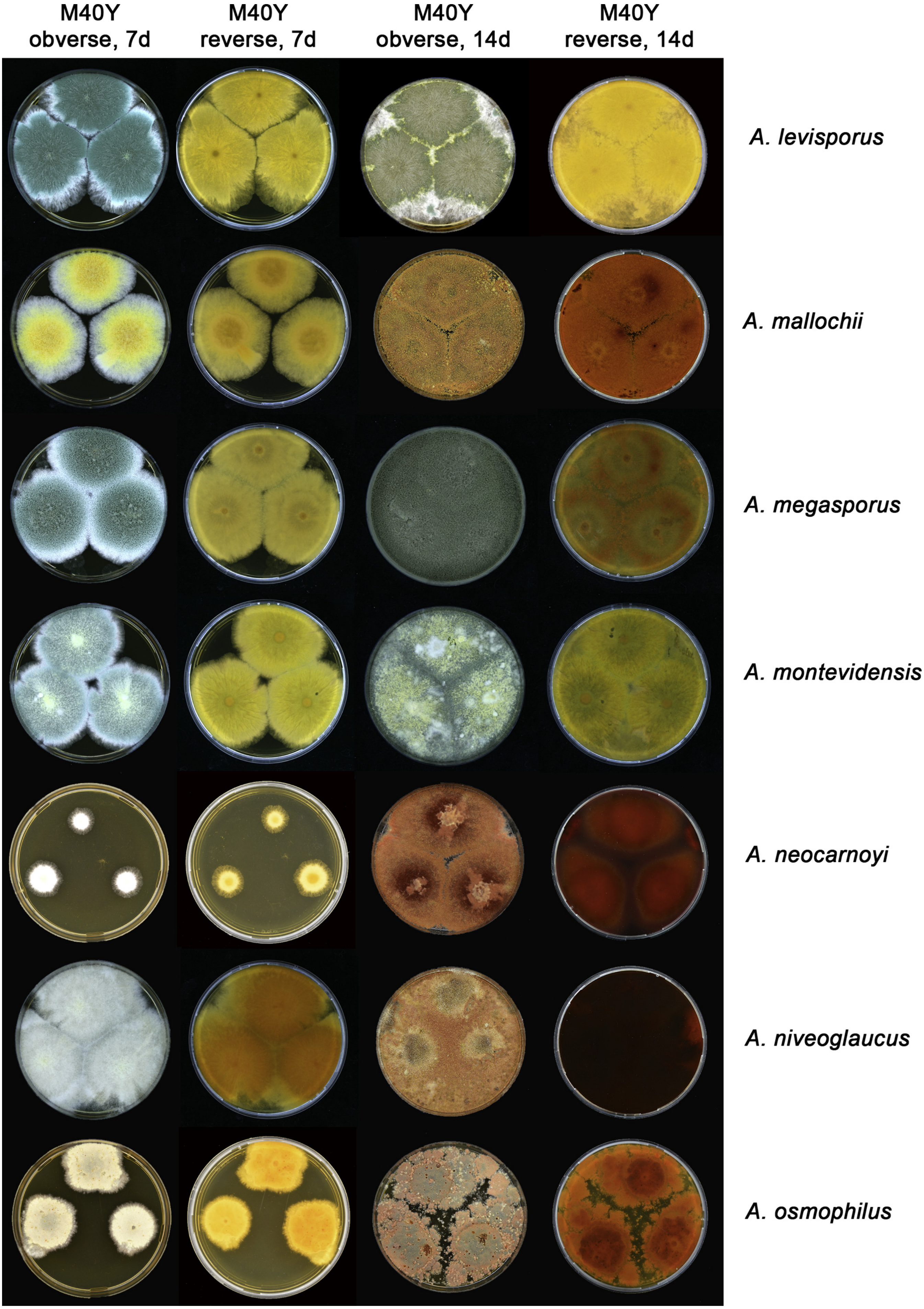


Fig. 15. Growth comparison of *Aspergillus* sect. *Aspergillus* species on M40Y for 7 d and 14 d at 25 °C.

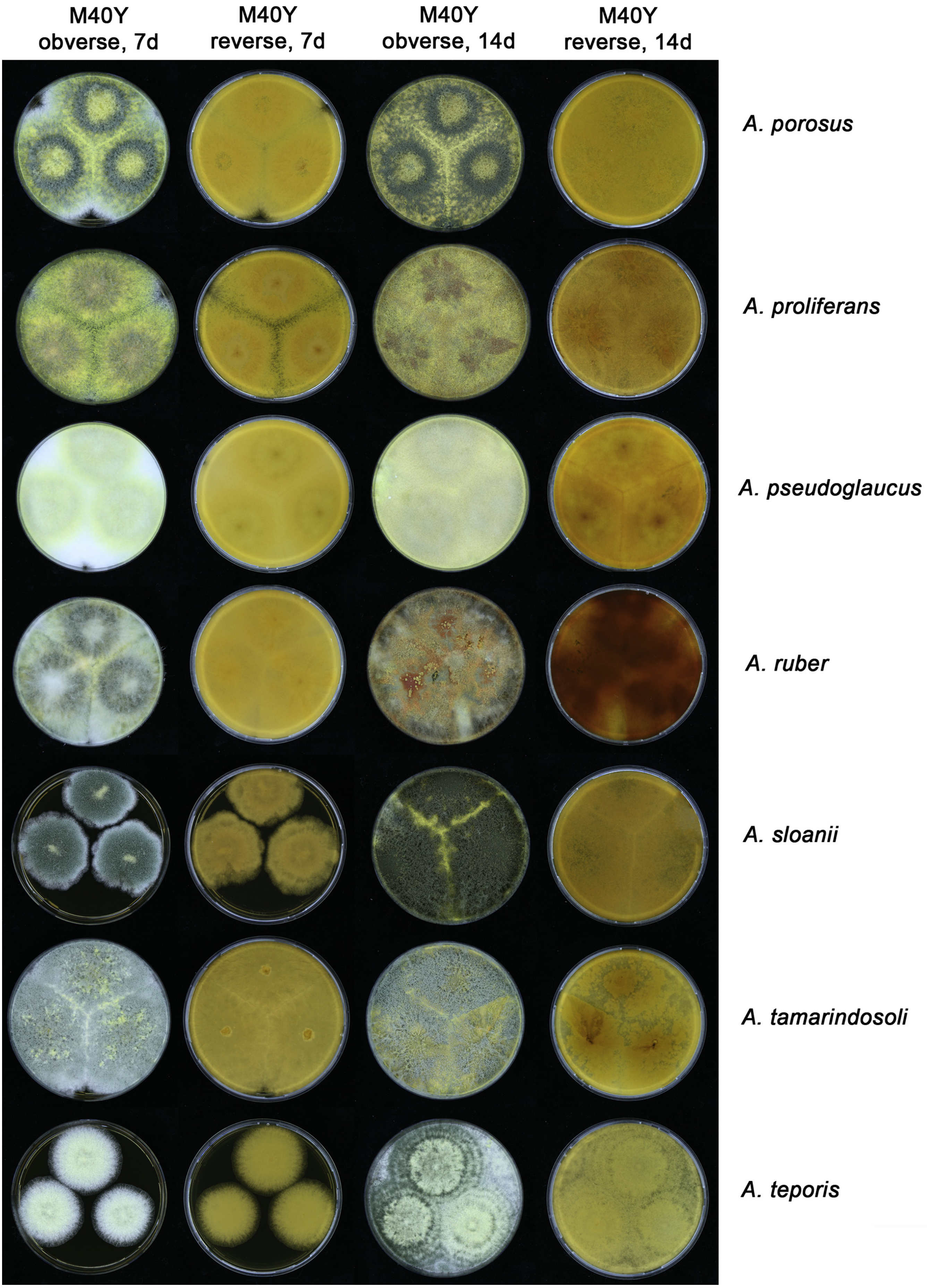


Fig. 16. Growth comparison of *Aspergillus* sect. *Aspergillus* species on M40Y for 7 d and 14 d at 25 °C.

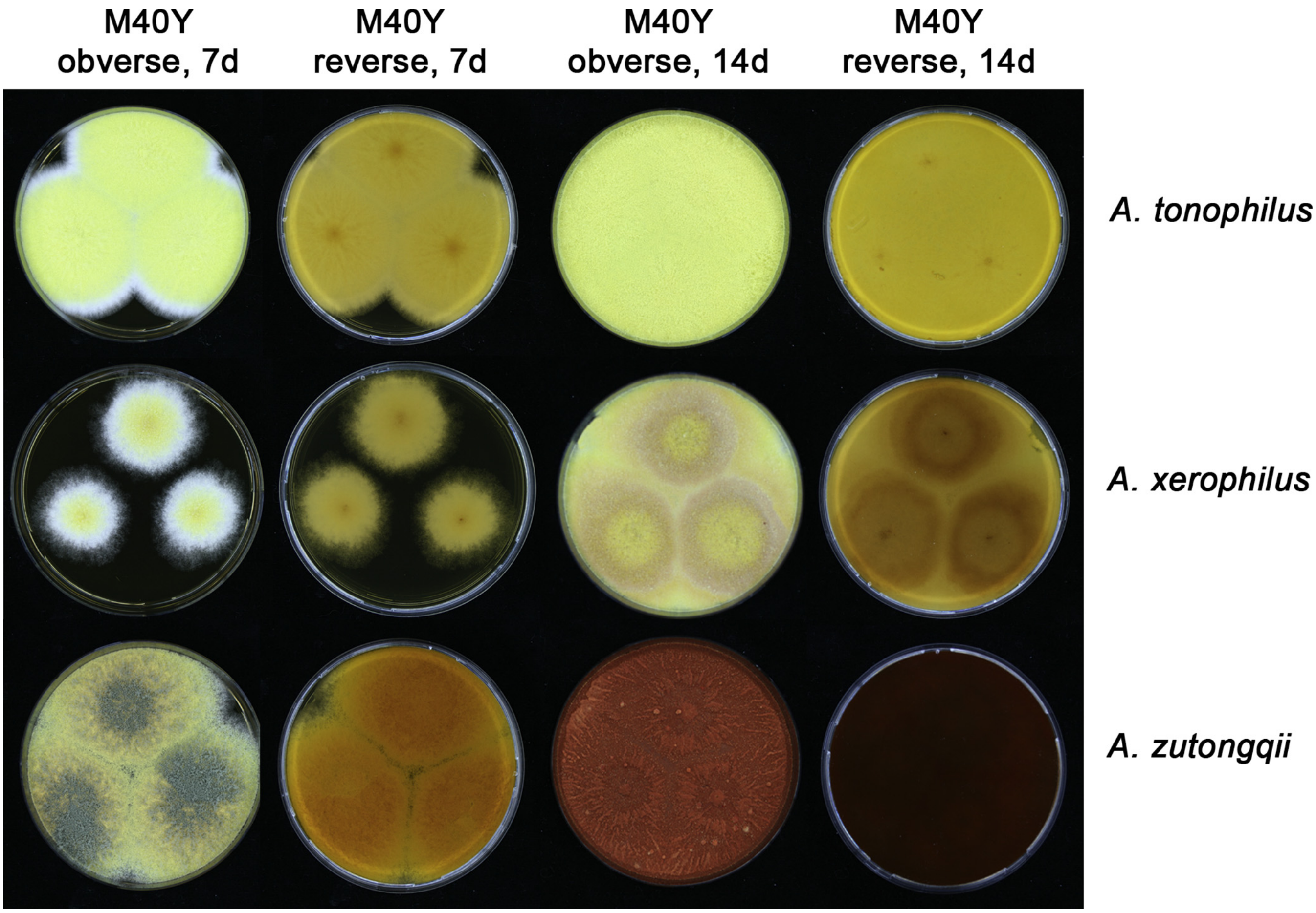


Fig. 17. Growth comparison of *Aspergillus* sect. *Aspergillus* species on M40Y for 7 d and 14 d at 25 °C.

further proved by phylogenetic analyses of Hubka *et al.* (2013a), where *A. athecius* was synonymized with *A. ruber*.

Clade classification in section *Aspergillus*

Aspergillus ruber clade

Most members of this clade produce non-crested ascospores or ascospores with reduced crests, the only exception is *A. cumulatus*, which produces irregular, low (<0.5 μm) crests. All species in this clade cannot grow on CY20S at 37 °C, four species (*A. appendiculatus*, *A. cumulates*, *A. mallochii*, *A. sloanii*) cannot grow on M60Y at 37 °C. Most species except *A. appendiculatus* can grow on CY20S at 25 °C, all species grow rapidly on M60Y at 25 °C.

Accepted species:
Aspergillus appendiculatus Blaser 1975, Sydowia 28: 38. [MB309209].
Aspergillus cumulatus D.H. Kim & S.B. Hong, J. Microbiol. Biotechnol. 24: 335. 2014. [MB807118].
Aspergillus mallochii Visagie, Yilmaz & Seifert, MycoKeys 19: 16. 2017. [MB819025].
Aspergillus pseudoglaucus Blochwitz, Ann. Mycol. 27: 207. 1929. [MB275429].
Aspergillus ruber (Jos. König *et al.*) Thom & Church, *Aspergillus*: 112. 1926. [MB490579].
Aspergillus sloanii Visagie, Hirooka & Samson, Stud. Mycol. 78: 108. 2014. [MB809194].
Aspergillus tonophilus Ohtsuki, Bot. Mag. (Tokyo) 75: 438. 1962. [MB326663].
Aspergillus zutongqii A.J. Chen, Frisvad & Samson, this study [MB818739].

Aspergillus glaucus clade

Members of this clade produce non-crested ascospores or ascospores with low crests (<0.5 μm) or irregular crests measuring 0.5–1 μm. All species in this clade cannot grow on CY20S and M60Y at 37 °C. Most species grow moderately on CY20S and grow rapidly on M60Y at 25 °C, except *A. neocarnoyi* grows restrictedly on CY20S at 25 °C (3–5 mm after 7 d).

Accepted species:
Aspergillus aerius A.J. Chen, Frisvad & Samson, this study [MB818731].
Aspergillus aurantiacoflavus Hubka, A.J. Chen, Jurjević & Samson, this study [MB818732].
Aspergillus brunneus Delacr., Bull. Soc. Mycol. France 9: 185. 1893. [MB204832].
Aspergillus glaucus (L.) Link, Mag. Ges. Naturf. Freunde Berlin 3: 16. 1809. [MB161735].
Aspergillus levisporus Hubka, A.J. Chen, Jurjević & Samson, this study [MB818735].
Aspergillus megasporus, Visagie, Yilmaz & Seifert, MycoKeys 19: 17. 2017. [MB819028].

Table 7. Extrolites reported from *Aspergillus* section *Aspergillus*.[1]

Biosynthetic family	Compounds	References	Producers
Cyclic dipeptides with a dimethylallyl group	LL-S-490β = N-a-acetylaszonalenine, rugulosuvine	Ellestad *et al.* 1973, Micheluz *et al.* 2016	*A. glaucus*, *A. pseudoglaucus*
Deoxybrevianamides[2]	Deoxybrevianamide E	Micheluz *et al.* 2016	*A. glaucus* (& *A penicillioides*)
Stachybotryamides[2]	Stachybotryamide	Micheluz *et al.* 2016	*A. glaucus*
Tryprostatins[2]	Tryprostatin B	Micheluz *et al.* 2016	*A. glaucus*
Tenellins[2]	Tenellin	Micheluz *et al.* 2016	*A. glaucus*
Echinulins	Echinulin, dehydroechinulin, didehydroechinulin, preechinulin, L-alanyl-L-tryptophan anhydride, (L-valyl-L-tryptophan anhydride, cryptoechinulin G, neoechinulin, neoechinulin A, neoechinulin B (= E-10), neoechinulin C (= cryotoechinulin A = E-8), neoechinulin D, neoechinulin E = cryptoechinulin C, dihydroneoechinulin B, isoechinulin A, isoechinulin B, isoechinulin C, dihydroxyisoechinulin A, rubrumazine A, rubrumazine B, rubrumazine C, tardioxopiperazine A, tardioxopiperazine B, dehydrovariecolorin L, variecolorin A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, golmaneone, 12-demethyl-12-oxo-eurotechinulin A, B, alkaloid E-7, cristatumin A, cristatumin B, cristatumin C,[3] cristatumin D, cristatumin E,[3] critatumin F, eurocristatine[3]	Quilico & Panazzi 1943, Quilico & Cardini 1950, Barbetta *et al.* 1969, Nakashima & Slater 1971, Allen 1972, Dossena *et al.* 1974, Cardillo *et al.* 1974, 1975, Marchelli *et al.* 1975, Nagasawa *et al.* 1975, 1976, Hamasaki *et al.* 1976a, b, Stipanovic & Schroeder 1976, Stipanovics *et al.* 1976, Inoue *et al.* 1977a, Marchelli *et al.* 1977, Gatti *et al.* 1978, Podojil *et al.* 1979, Fujimoto *et al.* 1999 (fungus was *A. pseudoglaucus*, misidentified as *Microascus tardifaciens*), Li *et al.* 2004a, b, Smetanina *et al.* 2007, Wang *et al.* 2007a, b, c, Li *et al.* 2008a, b, Slack *et al.* 2009, Almeida *et al.* 2010, Zhou *et al.* 2010 (misidentified as a *Penicillium griseofulvum*); Du *et al.* 2012, Gao *et al.* 2011, 2012a; Gomes *et al.* 2012, Yan *et al.* 2012, Gao *et al.* 2013 (misidentified as *A. effusus*), Wu *et al.* 2013, Miyake *et al.* 2014, Zou *et al.* 2014, Meng *et al.* 2015, Micheluz *et al.* 2016, Visagie *et al.* 2017	*A. brunneus*, *A. chevalieri*, *A. cristatus*, *A. glaucus*, *A. mallochii*, *A. megasporus*, *A. montevidensis*, *A. proliferans*, *A. pseudoglaucus*, *A. ruber* (Arestricticins A, B, cristatin A and asperglaucide were reported from *A. restrictus* and *A. penicillioides* (Itabashi *et al.* 2006), indicating a strong relationship between species in sections *Aspergillus* and *Restricti*.)
Quinolone	Quinolactacin A1, Quinolactacin A2, Quinolactacin B	Visagie *et al.* 2017	*A. megasporus*
Chimeric echinulins and auroglaucins	Cryptoechinulin B (= aurechinulin), (+) and (−)-cryptoechinulin D, 7-O-methylvariecolortide A, variecolortide A, (+) & (−) variecolortide B, (+) & (−) variecolortide C, (+) & (−) 7-isopentenylcryptoechinuline D, dihydrocryptoechinulin D, effusin A	Gatti *et al.* 1976, Inoue *et al.* 1977b, Li *et al.* 2010, Wang *et al.* 2007b (misidentified as *A. variecolor*); Kuttruff *et al.* 2011, Yan *et al.* 2012, Gao *et al.* 2012b (misidentified as *A. effusus*), Gao *et al.* 2013 (misidentified as *A. effusus*), Chen *et al.* 2014	*Aspergillus montevidensis*, *A. ruber*
Anthraquinones	Catenarin, emodic acid, emodin (= parietin), erythroglaucin, fallacinol, physcion, questin (= emodin 8-O-methylether), questinol, rubrocristin, variecolorquinone A, (2S)-2,3-dihydroxypropyl-1,6,8-trihydroxy-3-methyl-9,10-dioxoanthracene-2-carboxylate, 3-O-(α-D-ribofuranosyl)questinol, 3-O-(α-D-ribofuranosyl)questin, rubrocristin, viocristin, isoviocristin, hydroxyviocristin, eurorubrin, asperinine A, B, ω-hydroxyemodin-5-merthyether, ω-hydroxyrubrocristin	Anslow & Raistrick 1940, Bachmann *et al.* 1979, 1982, Anke *et al.* 1980a, b, Fujimoto *et al.* 1999, Engstrom *et al.* 1982, Laatsch & Anke 1982, Arai *et al.* 1989, Wang *et al.* 2006 (as *Chaetomium globosum*), Smetanina *et al.* 2007, Wang *et al.* 2007c (fungus misidentified as *A. variecolor*), Du *et al.* 2008, Wang *et al.* 2008, Li *et al.* 2009, Gomes *et al.* 2012, Almeida *et al.* 2010, Yan *et al.* 2012, Du *et al.* 2014, Micheluz *et al.* 2016, Visagie *et al.* 2017	*A. brunneus*, *A. chevalieri*, *A. cristatus*, *A. glaucus*, *A. intermedius*, *A. leucocarpus*, *A. mallochii*, *A. megasporus*, *A. neocarnoyi*, *A. niveoglaucus*, *A. pseudoglaucus*, *A. ruber*, *A. tonophilus* (Citreorosein was reported from *A. penicillioides* by Micheluz *et al.* 2016)
Asperflavins	Anhydroasperflavin, asperflavin, asperflavin ribofuranoside, isoasperflavin	Grove 1972a (misidentified as *A. flavus*), Anke *et al.* 1978, Fujimoto *et al.* 1999, Li *et al.* 2006 (misidentified as *Microsporum*), Smetanina *et al.* 2007, Du *et al.* 2008, 2014	*A. glaucus*, *A. pseudoglaucus*, *A. megasporus*
Isotorachrysones	Isotorachrysone, isotarachrysone 6-O-α-D-ribofuranoside, 8-methoxy-3-methyl-1-naphthalenol-6-O-α-D-ribofuranoside, 8-methoxy-1-naphthalenol-6-O-α-D-ribofuranoside, (+)-variecolorquinone A, aspergiodiquinone	Wang *et al.* 2007a (misidentified as *A. variecolor*), Du *et al.* 2008, Sun *et al.* 2013	*A. glaucus*
Aspergiolides	Aspergiolide A, B, C, D	Du *et al.* 2007, 2008, 2011, Sun *et al.* 2009, 2013, Tao *et al.* 2009	*A. glaucus*
Eurotionones	Eurotinone, variecolorquinone B, 2-methyleurotinone, 9-dehydroxyeurotinone, 2-O-methyl-9-dehydroxyeurotinone, 2-O-methyl-4-O-(α-D-ribofuranosyl)-9-	Wang *et al.* 2007c, Li *et al.* 2009, Yan *et al.* 2012, Miyake *et al.* 2014, Meng *et al.* 2016	*A. ruber*

(*continued on next page*)

Table 7. (Continued).

Biosynthetic family	Compounds	References	Producers
	dehydroxyeurotinone, all related to anthraquinones, (+) & (−) europhenol A		
Bianthrons	(*trans*) & (*cis*)-emodin-physcion bianthrone, physcionanthrone (= physciondianthranol), physcion bianthrone (= physcion-dianthrone = physcion anthrone dimer), physcion-anthrone A (= physcion-9-anthrone), physcion anthrone B	Ashley *et al.* 1939, Bachmann *et al.* 1979, Anke *et al.* 1980a, b	*A. cristatus*, *A. chevalieri*
Asperentins	Asperentin (=cladosporin), cladosporin 8-O-methylether (= asperentin 8-O-methyl ether), aspyran, asperentin-6-O-methyl ether, 5′-hydroxy-asperentin-8-methyl ether, 5′-hydroxyasperentin, 4′-hydroxyasperentin, (isocladosporin), 6-O-α-D-ribosylasperentin, 6-O-α-D-ribosyl-8-O-methylasperentin, 5-hydroxyl-6-O-methylasperentin	Grove 1972b, 1973, Cattel *et al.* 1973 (misidentified as *A. flavus*), Podojil *et al.* 1979, Fujimoto *et al.* 1999, Wang *et al.* 2006 (as *Chaetomium globosum*), Slack *et al.* 2009, Kimura *et al.* 2012, Wang *et al.* 2013 (as *Cladosporium cladosporioides*), Kozlovsky *et al.* 2014, Tang *et al.* 2014, Greco *et al.* 2015, Cochrane *et al.* 2016 (from *Cladosporium cladosporioides*)	*A. chevalieri*, *A. montevidensis*, *A. proliferans*, *A. pseudoglaucus*, *A. ruber*
Mycophenolic acids	5,7-dihydroxy-4-methylphthalide, 6-farnesyl-5,7-dihydroxy-4-methylphthalide , mycophenolic acid	Grove 1972a, b (misidentified as *A. flavus*), Burkin & Kononenko 2010, Gao *et al.* 2011, 2012a, b, Séguin *et al.* 2014	*A. pseudoglaucus*, *A. ruber* (traces of mycophenolic acid), *A. montevidensis* (traces of mycophenolic acid), *A. chevalieri* (traces of mycophenolic acid)
Pseurotins[2]	Pseurotin A & D	Micheluz *et al.* 2016	*A. glaucus*
Orsellinic acid derivatives	Cristatumside A	Du *et al.* 2014	*A. cristatus*
Kotanins	Desmethylkotanin, kotanin	Büchi *et al.* 1971	*A. glaucus*
Auroglaucins	Auroglaucin, flavoglaucin, dihydroauroglaucin, isodihydroauroglaucin, isotetrahydroauroglaucin (= dihydroflavoglaucin), chaetopyranin, 2-(2′,3-epoxy-1′,3-heptadienyl)-6-hydroxy-5-(3-methyl-2-butenyl)benzaldehyde, tetrahydroauroglaucin, (E)-2-(hept-1-enyl)-3-(hydroxymethyl)-5-(3-methylbut-2-enyl) benzene-1,4-diol, (E)-4-(hept-1-enyl)-7-(3-methylbut-2-enyl)-2,3-dihydrobenzofuran-2,5-diol, eurotirumin, 2-(2′,3-epoxy-1′-heptenyl)-6-hydroxy-5-(3″-methyl-2″-butenyl)benaldehyde, (E)-6-hydroxy-7-(3-methyl-2-butenyl)-2-(3-oxobut-1-enyl) chroman-5-carbaldehyde, 2-(1′,5′-heptadienyl)3,6-dihydroxy-5-(3″-methyl-2″butenyl)benzaldehyde, aspergentisyl A, B, aspergin	Gould & Raistrick 1934, Ashley *et al.* 1939, Quilico *et al.* 1949, Birch 1958, Inoue *et al.* 1977c, Hamasaki *et al.* 1980, 1981, Ishikawa *et al.* 1984, 1985, Li *et al.* 2006, Wang *et al.* 2006 (as *Chaetomium globosum*), Li *et al.* 2008a, b, Miyake *et al.* 2009, Slack *et al.* 2009, Almeida *et al.* 2010, Miyake *et al.* 2010a, b, Gao *et al.* 2011, 2012a, b, Gao *et al.* 2013 (misidentified as *A. effusus*), Sun *et al.* 2013, Wu *et al.* 2013, Miyake *et al.* 2014, Visagie *et al.* 2017	*A. brunneus*, *A. glaucus*, *A. glaucus*? (as *Microsporum* sp.), *A. chevalieri*, *A. cristatus*, *A glaucus*, *A. montevidensis*, *A. mallochii*, *A. pseudoglaucus*, *A. ruber*
Heveadrides	Epiheveadride, heveadride	Slack *et al.* 2009	*A. glaucus*, *A. montevidensis*, *A. ruber*
Chaetoviridins	Chaetoviridin A	Micheluz *et al.* 2016	*A. glaucus*
Eurocin	Eurocin	Oeemig *et al.* 2012	*A. montevidensis*
Diterpene antibiotics	LL-S491β, LL-S491γ	Ellestad *et al.* 1972	*A. chevalieri*
Asperglaucide	Asperglaucide	Cox *et al.* 1976	*A. glaucus*
Hopane type triterpenoids	2-Hydroxydiplopterol	Wang *et al.* 2009 (misidentified as *A variecolor*)	*Aspergillus* section *Aspergillus* species
Mycotoxin production by *Aspergillus* section *Aspergillus* strains checked but not confirmed in this study			
Citrinin (produced by a contaminant?)		Li *et al.* 2006	*A. glaucus*? (as *Microsporum* sp.)
Aflatoxins (not produced) (Bachmann *et al.* 1979, 1982, Blaser *et al.*, 1980, Varga *et al.* 2009)		Kulik & Holaday, 1966, Leitao *et al.* 1989, Jayraman & Kalyanasundaram 1990, El-Kady *et al.* 1994, Ahmed *et al.* 2005, Fraga *et al.* 2007, 2008	*A. chevalieri*, *A. intermedius*, *A. pseudoglaucus*, *A. ruber*
Sterigmatocystin (not produced) (Rank *et al.* 2011)		Schroeder & Kelton, 1975, Moubasher *et al.* 1977, Szebiotko *et al.* 1981, Karo & Hadlok, 1982, Soboleva & Kurmanov, 1984, El-Kady *et al.* 1994, Ahmed *et al.* 2005	*A. chevalieri*, *A. intermedius*, *A. montevidensis*, *A. pseudoglaucus*, *A. ruber*

Table 7. (Continued).

Biosynthetic family	Compounds	References	Producers
Xanthocillin X (not produced) (Bachmann *et al.* 1979, 1982, Blaser *et al.* 1980)		Coveney *et al.* 1966	*A. glaucus*
Gliotoxin (not produced) (Bachmann *et al.* 1979, 1982, Blaser *et al.* 1980)		Wilkinson & Spilsbury 1965, El-Kady *et al.* 1994	*A. chevalieri*, *A. intermedius*, *A. pseudoglaucus*
Ochratoxin A (not produced) (Bachmann *et al.* 1979, 1982, Blaser *et al.* 1980)		Chelkowski *et al.* 1987, El-Kady *et al.* 1994, Al-Julaifi 2003	*A. glaucus*, *A. montevidensis*, *A. pseudoglaucus*

[1] Chevalone A-D, aszonapyrone A-B, eurochevalierine and CJ-12662 reported from *Eurotium chevalieri* were produced by a strain from *Aspergillus* section *Fumigati* (see Frisvad & Larsen 2016).

[2] These compounds may have been produced by a strain of *Aspergillus* section *Fumigati* contaminating *A. pseudoglaucus* (*Eurotium repens*), as they have been found co-occurring in *Aspergillus fumigatus* (see Frisvad & Larsen 2016), but never in *Aspergillus* section *Aspergillus*.

[3] Diketopiperazine dimers.

Table 8. Extrolites found in the different species of *Aspergillus* section *Aspergillus*. Tetracyclic means compounds with a UV spectrum typical of BMS-192548 (Shu *et al.* 1995) or similar UV spectra.

Species	Extrolites
Aspergillus aerius	Auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, tetracyclic, tetrahydroauroglaucin
A. appendiculatus	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, questin, questinol, tetracyclic, tetrahydroauroglaucin, “MYO”
A. aurantiacoflavus	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, epiheveadrides, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, questin, questinol, tetracyclic, tetrahydroauroglaucin
A. brunneus	Asperflavin, asperentins, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, 5-farnesyl-5,7-dihydroxy-4-methylphthalide, erythroglaucin, flavoglaucin, isoechinulins, mycophenolic acid, neoechinulins, physcion, questin, tetracyclic, tetrahydroauroglaucin
A. caperatus	Auroglaucin, a bisanthron, dihydroauroglaucin, echinulins, epiheveadrides, flavoglaucin, isoechinulins, neoechinulins, physcion, tetrahydroauroglaucin
A. chevalieri	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, epiheveadrides, flavoglaucin, isoechinulins, neoechinulins, physcion, questin, questinol, tetracyclic, tetrahydroauroglaucin, unique: “MYO”
A. cibarius	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, erythroglaucin, flavoglaucin, neoechinulins physcion, tetracyclic, tetrahydroauroglaucin
A. costiformis	Auroglaucin, dihydroauroglaucin, echinulins, epiheveadrides, flavoglaucin, isoechinulins, neoechinulins, physcion, tetrahydroauroglaucin
A. cristatus	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, epiheveadrides, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, tetrahydroauroglaucin, “MYO”
A. cumulatus	Auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, tetracyclic, tetrahydroauroglaucin (DTO 308-D8: “canescins”; DTO 355-G9 produces another type of indolealkaloids than echinulins in addition to echinulins, similar to 12,13-dehydro-deoxybrevianamide E)
A. endophyticus	Auroglaucin, bisanthrones, dihydroauroglaucin, echinulins (for all species we did find preechinulin, echinulin, neoechinulin A and B), emodin, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, tetrahydroauroglaucin
A. glaucus	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, epiheveadrides (traces), erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, questin, questinol, tetracyclic, tetrahydroauroglaucin
A. intermedius	Asperflavin, auroglaucin, dihydroauroglaucin, echinulins, epiheveadrides, flavoglaucin, isoechinulins, LL-S491β, neoechinulins, physcion, questin, tetrahydroauroglaucin
A. leucocarpus	An apolar indoloterpene, echinulins, epiheveadrides, neoechinulins, “MUDI” 1-3
A. levisporus	Auroglaucin, dihydroauroglaucin, echinulins, flavoglaucin, isoechinulins, neoechinulins, tetrahydroauroglaucin, unique: “WOF” 1 & 2
A. mallochii	Auroglaucin, dihydroauroglaucin, echinulins, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, tetracyclic, tetrahydroauroglaucin
A. megasporus	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulin, emodin, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, preechinulin, physcion, quinolactacin (A1, A2, B), tetracyclic, tetrahydroauroglaucin
A. montevidensis	Apolar indoloterpenes, asperflavin in few isolates, auroglaucin, dihydroauroglaucin, echinulins, epiheveadrides, flavoglaucin, isoechinulins, neoechinulins, tetrahydroauroglaucin

(*continued on next page*)

Table 8. (Continued).

Species	Extrolites
A. neocarnoyi	Asperentins, asperflavin, auroglaucin, a bisanthron, dihydroauroglaucin, echinulins, flavoglaucin, neoechinulins, questin, questinol, tetracyclic, tetrahydroauroglaucin
A. niveoglaucus	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, erythroglaucin, flavoglaucin, mycophenolic acid (tentatively identified), neoechinulins, physcion, questin, questinol, siderin (in DTO 355-C4), tetracyclic, tetrahydroauroglaucin
A. osmophilus	Asperflavin, auroglaucin, flavoglaucin, dihydroauroglaucin, tetrahydroauroglaucin, echinulin and neoechinulin A.
A. porosus	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, epiheveadrides, isoechinulins, flavoglaucin, neoechinulins, physcion, tetrahydroauroglaucin
A. proliferans	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, epiheveadrides, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, questin, tetracyclic, tetrahydroauroglaucin
A. pseudoglaucus	Asperentins, asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, erythroglaucin, 6-farnesyl-5,7-dihydroxy-4-methylphthalide, flavoglaucin, isoechinulins, mycophenolic acid, neoechinulins, physcion, questin, questinol, tetracyclic, tetrahydroauroglaucin
A. ruber	Auroglaucin, bisanthrons, catenarin, dihydroauroglaucin, echinulins, epiheveadrides, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, physcion, questin, questinol, tetracyclic, tetrahydroauroglaucin (Ex type of *A. athecius* CBS 464.65 produced breviones and no red anthraquinones)
A. sloanii	Auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, flavoglaucin, physcion, tetracyclic, tetrahydroauroglaucin
A. tamarindosoli	Asperflavin, auroglaucin, bisanthrons, echinulins, emodin, dihydroauroglaucin, epiheveadrides, flavoglaucin, isoechinulins, neoechinulins, physcion, tetrahydroauroglaucin, unique: “MYO”
A. teporis	Echinulins, epiheveadrides, isoechinulins, neoechinulins, unique: “KYF” 1 & 2
A. tonophilus	Auroglaucin, bisanthrons (few), dihydroauroglaucin, echinulins, flavoglaucin, an apolar indoloterpene, isoechinulins, neoechinulins, tetrahydroauroglaucin
A. xerophilus	Bisanthrons, dihydroauroglaucin, echinulins, erythroglaucin, isoechinulins, neoechinulins, physcion, sulochrin, tetracyclic, unique: “XERO”
A. zutongqii	Asperflavin, auroglaucin, bisanthrons, dihydroauroglaucin, echinulins, emodin, epiheveadrides, erythroglaucin, flavoglaucin, isoechinulins, neoechinulins, (tetracyclic), tetrahydroauroglaucin

Table 9. Identification of indoor section *Aspergillus* species from fifteen countries.

Species	Strain no.	Substrate	Location	*CaM* GenBank accession nr.
Aspergillus aerius	CBS 141771 = DTO 241-G7	Air treatment system in plant production	The Netherlands	LT670991
A. appendiculatus	DTO 197-F5	Air, bakery	Tilburg, the Netherlands	LT671231
A. chevalieri	DTO 080-H3	Air, house	Stuttgart, Germany	LT671221
	DTO 106-E5	Vultures enclosure (indoor)	Amsterdam, the Netherlands	LT671222
	DTO 124-E8	Air in food related factory	Ospel, the Netherlands	LT671223
	DTO 130-E7	Indoor environment	Thailand	LT671224
	DTO 131-B6	Indoor environment	Thailand	LT671225
	DTO 177-B1	Air, bakery	Heerde, the Netherlands	LT671226
	DTO 177-B3	Air, bakery	Heerde, the Netherlands	LT671227
	DTO 268-B7	Houst dust	Mexico	LT671229
	DTO 266-F8	Houst dust	Thailand	LT671230
	EMSL No. 2223	Air, hospital	Fairfax, VA, USA	LT671218
	EMSL No. 56	Indoor air	California, USA	LT671219
	EMSL No. 2871	Indoor air, basement	Denver, CO, USA	LT671220
A. cibarius	DTO 123-E7	Air, office	Zutphen, the Netherlands	LT671232
	DTO 124-B9	Air in food related factory	Ospel, the Netherlands	LT671233
	DTO 197-F6	Air, bakery	Tilburg, the Netherlands	LT671234
A. glaucus	EMSL No. 2529	Air, office	Puerto Rico	LT671071
	DTO 155-G4	Indoor, paper	The Netherlands	LT671257
	EMSL No. 3317 = CCF 5382 = DTO 355-H2	Indoor air, bedroom	NY, USA	LT671074
A. intermedius	CCF 5377 = DTO 355-G5	Air, surgical operating room	Prague, Czech Republic	LT671080
A. leucocarpus	DTO 357-A2 = KAS 7576	Houst dust	Canada	LT671089
A. montevidensis	DTO 008-H7 = CBS 119376	Indoor environment	Germany	LT671235

Table 9. (Continued).

Species	Strain no.	Substrate	Location	*CaM* GenBank accession nr.
	DTO 072-E7	Indoor, archive	Amsterdam, the Netherlands	LT671236
	DTO 108-F4	Indoor environment	France	LT671237
	DTO 123-D7	Air, office	Zutphen, the Netherlands	LT671238
	DTO 126-A3	Swab sample, kitchen cabinet drawer next to sink	The Netherlands	LT671239
	DTO 146-E3	Indoor environment	Hungary	LT671240
	DTO 146-E4	Indoor environment	Hungary	LT671241
	DTO 146-E6	Indoor environment	Hungary	LT671242
	DTO 147-E4	Indoor environment	Hungary	LT671243
	DTO 177-A8	Air, bakery	Heerde, the Netherlands	LT671244
	DTO 177-A9	Air, bakery	Heerde, the Netherlands	LT671245
	DTO 177-B2	Air, bakery	Heerde, the Netherlands	LT671246
	DTO 177-B6	Air, bakery	Heerde, the Netherlands	LT671247
	DTO 177-B7	Air, bakery	Heerde, the Netherlands	LT671248
	DTO 299-A2	Indoor hospital air	Turkey	LT671249
	DTO 180-B6	House dust	South Africa	LT671250
	DTO 267-H2	House dust	Thailand	LT671251
	EMSL No. 1589	Air, green house	Delaware, USA	LT671252
	EMSL No. 2730	Black HEPA filter	Edwardsville, IL, USA	LT671254
	EMSL No. 2934 = CCF 5379 = DTO 355-H3	Indoor air, bedroom	Mahanoy City, PA, USA	LT671098
A. niveoglaucus	DTO 177-B4	Air, bakery	Heerde, the Netherlands	LT671255
	IHEM 1811 = DTO 355-C3	Indoor air	Namur, Belgium	LT671116
	EMSL No. 2211	Air, bathroom	Great Falls, MT, USA	LT671113
A. proliferans	DTO 124-C8	Air in food related factory	Ospel, the Netherlands	LT671256
	DTO 197-F7	Air, bakery	Tilburg, the Netherlands	LT671258
	DTO 197-F8	Air, bakery	Tilburg, the Netherlands	LT671259
	DTO 331-D1	Air, house	Noordwijk, the Netherlands	LT671260
	EMSL No. 2207 = CCF 5395 = DTO 355-H5	Air of living room	Yardley, PA, USA	LT671149
	EMSL No. 2791 = CCF 5392 = DTO 355-H6	Indoor air, basement	Troy, NY, USA	LT671152
A. pseudoglaucus	DTO 011-E9	Indoor air	Loosdrecht, the Netherlands	LT671264
	DTO 244-I1	Houst dust	UK	LT671265
	DTO 244-I7	Houst dust	UK	LT671266
	DTO 039-F5	Indoor environment from mortel (cement)	Düsseldorf, Germany	LT671267
	DTO 072-E6	Indoor, archive	Amsterdam, the Netherlands	LT671268
	DTO 087-G6	Air in warehouse, Citronas	The Netherlands	LT671269
	DTO 106-D1	Elephants enclosure (indoor)	Amsterdam, the Netherlands	LT671270
	DTO 106-E2	Zebra enclosure (indoor)	Amsterdam, the Netherlands	LT671271
	DTO 115-F5	Indoor	Hungary	LT671272
	DTO 117-F9	Indoor, archive	Giessenlanden, the Netherlands	LT671273
	DTO 123-D8	Air, office	Zutphen, the Netherlands	LT671274
	DTO 123-I2	Air, factory	Kerkrade, the Netherlands	LT671275
	DTO 124-D3	Air in food related factory	Ospel, the Netherlands	LT671276
	DTO 126-A2	Swab sample, kitchen cabinet drawer next to sink	The Netherlands	LT671277
	DTO 147-B6	Indoor environment	Hungary	LT671278
	DTO 147-D1	Indoor environment	Hungary	LT671279

(*continued on next page*)

Table 9. (Continued).

Species	Strain no.	Substrate	Location	*CaM* GenBank accession nr.
	DTO 147-H9	Indoor environment	Hungary	LT671280
	DTO 177-B5	Air, bakery	Heerde, the Netherlands	LT671281
	DTO 241-H5	Air treatment system in production plant	Goes, the Netherlands	LT671282
	EMSL No. 2474 = CCF 5387 = DTO 355-I4	Indoor air, basement	Piscataway, NJ, USA	LT671167
	EMSL No. 2779 = CCF 5389 = DTO 355-I3	Air in front of air conditioning vent	Melbourne, FL, USA	LT671161
	EMSL No. 1022	Indoor air of home	New Jersey, USA	LT671283
	EMSL No. 1415	Indoor air of home	Massachusetts, USA	LT671284
	EMSL No. 1643	Indoor air of hospital	Alabama, USA	LT671285
	EMSL No. 1918	Air, living room	New York, NY, USA	LT671286
	EMSL No. 1919	Air, bedroom	Fort Salonga, NY, USA	LT671287
	EMSL No. 1966	Air, hospital	New York, NY, USA	LT671288
	EMSL No. 2222	Air, bedroom	Cinnaminson, NJ, USA	LT671289
	EMSL No. 1245	Air, home	New Jersey, USA	LT671290
	EMSL No. 1246	Air, home	New Jersey, USA	LT671291
	EMSL No. 2130	Air, hospital	Trinidad & Tobago	LT671292
	EMSL No. 2472	Air, basement	Piscataway, NJ, USA	LT671293
	EMSL No. 2473	Air, basement	Piscataway, NJ, USA	LT671294
	EMSL No. 2475	Air, basement	Piscataway, NJ, USA	LT671295
	EMSL No. 2832	Carpet dust, Harker Heights Trails	TX, USA	LT671296
	EMSL No. 2834	Air, hospital	Chicago, IL, USA	LT671297
	EMSL No. 2844	Swab, bedroom	Norman, OK, USA	LT671298
	EMSL No. 2845	Swab, bedroom	Norman, OK, USA	LT671299
	EMSL No. 2860	Air, living room	Bowling Green, KY, USA	LT671300
	EMSL No. 2861	Air, living room	Bowling Green, KY, USA	LT671301
	EMSL No. 2930	Air, living room	Big Rapids, RI, USA	LT671302
	EMSL No. 1780 = CCF 5388 = DTO 355-I2	House dust	Pennsylvania, USA	LT671158
	EMSL No. 2809 = CCF 5386	Indoor air, office	Endicott, NY, USA	LT671164
A. ruber	DTO 146-E2	Indoor environment	Hungary	LT671261
	DTO 267-H3	House dust	Thailand	LT671262

Aspergillus niveoglaucus Thom & Raper, U.S.D.A. Misc. Pub. 426: 35. 1941. [MB120985].
Aspergillus neocarnoyi Kozak., Mycol. Pap. 161: 63. 1989. [MB127756].
Aspergillus proliferans G. Sm., Trans. Brit. Mycol. Soc. 26: 26. 1943. [MB284312].

Aspergillus chevalieri clade

Members of this clade produce ascospores with high crests (≥ 0.5 μm). All species in this clade can grow on M60Y at 37 °C. Most species except *A. caperatus* and *A. costiformis* can grow on CY20S at 37 °C. All species grow rapidly on CY20S and M60Y at 25 °C.

Accepted species:
Aspergillus caperatus A.J. Chen, Frisvad & Samson, this study [MB818733].
Aspergillus chevalieri (L. Mangin) Thom & Church, The Aspergilli: 111. 1926. [MB292839].
Aspergillus costiformis H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14: 10. 1995. [MB363444].
Aspergillus cristatus Raper & Fennell, Gen. *Aspergillus*: 169. 1965. [MB326622].
Aspergillus intermedius Blaser, Sydowia 28: 41. 1975. [MB309226].
Aspergillus montevidensis Talice & Mackinnon, Compt. Rend. Soc. Biol. Fr. 108: 1007. 1931. [MB309231].
Aspergillus porosus A.J. Chen, Frisvad & Samson, this study [MB818736].

Aspergillus xerophilus clade

Members of this clade produce ascospores with low crests (≤ 0.5 μm), cannot grow on CYA, MEA, CY20S, while grow rapidly on M60Y. *Aspergillus osmophilus* grows rapidly on M60Y at 37 °C, while *A. xerophilus* does not grow under this condition.

Accepted species:
Aspergillus osmophilus Asgari & Zare, Mycoscience 55: 58. 2013. [MB803278].

Aspergillus xerophilus Samson & Mouch., Antonie van Leeuwenhoek 41: 348. 1975. [MB309251].

Other species:
Aspergillus cibarius S.B. Hong & Samson, J. Microbiol. 50: 713. 2012. [MB800861].
Aspergillus endophyticus Hubka, A.J. Chen, & Samson, this study [MB818734].
Aspergillus leucocarpus Hadlok & Stolk, Antonie van Leeuwenhoek 35: 9. 1969. [MB326642].
Aspergillus tamarindosoli A.J. Chen, Frisvad & Samson, this study [MB818737].
Aspergillus teporis A.J. Chen, Frisvad & Samson, this study [MB818738].

SPECIES DESCRIPTIONS

Aspergillus aerius A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB818731. Fig. 18.

Etymology: Name refers to its origin, isolated from air treatment system.

Diagnosis: Large (6.5–8 × 4.5–6 μm), smooth ascospores with roughness along equatorial ridges, tuberculate conidia measuring (5–)10–13 × 6–10 μm.

Typus: **The Netherlands**, air treatment system in production plant, 2013, isolated by J. Houbraken (holotype CBS H-22823, culture ex-type: CBS 141771 = DTO 241-G7 = IBT 34446).

ITS barcode: LT670916. (Alternative markers: *BenA* = LT670990; *CaM* = LT670991; *RPB2* = LT670992).

Colony diam, 7 d (mm): CYA 10–12; MEA 7–10; CY20S 17–20; CY20S 30 °C 14–15; CY20S 37 °C No growth; M40Y 65–66; M60Y >75; M60Y 30 °C >75; M60Y 37 °C No growth; CYAS 35–36; DG18 40–44; MEA10S 63–65.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium pale luteous (11) to sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse pale luteous (11). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) to orange (7); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse ochreous (44). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) to orange (7); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse buff (45). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse amber (47). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 190–275 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth, 6.5–8 × 4.5–6 μm, rough along equatorial ridges, in side view lenticular, furrow present, crests absent. Conidiophores with smooth stipes, hyaline or light brown, 500–1 000 × 7–15.5 μm. Vesicles globose to subglobose, 26–41 μm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 7.5–12.5 × 5–8 μm. Conidia globose, subglobose to ellipsoidal, tuberculate, (5–)10–13 × 6–10 μm.

Distinguishing characters: The large ascospores of *A. aerius* resemble those of *A. brunneus*, but *A. brunneus* produces larger conidia, that are infrequently ellipsoidal (8–15 × 8–13 μm).

Aspergillus appendiculatus Blaser 1975, Sydowia 28: 38. MycoBank MB309209. Fig. 19.

Synonyms: *Eurotium appendiculatum* Blaser, Sydowia 28: 38. 1975.

Aspergillus aridicola H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14: 88. 1995.

Eurotium aridicola H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14: 88. 1995.

Typus: ZT 8286, holotype. Culture ex-type: CBS 374.75 = IMI 278374 = FRR 2793 = JCM 1566 = PIL 588 = IBT 34507.

ITS barcode: HE615132. (Alternative markers: *BenA* = HE801333; *CaM* = HE801318; *RPB2* = HE801307).

Colony diam, 7 d (mm): CYA No growth; MEA No growth; CY20S No growth; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y 50–52; M60Y 50–59; M60Y 30 °C 44–49; M60Y 37 °C No growth; CYAS 19–20; DG18 35–38; MEA10S 26–28.

Colony characters: M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white and sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white and sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse light citrine green (67). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white and sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse sulphur yellow (15) in the centre, citrine green (67) in the edge. MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium white; margins entire; texture floccose; sporulation moderately dense; conidia

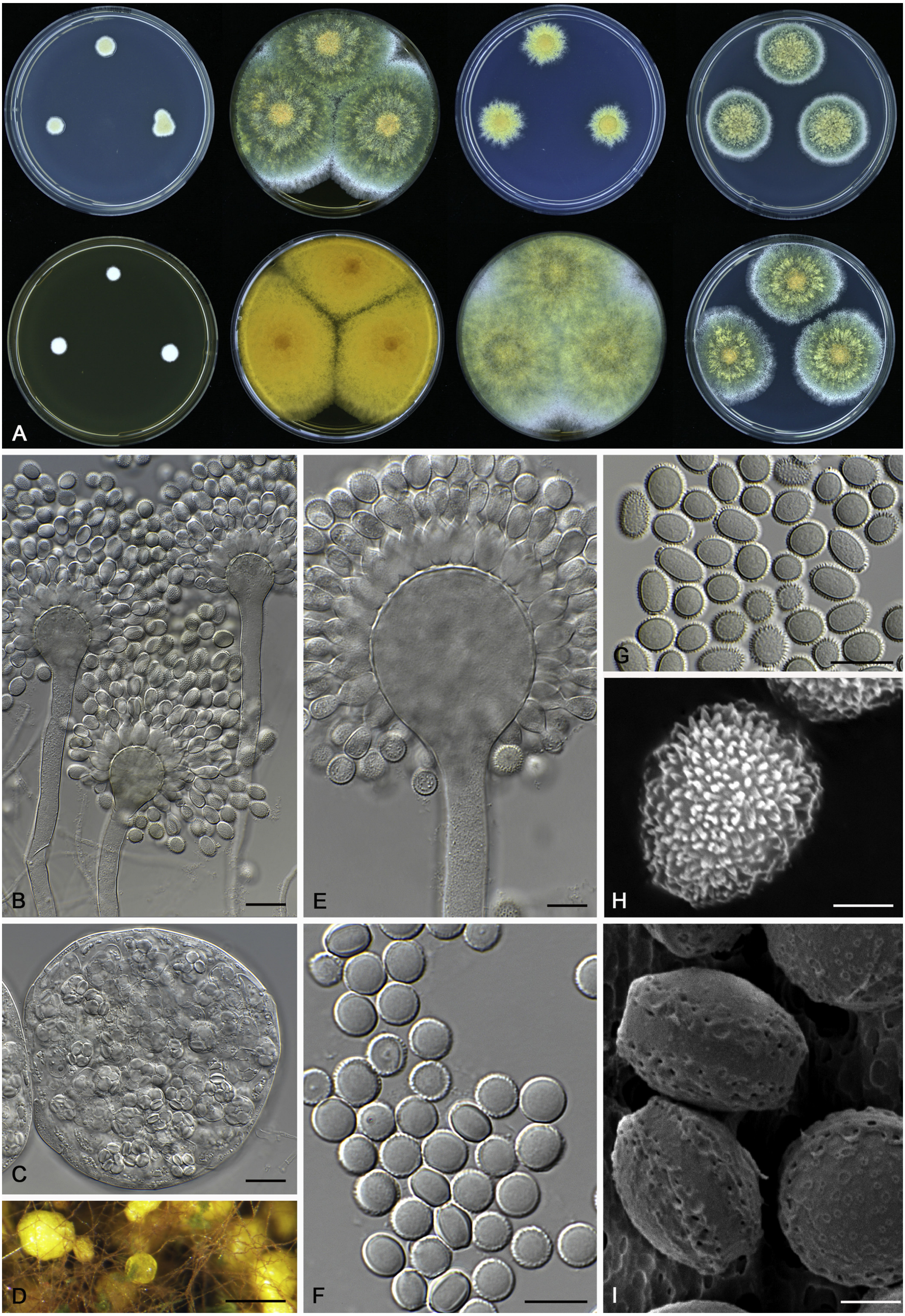


Fig. 18. *Aspergillus aerius* CBS 141771^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

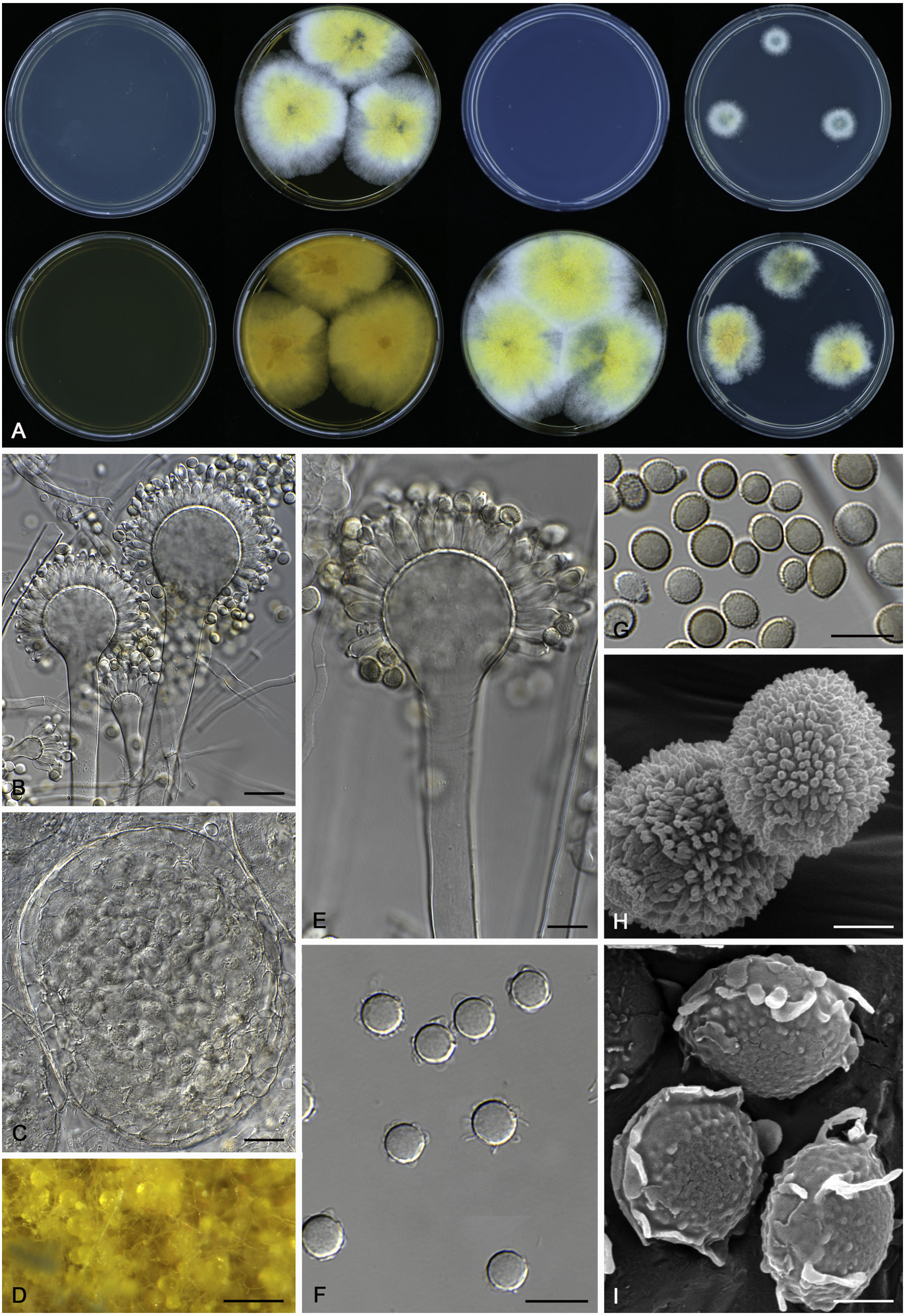


Fig. 19. *Aspergillus appendiculatus* CBS 374.75^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

en masse greyish green (50); soluble pigments absent; exudates absent; reverse sulphur yellow (15).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–225 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies slightly rough, 5–7.5 × 4–5.5 µm, in side view lenticular, furrow absent or showing as a trace, crests with filiform appendages or petaliform, petals 1–1.5 µm wide at highest parts. Conidiophores with smooth stipes, hyaline or light brown, 800–2 000 × 7–12(–14.5) µm. Vesicles globose to subglobose, 30–64 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 8–16 × 4.5–7.5 µm. Conidia globose, subglobose to ellipsoidal, tuberculate, 5–10(–12) × 5–7(–8.5) µm.

Distinguishing characters: *Aspergillus appendiculatus* is typically characterized by petaliform crests on ascospores. Similar ascospores are also produced by *A. mallochii*, which are smaller in size (4–6 × 3–5 µm).

Additional materials examined: **Canada**, House dust, 2015, isolated by C.M. Visagie, DTO 357-A3 = KAS 7579. **China**, Tibet, sheep dung, isolated by H.Z. Kong & Z.T. Qi, CBS 101746 = CGMCC 3.04673 (AS 3.4673).

Aspergillus aurantiacoflavus Hubka, A.J. Chen, Jurjević & Samson, **sp. nov.** MycoBank MB818732. Fig. 20.

Etymology: Name refers to its orange and yellow colony, *aurantiacus* = orange, *flavus* = yellow.

Diagnosis: Orange and yellow colony, verruculose ascospores measuring 4–5.5 × 3–5 µm.

Typus: **USA**, CA, San Diego, baby carrier backpack, 2015, isolated by Ž. Jurjević (holotype CBS H-22827, culture ex-type: CBS 141930 = EMSL No. 2903 = CCF 5393 = DTO 355-I1 = IBT 34485).

ITS barcode: LT670917. (Alternative markers: *BenA* = LT670993; *CaM* = LT670994; *RPB2* = LT670995).

Colony diam, 7 d (mm): CYA 2–3; MEA 2–3; CY20S 23–25; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y 65–70; M60Y 70–>75; M60Y 30 °C >75; M60Y 37 °C No growth; CYAS 38–40; DG18 44–45; MEA10S 44–45.

Colony characters: CY20S 25 °C, 7 d: Colonies low to moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation absent to sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse pale luteous (11) or buff (45). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation sparse; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) or orange (7) at centre, ochreous (44) at edge. M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation absent to moderately dense; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) or orange (7) at centre, ochreous (44) at edge. DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) or orange (7) at centre, ochreous (44) at edge. MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15) and orange (7); margins entire; texture floccose; sporulation absent to moderately dense; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) or orange (7) at centre, ochreous (44) at edge.

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 110–250 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose, 4–5.5 × 3–5 µm, in side view lenticular, furrow present, crests irregular, <0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 250–800 × 7.5–12 µm. Vesicles globose to subglobose, 30–45 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6–11 × 3.5–6.5 µm. Conidia globose to subglobose, tuberculate, 5–9 × 4–7 µm.

Distinguishing characters: Phylogenetically *A. aurantiacoflavus* is closely related to *A. proliferans* and *A. glaucus*, but *A. proliferans* produces non-crested ascospores; *A. glaucus* produces larger ascospores (5.5–7.5 × 3.5–6 µm).

Additional materials examined: **USA**, IL, Chicago, rubber toy import from China, 2015, isolated by Ž. Jurjević, CCF 5562 = EMSL No. 2690, CCF 5563 = EMSL No. 2691, CCF 5564 = EMSL No. 2692, EMSL No. 2693 = CCF 5391 = DTO 355-H7, CCF 5565 = EMSL No. 2694. **USA**, New Jersey, Cherry Hill, cake spread, 2015, isolated by Ž. Jurjević, EMSL No. 3024 = CCF 5394 = DTO 355-H9.

Aspergillus brunneus Delacr., Bull. Soc. Mycol. France 9: 185. 1893. MycoBank MB204832. Fig. 21.
Synonyms: *Eurotium echinulatum* Delacr., Bull. Soc. Mycol. France 9: 266. 1893.
Aspergillus echinulatus (Delacr.) Thom & Church, The Aspergilli: 107. 1926.
Aspergillus medius R. Meissn., Bot. Z.: 356. 1897.
Eurotium medium R. Meissn., Bot. Z.: 356. 1897.
Eurotium verruculosum Vuill. Bull. Soc. Mycol. France 34: 83. 1918.

Typus: IMI 211378, epitype (Hubka *et al.* 2013a). Culture ex-type: CBS 112.26 = CBS 524.65 = IBT 5341 = NRRL 131 = NRRL 134 = ATCC 1021 = IFO 5862 = IMI 211378 = QM 7406 = Thom 4481 = Thom 5633.4 = WB 131.

ITS barcode: EF652060. (Alternative markers: *BenA* = EF651907; *CaM* = EF651998; *RPB2* = EF651939).

Colony diam, 7 d (mm): CYA 11–12; MEA 3–5; CY20S 30–34; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y

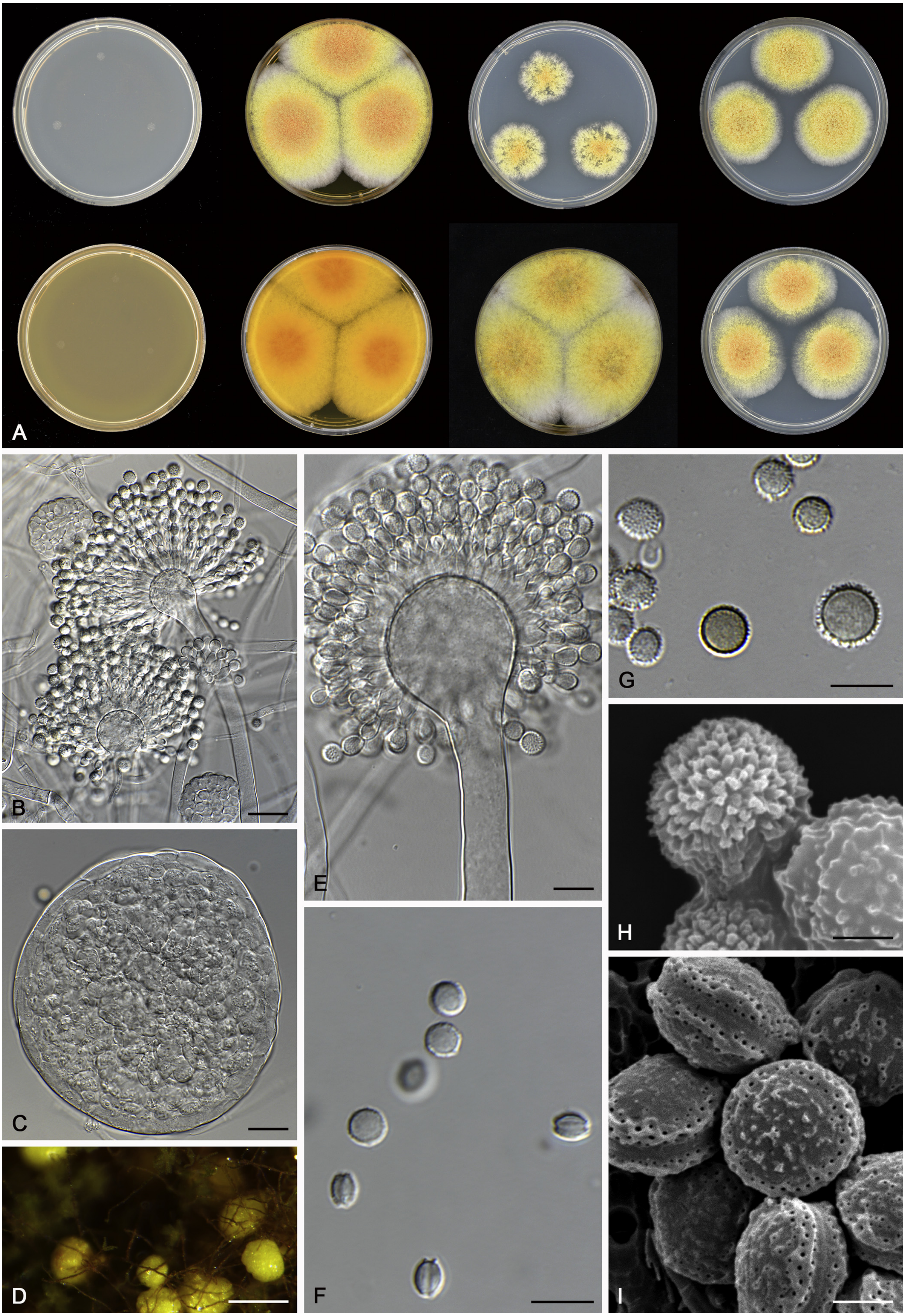


Fig. 20. *Aspergillus aurantiacoflavus* CBS 141930^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

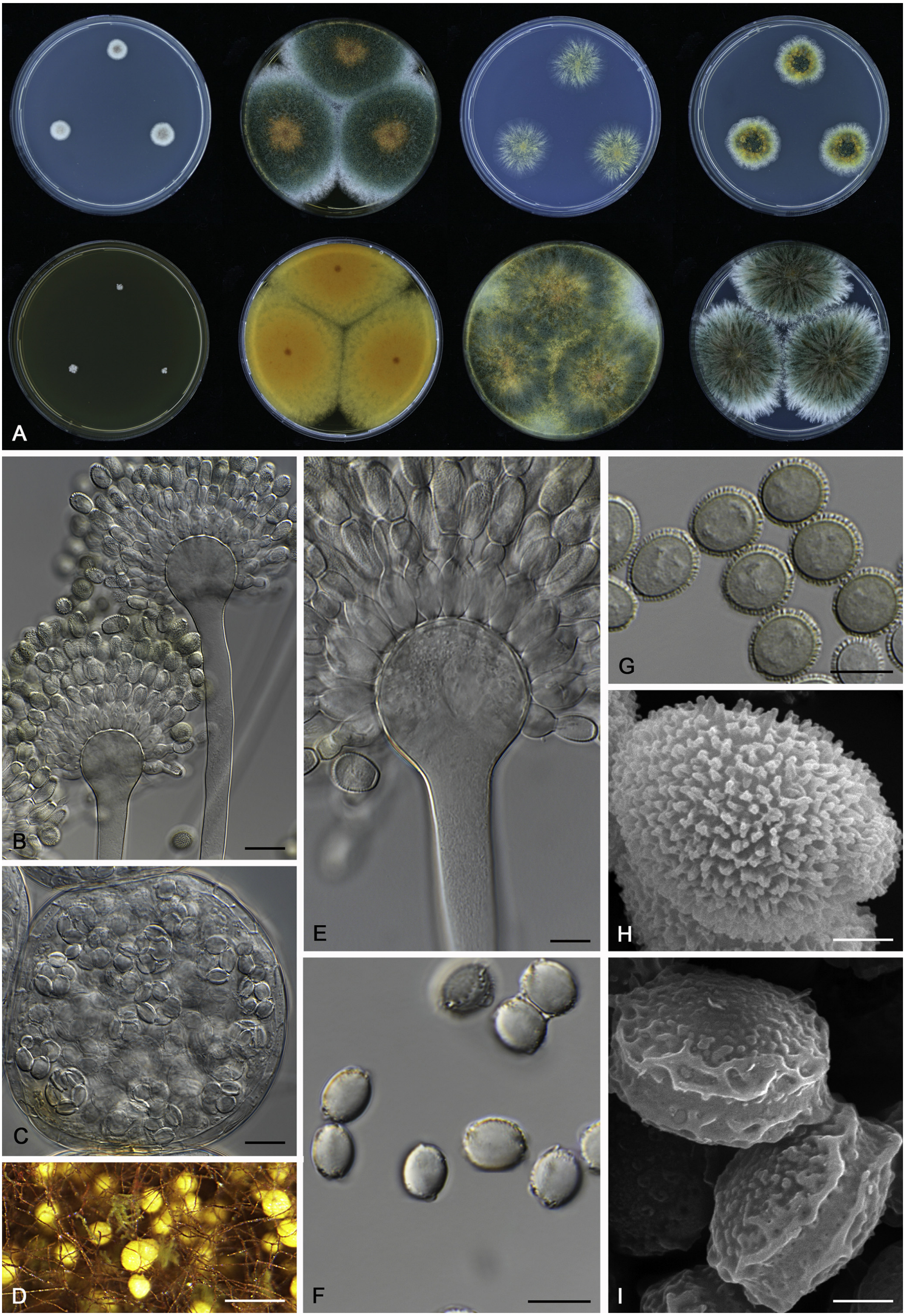


Fig. 21. *Aspergillus brunneus* CBS 112.26^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

65–72; M60Y >75; M60Y 30 °C 60–65; M60Y 37 °C No growth; CYAS 26–27; DG18 60–61; MEA10S 48–52.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse fulvous (43). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7), later turn into bay (6); texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7); texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7); texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7); texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse fulvous (43). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium orange (7); margins entire; texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse fulvous (43).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 110–240 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies rough along equatorial ridges, 7–10 × 6–8 µm, in side view lenticular, furrow present, crests irregular, <0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 700–1 200 × 7–18 µm. Vesicles globose to subglobose, 32–58 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 10–18.5 × 7–12.5 µm. Conidia globose to subglobose, tuberculate, 8–15 × 8–13 µm.

Distinguishing characters: *Aspergillus brunneus* is close to *A. neocarnoyi* and *A. osmophilus* in ascospore size and ornamentation, but the latter two are more xerophilic, and show no growth on MEA and CYA. In addition, *A. brunneus* grows faster on CY20S.

Additional materials examined: **Canada**, house dust, 2015, isolated by C.M. Visagie, DTO 357-A1 = KAS7575. **Canada**, Manitoba, unknown source, isolated by M. Desjardins, DTO 197-B3 = CBS 117328. Unknown source, isolated by G. Smith, NRRL 133 = CCF 5586. Unknown source, isolated by W. McRae, NRRL 124 = CBS 113.27 = CCF 5585.

Aspergillus caperatus A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB818733. Fig. 22.

Etymology: Name refers to the wrinkled ornamentation on conidia.

Diagnosis: Verruculose to rugulose ascospores with crests measuring 0.5–1 µm, lobate-reticulate conidia, no growth on CY20S at 37 °C.

Typus: **South Africa**, Robben Island, soil, 2015, collected by P. Crous, isolated by M. Meijer (holotype CBS H-22825, culture ex-type: CBS 141774 = DTO 337-E6 = IBT 34451).

ITS barcode: LT670922. (Alternative markers: *BenA* = LT671008; *CaM* = LT671009; *RPB2* = LT671010).

Colony diam, 7 d (mm): CYA 19–20; MEA 14–15; CY20S 55–56; CY20S 30 °C 52–53; CY20S 37 °C No growth; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C >75; CYAS 41–44; DG18 49–50; MEA10S 58–63.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12) to sulphur yellow (15). M40Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse sulphur yellow (15). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse sulphur yellow (15). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 130–220 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose to rugulose, 3.5–4.5 × 2.5–4 µm, in side view lenticular, furrow pronounced, crests 0.5–1 µm. Conidiophores with smooth stipes, hyaline or light brown, 250–500 × 6.5–9(–12) µm. Vesicles globose to subglobose, 26–45 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 7.5–12 × 4–7.5 µm. Conidia globose to subglobose, lobate-reticulate, 3.5–5.5 × 3.5–4.5 µm.

Distinguishing characters: Phylogenetically *A. caperatus* is closely related to *A. montevidensis*, *A. intermedius* and *A. porosus*, but *A. montevidensis* produces larger ascospores (4–6 × 3–4.5 µm), *A. intermedius* produces microtuberculate conidia and *A. porosus* is characterized by pitted ascospores. In addition, *A. caperatus* does not grow on CY20S at 37 °C compared to other three species.

Aspergillus chevalieri (L. Mangin) Thom & Church, The Aspergilli: 111. 1926. MycoBank MB292839. Fig. 23.

Synonyms: *Eurotium chevalieri* L. Mangin, Ann. Sci. Nat., Bot.: 361. 1909.
Aspergillus chevalieri var. *multiascosporus* Nakaz. *et al.*, J. Agr. Chem. Soc. Japan 10: 135–192. 1934.
Aspergillus allocotus Bat. & H. Maia, Anais Soc. Biol. Pernambuco 15: 181. 1957.
Aspergillus equitis Samson & W. Gams, Advances in *Penicillium* and *Aspergillus* Systematics: 36. 1985.

Typus: IMI 211382, neotype (Samson & Gams 1985). Culture ex-type: CBS 522.65 = NRRL 78 = ATCC 16443 = IMI 211382 = NRRL A-7803 = Thom 4125.3 = WB 78 = IBT 5680.

ITS barcode: EF652068. (Alternative markers: *BenA* = EF651911; *CaM* = EF652002; *RPB2* = EF651954).

Colony diam, 7 d (mm): CYA 17–25; MEA 17–27; CY20S 23–67; CY20S 30 °C 23–60; CY20S 37 °C 3–33; M40Y 50–>75; M60Y 60–>75; M60Y 30 °C 55–>75; M60Y 37 °C >75; CYAS 23–55; DG18 27–45; MEA10S 40–52.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium straw (46) to sulphur yellow (15) to orange (7); texture velvety; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) or fulvous (43) fading into sulphur yellow (15). M40Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15) and white or orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse fulvous (43) or luteous (12) or ochreous (44). M60Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15) and white or orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12) to ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) or white or grey olivaceous (107) or orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12) to ochreous (44) fading into sulphur yellow (15) or luteous (12). DG18 25 °C, 7 d: Colonies moderately deep, plane or slightly sulcate; margins entire; mycelium sulphur yellow (15) and white or orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12) or ochreous (44) fading into sulphur yellow (15) or rust (39). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15) and white or orange (7); margins entire; texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12) or ochreous (44) or fulvous (43).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–250 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth to slightly verruculose, 3.5–5.5 × 3–4 µm, in side view lenticular, furrow present, crests 0.5–1 µm. Conidiophores with smooth stipes, hyaline or light brown, 200–1 000 × 6–12 µm. Vesicles globose to subglobose, 23–47 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 5.5–7.5(–10) × 3–5 µm. Conidia globose, subglobose to ellipsoidal, tuberculate to lobate-reticulate, 3–4(–6) × 2.5–3.5(–5) µm.

Distinguishing characters: Phylogenetically *A. chevalieri* is closely related to *A. cristatus* and *A. costiformis*, but *A. cristatus* produces verruculose to rugulose ascospores, while *A. costiformis* produces large rugulose ascospores (5.5–7 × 5–6.5 µm). Morphologically, *A. chevalieri* is close to *A. intermedius* and *A. caperatus* in ascospore size and ornamentation, but *A. intermedius* produces microtuberculate conidia, *A. caperatus* produces mainly globose and averagely larger conidia (3.5–5.5 × 3.5–4.5 µm).

Additional materials examined: **Brazil**, corn kernels, 2008, isolated by J. Houbraken, DTO 061-A2. **China**, Guizhou, liquor starter, CGMCC 3.06736, CGMCC 3.06722. **China**, unknown source, CGMCC 3.01302, CGMCC 3.01303, CGMCC 3.12591, CGMCC 3.01299, CGMCC 3.01301. **China**, Beijing, unknown source, CGMCC 3.06135, CGMCC 3.06136. **China**, Yunnan, moldy weeds, CGMCC 3.06491. **China**, Yunnan, moldy bamboo, CGMCC 3.06490. **China**, Ningxia, soil, CGMCC 3.06133. **China**, Yunnan, soil under corn, CGMCC 3.06487. **China**, Yunnan, soil, CGMCC 3.06489. **China**, Guizhou, liquor starter, CGMCC 3.06753. **China**, Beijing, soil, CGMCC 3.06134. **China**, Beijing, feed, CGMCC 3.07889. **China**, Tibet, soil, 2001, CGMCC 3.06132 = DTO 348-G5. **China**, Yunnan, moldy peel, 2001, CGMCC 3.06492 = DTO 348-H3. **Czech Republic**, Brno, rice, 1999, isolated by V. Ostrý, CCF 3291 = DTO 355-B6. **Czech Republic**, Prague, semolina, 1979, isolated by V. Muzikář, CCF 1676 = DTO 355-B7. **Czech Republic**, semolina, 1979, isolated by V. Muzikář, CCF 1663. **Czech Republic**, Brno, seeds of *Carum carvi*, 2000, isolated by V. Ostrý, CCF 3211. **India**, keratitis, CBS 123900. **Japan**, unknown source, isolated by R. Nakazawa, CBS 113.34 = NRRL 88 = WB 88 = DTO 196-H7 (Isotype of *Aspergillus chevalieri* var. *multiascosporus*). **Madagascar**, soil, 2008, isolated by J. Houbraken, CBS 141769 = DTO 088-D7. **Madagascar**, soil, 2008, isolated by J. Houbraken, DTO 092-D3. **Portugal**, unknown source, CBS 126335. **South Korea**, soybeans, 2012, isolated by D.H. Kim, CCF 4788 = KACC 47145 = DTO 355-B8. **Thailand**, Hua Hin, soil under tamarind, 2007, isolated by R.A. Samson & J. Houbraken, DTO 054-A9. **The Netherlands**, Quail bedding, 2014, isolated by M. Meijer, DTO 316-G5. **The Netherlands**, milk powder, 2016, isolated by J. Houbraken, DTO 346-C5. **The Netherlands**, animal feed kernels, 2016, isolated by J. Houbraken, DTO 346-B8. **The Netherlands**, garlic butter, isolated by J. Houbraken, DTO 239-H5. **The Netherlands**, animal feed kernels, 2016, isolated by J. Houbraken, DTO 346-B7. **USA**, Indiana, Indianapolis, unknown source, isolated by Dr. Adams, NRRL 79. **USA**, culture contamination, isolated by D.I. Fennell, NRRL 4755. **USA**, CA, child carrier, 2015, isolated by Ž. Jurjević, EMSL No. 2739, EMSL No. 2768. **USA**, AZ, Tempe, office chair, 2015, isolated by Ž. Jurjević, EMSL No. 2931. Unknown source, isolated by S. Suhendriani, DTO 238-E3.

Notes: Raper & Fennell (1965) indicated that *Aspergillus chevalieri* var. *multiascosporus* showed definitely identical colony character of *A. chevalieri*, and included it with *A. chevalieri*. Hubka *et al.* (2013a) synonymized *A. chevalieri* var. *multiascosporus* with *A. chevalieri* and our morphological observation and molecular data (*CaM*) supported this treatment. *Aspergillus allocotus* was considered a synonym based on type culture WB 4909 (Raper & Fennell 1965), which was followed by Kozakiewicz (1989) and Hubka *et al.* (2013a). *Aspergillus equitis* was proposed as epithet for the anamorph of *Eurotium chevalieri* (Samson & Gams 1985). It was synonymized with *A. chevalieri* by Hubka *et al.* (2013a).

Aspergillus cibarius S.B. Hong & Samson, J. Microbiol. 50: 713. 2012. MycoBank MB800861. Fig. 24.

Typus: KACC 46346, holotype. Culture ex-type: KACC 46346 = DTO 197-D3 = IBT 32307.

ITS barcode: JQ918177. (Alternative markers: *BenA* = JQ918180; *CaM* = JQ918183; *RPB2* = JQ918186).

Colony diam, 7 d (mm): CYA 16–18; MEA 2–10; CY20S 18–32; CY20S 30 °C 2–5; CY20S 37 °C No growth; M40Y 65–75; M60Y 65–>75; M60Y 30 °C 60–>75; M60Y 37 °C 0–9; CYAS 31–42; DG18 40–43; MEA10S 43–50.

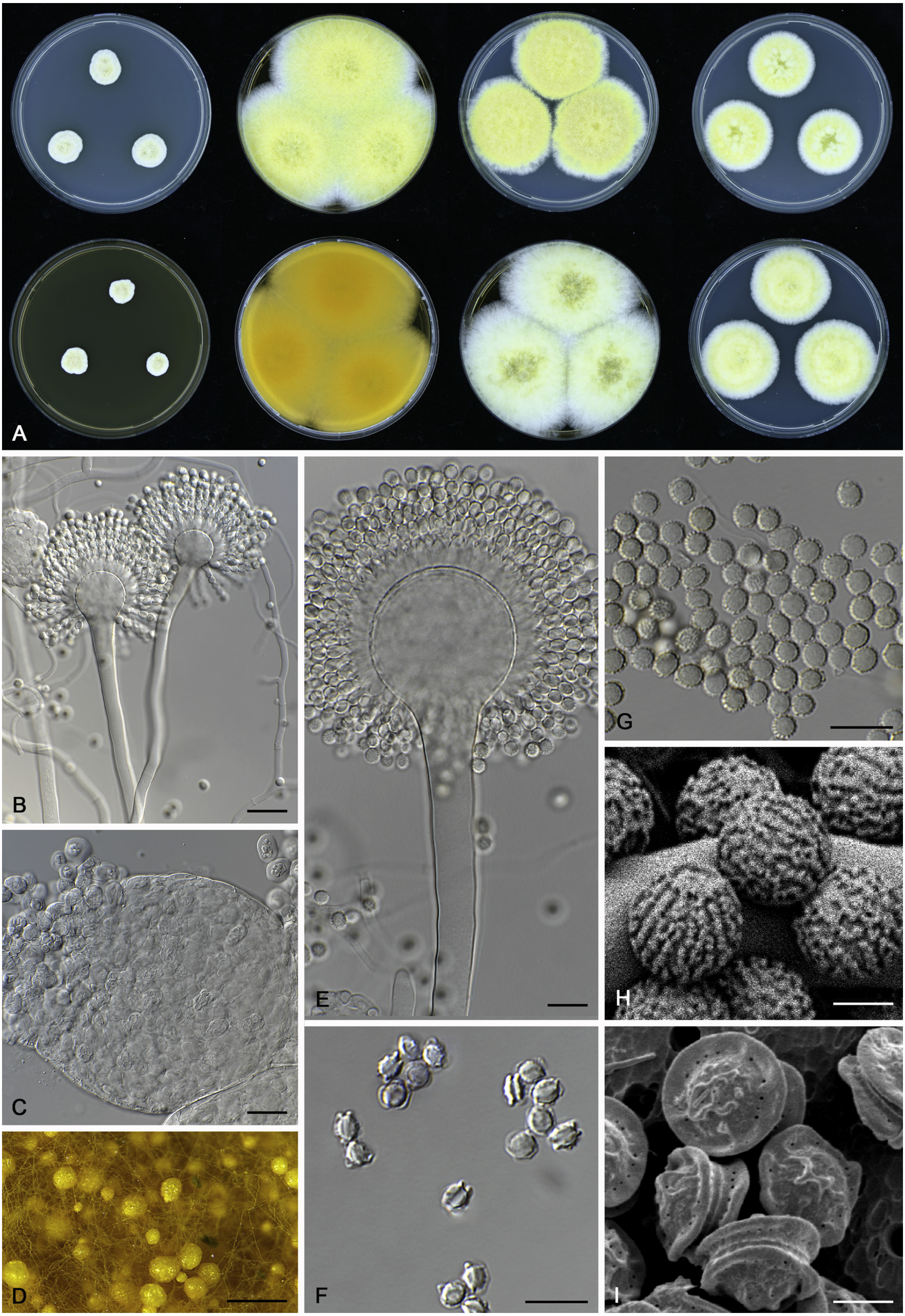


Fig. 22. *Aspergillus caperatus* CBS 141774^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

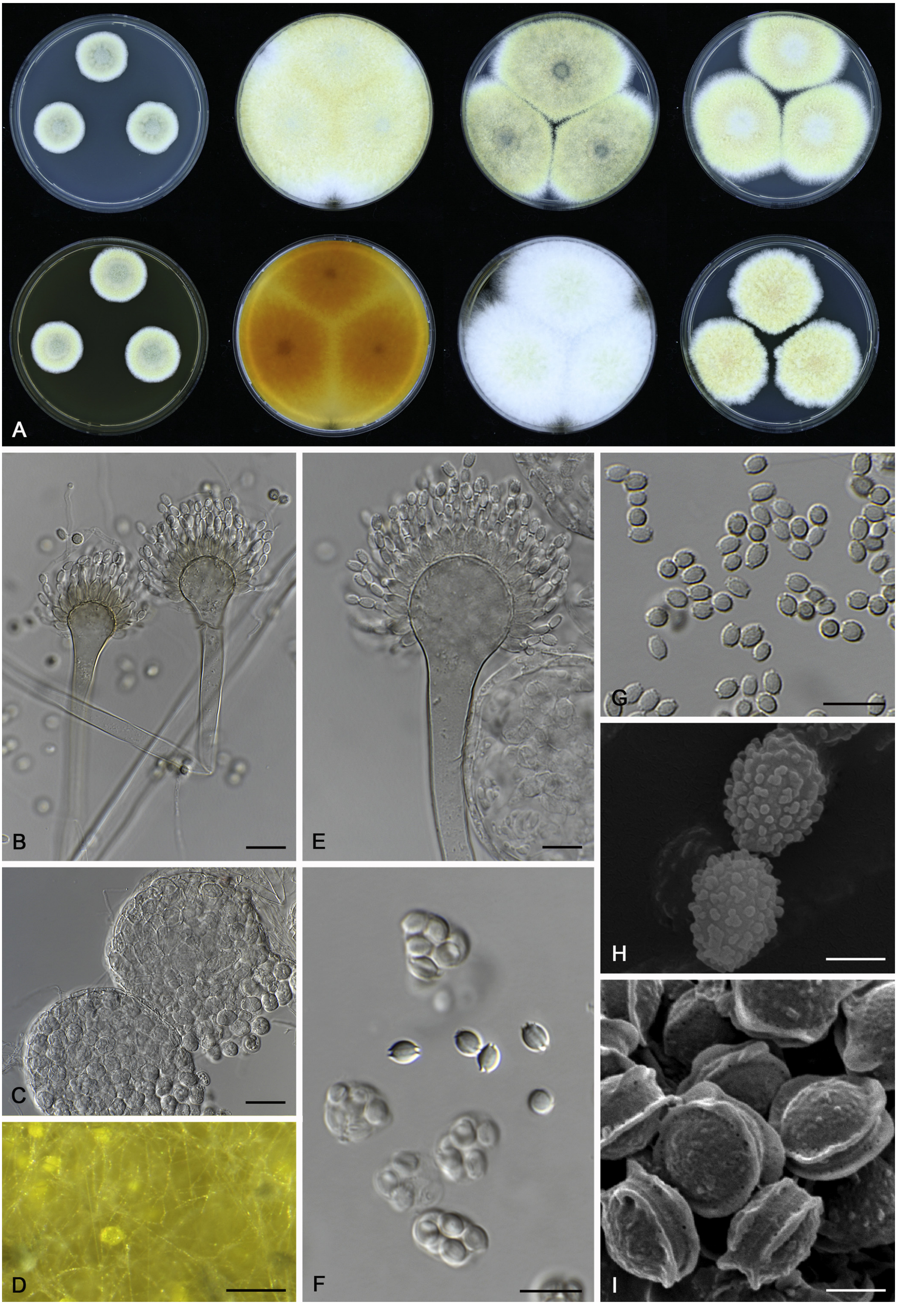


Fig. 23. *Aspergillus chevalieri* CBS 522.65^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

Colony characters: CY20S 25 °C, 7 d: Colonies low to moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse straw (46). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7) at centre, sulphur yellow (15) at edge, later turn to rust (39); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation absent or moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7) at centre, sulphur yellow (15) at edge; texture floccose; sporulation absent or sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7) at centre, sulphur yellow (15) at edge; texture floccose; sporulation absent or sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse straw (46). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium orange (7) at centre, sulphur yellow (15) at edge; margins entire; texture floccose; sporulation absent or sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse straw (46).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–200 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies rough along equatorial ridges, 4–5.5 × 3–5 µm, in side view lenticular, furrow present, crests irregular, < 0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 500–700 × 8–14 µm. Vesicles globose to subglobose, 32–58 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6–11 × 3–5.5 µm. Conidia subglobose to ellipsoidal, tuberculate, 4–7 × 3.5–5.5 µm.

Distinguishing characters: Phylogenetically *A. cibarius* is distinct from other taxa in sect. *Aspergillus*, located at a basal position adjacent to the *A. ruber* and *A. glaucus* clades. Morphologically, the size, ornamentation and irregular crests of ascospores of *A. cibarius* resemble those of *A. aurantiacoflavus*, *A. cumulates*, *A. niveoglaucus* and *A. xerophilus*, but *A. aurantiacoflavus* produces orange and yellow colonies and grows slower on CYA and MEA, *A. cumulatus* produces globose conidia, *A. niveoglaucus* does not grow on CY20S at 30 °C, *A. xerophilus* is more xerophilic and does not grow on CYA and MEA.

Additional materials examined: **China**, Hebei, soil, 2001, CGMCC 3.06498 = DTO 348-H7. **China**, 1952, CGMCC 3.00450 = DTO 348-B5. **China**, tea, CGMCC 3.00451. **China**, Hebei, faeces, CGMCC 3.06501. **Czech Republic**, Prague, toenail of 56-year-old woman, 2010, isolated by P. Lysková, CCF 4098 = NRRL 62493 = DTO 354-I8. **Czech Republic**, Prague, toenail of 63-year-old man, 2012, isolated by P. Lysková, CCF 4235 = NRRL 62492 = DTO 354-I7. **Spain**, Nerja cave, near Málaga, cave sediment (entrance chambre), 2011, isolated by A. Nováková, CCF 4264 = DTO 354-I9. **The Netherlands**, black bean, 2012, isolated by M. Meijer, KACC 49766 = CCF 4784. **The Netherlands**, almond bar, 2014, isolated by T.V. Doorn, DTO 322-A6. **The Netherlands**, fruit pulp, 2014, isolated by T.V. Doorn, DTO 303-B8. **USA**, DC, Washington, chocolate glazed frosted donut, 2014, isolated by Ž. Jurjević, EMSL No. 2500. **USA**, NY, Elmsford, valet drover, swab, 2014, isolated by Ž. Jurjević, EMSL No. 2644. **USA**, CA, Danville, chocolate chip cookies, 2015, EMSL No. 2866. **USA**, DC, Washington, chocolate glazed frosted donut, 2014, isolated by Ž. Jurjević, EMSL No. 2499. **USA**, Pennsylvania, child's shoes, 2012, isolated by Ž. Jurjević, EMSL No. 1652 = CCF 5385 = DTO 355-G6. **USA**, Washington DC, chocolate glazed frosted donut, 2014, isolated by Ž. Jurjević, EMSL No. 2498 = CCF 5383 = DTO 355-G7. **USA**, California, Danville, chocolate chip cookies, 2015, isolated by Ž. Jurjević, EMSL No. 2865 = CCF 5384 = DTO 355-G8.

Aspergillus costiformis H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14: 10. 1995. MycoBank MB363444. Fig. 25.

Synonyms: *Eurotium costiforme* H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14: 10. 1995.

Typus: HMAS 62766, holotype. Culture ex-type: CBS 101749 = CGMCC 3.04664 = DTO 348-D8 = IBT 34456 = IBT 33662.

ITS barcode: HE615136. (Alternative markers: *BenA* = HE801338; *CaM* = HE801320; *RPB2* = HE801309).

Colony diam, 7 d (mm): CYA 9–10; MEA 13–18; CY20S 40–41; CY20S 30 °C 35–42; CY20S 37 °C No growth; M40Y 60–61; M60Y 47–54; M60Y 30 °C 60–70; M60Y 37 °C 70–>75; CYAS 9–11; DG18 36–38; MEA10S 24–25.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture velvety; sporulation absent; soluble pigments absent; exudates absent; reverse sulphur yellow (15). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture velvety; sporulation absent; soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture velvety; sporulation absent; soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture velvety; sporulation absent; soluble pigments absent; exudates absent; reverse straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture velvety; sporulation absent; soluble pigments absent; exudates absent; reverse straw (46). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15); margins entire; texture velvety; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse straw (46).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–255 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies rugulose, 5.5–7 × 5–6.5 µm, in side view lenticular, furrow pronounced, crests 0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 500–800 × 7–13 µm. Vesicles globose to subglobose, 20–45(–60) µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6–9.5 × 3–4.5(–5.5) µm. Conidia globose to subglobose, microtuberculate, 4–5.5(–6.5) × 3–4.5(–5.5) µm.

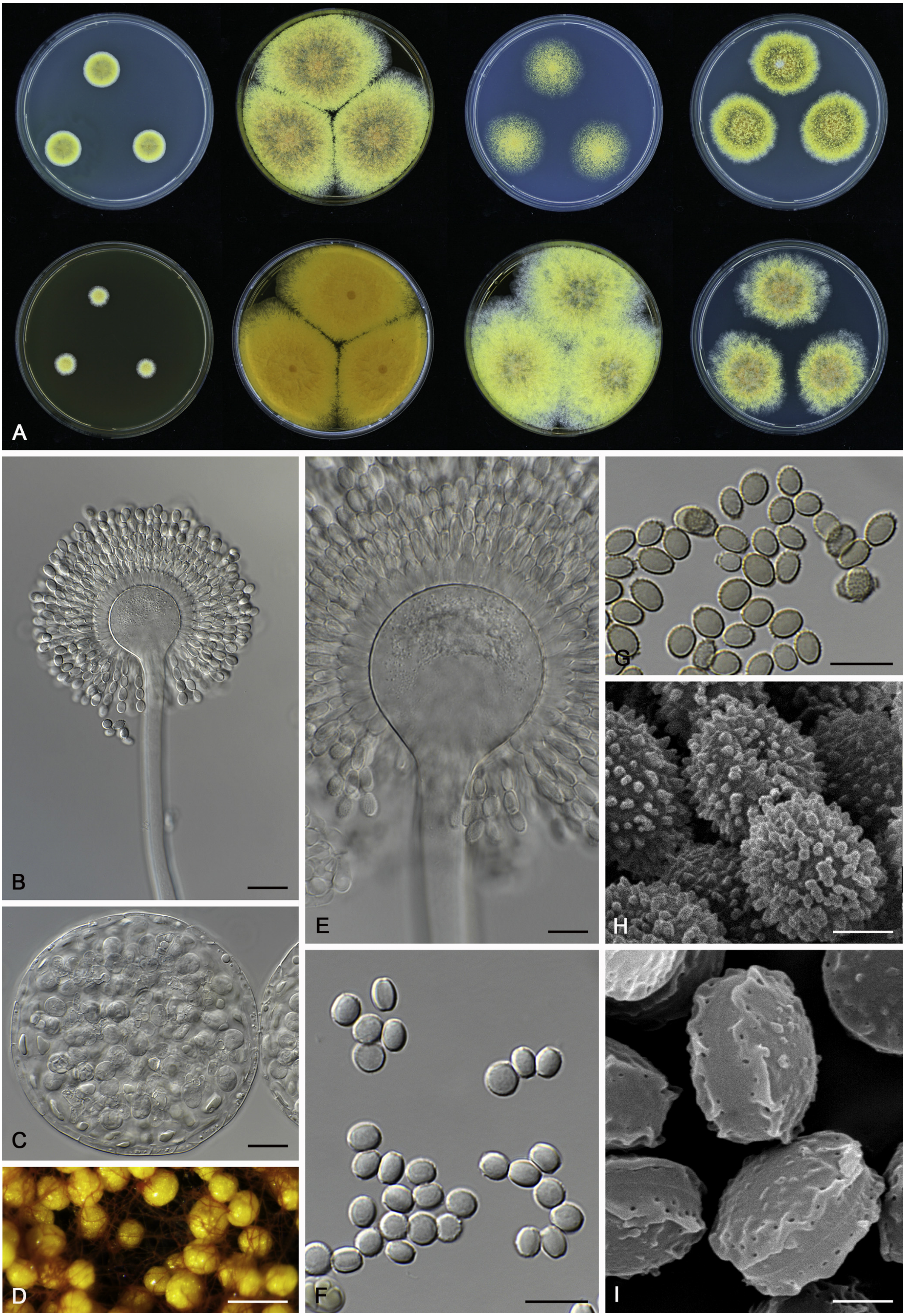


Fig. 24. *Aspergillus cibarius* KACC 46346^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E−G = 10 µm; H, I = 2 µm.

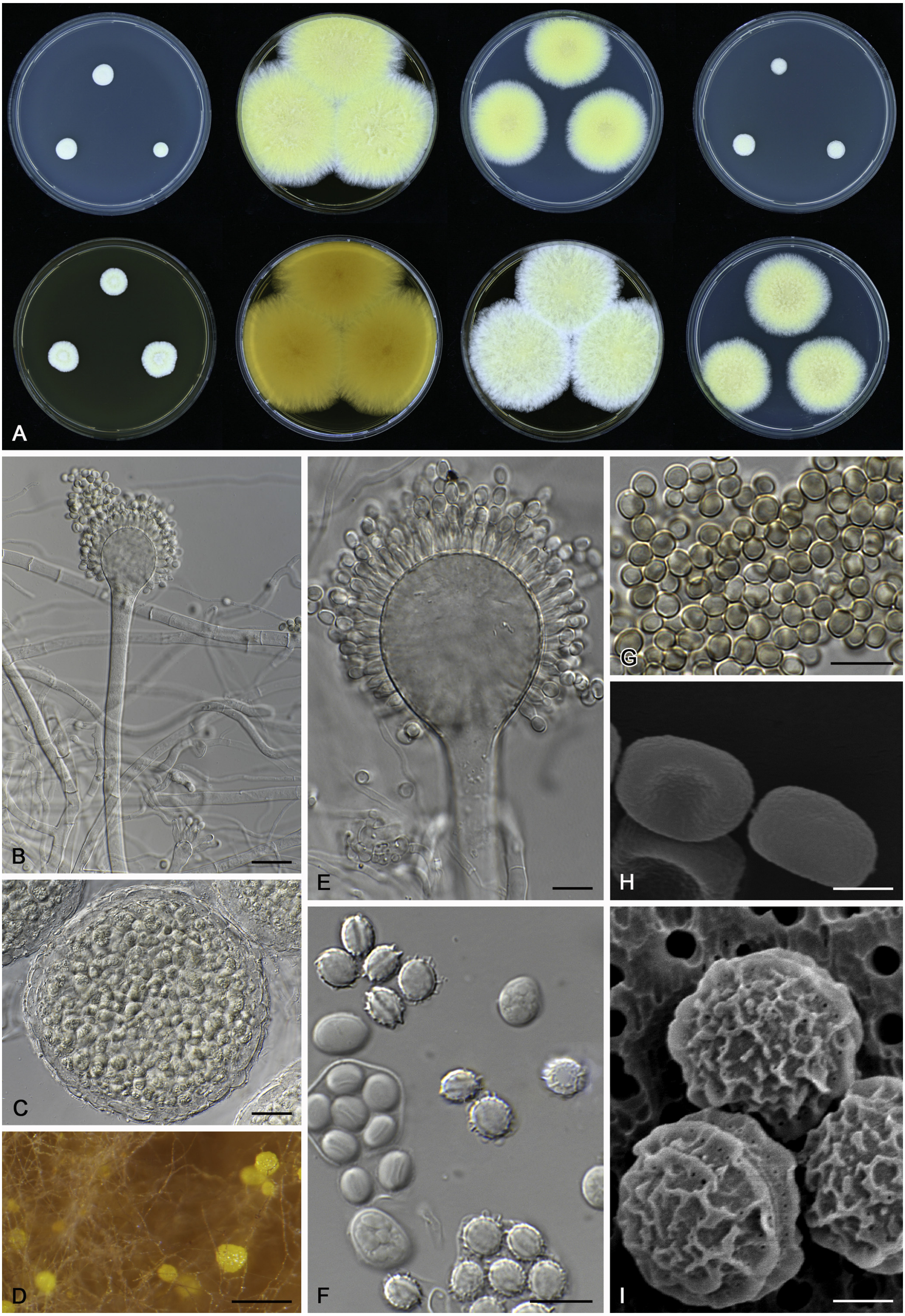


Fig. 25. *Aspergillus costiformis* CBS 101749^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

Distinguishing characters: *Aspergillus costiformis* is characterized by large, rugulose ascospores and microtuberculate conidia. *Aspergillus neocarnoyi* also produces large, verruculose to rugulose ascospores, but differs in larger, tuberculate conidia measuring 8–15.5 × 6–10 µm.

Additional materials examined: **China**, Hebei, moldy box, 2001, CGMCC 3.06520 = DTO 348-I5. **Czech Republic**, Prague, toenail of 5-year-old boy, 2010, isolated by P. Lysková, CCF 4097 = NRRL 62483 = DTO 354-I3. **The Netherlands**, cellophane, 2015, isolated by J. Houbraken, DTO 326-B4.

Aspergillus cristatus Raper & Fennell, Gen. *Aspergillus*: 169. 1965. MycoBank MB326622. Fig. 26.
Synonyms: *Eurotium cristatum* (Raper & Fennell) Malloch & Cain, Canad. J. Bot. 50: 64. 1972.
Aspergillus cristatellus Kozak., Mycol. Pap. 161: 81. 1989.

Typus: IMI 172280, neotype (Hubka *et al.* 2013a). Culture ex-type: CBS 123.53 = NRRL 4222 = ATCC 16468 = BCRC 33090 = FRR 1167 = IBT 5355 = IHEM 5619 = IMI 172280 = JCM 1569 = MUCL 15644 = WB 4222.

ITS barcode: EF652078. (Alternative markers: *BenA* = EF651914; *CaM* = EF652001; *RPB2* = EF651957).

Colony diam, 7 d (mm): CYA 20–32; MEA 18–36; CY20S 57–75; CY20S 30 °C 55–70; CY20S 37 °C 42–51; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C >75; CYAS 35–56; DG18 38–53; MEA10S 43–70.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15) or orange (7); texture velvety to floccose; sporulation absent to dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse straw (46) or sulphur yellow (15) or fulvous (43). M40Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate or plane; margins entire; mycelium sulphur yellow (15); texture velvety to floccose; sporulation absent to dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse to moderately dense; conidia *en masse* grayish green (50) to dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation absent to moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44) fading into straw (46) or sulphur yellow (15). DG18 25 °C, 7 d: Colonies moderately deep, slightly sulcate or plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation absent to moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse straw (46), ochreous (44) or sulphur yellow (15). MEA10S 25 °C, 7 d: Colonies moderately deep, plane or slightly sulcate; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–200 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose to rugulose, 4.5–6 × 4–6 µm, in side view lenticular, furrow present, crests 1.2–1.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 300–500 × (6–)8–12 µm. Vesicles globose to subglobose, (26–)35–51 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 5.5–9 × 3.5–6 µm. Conidia globose, subglobose to ellipsoidal, tuberculate, 4–6.5 × 3.5–5 µm.

Distinguishing characters: Phylogenetically *A. cristatus* is closely related to *A. chevalieri* and *A. costiformis*, but *A. chevalieri* produces smooth to slightly verruculose ascospores, and *A. costiformis* produces larger ascospores and microtuberculate conidia.

Additional materials examined: **China**, unknown source, CGMCC 3.02167, CGMCC 3.03972, CGMCC 3.06140, CGMCC 3.06141, CGMCC 3.00449, CGMCC 3.06139, CGMCC 3.00448, CGMCC 3.00463. **China**, Hubei, tea, CGMCC 3.07927. **China**, Zhejiang, tea, CGMCC 3.07934. **China**, Beijing, unknown source, CGMCC 3.06131. **China**, Yuannan, tea, CGMCC 3.07925, CGMCC 3.07926. **China**, Sichuan, tea, CGMCC 3.07924. **China**, Yunnan, Pu'er tea, CGMCC 3.15365. **China**, Hunan, tea, CGMCC 3.07928. **China**, Hunan, Fuzhuan brick tea, CGMCC 3.06086, CGMCC 3.06088, CGMCC 3.06087, CGMCC 3.06089, CGMCC 3.07930. **China**, Chongqing, tea, CGMCC 3.07929. **China**, Guangxi, tea, CGMCC 3.06083. **China**, Liaoning, unknown source, CGMCC 3.06085. **China**, Hubei, soil, CGMCC 3.06082. **China**, Hunan, tea, CGMCC 3.06084. **China**, Hunan, tea block, 2013, isolated by Q.L. Pan & L. Wang, CCF 4701 = DTO 355-B1. **China**, Guangxi, tea block, 2013, isolated by Q.L. Pan & L. Wang, CCF 4702 = DTO 355-B2. **China**, Hubei, soil, 2001, CGMCC 3.06081 = DTO 348-E9. **Zaire**, Kinshasa, soil, 1984, IHEM 2423 = DTO 355-B3.

Aspergillus cumulatus D.H. Kim & S.B. Hong, J. Microbiol. Biotechnol. 24: 335. 2014. MycoBank MB807118. Fig. 27.

Typus: KACC 47316, holotype. Culture ex-type: KACC 47316 = DTO 303-D9 = IBT 34470 = IBT 33670.

ITS barcode: KF928303. (Alternative markers: *BenA* = KF928297; *CaM* = KF928300; *RPB2* = KF928294).

Colony diam, 7 d (mm): CYA 7–10; MEA 4–5; CY20S 28–35; CY20S 30 °C 9–17; CY20S 37 °C No growth; M40Y 70–75; M60Y >75; M60Y 30 °C 62–70; M60Y 37 °C No growth; CYAS 33–42; DG18 35–47; MEA10S 65–68.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane to sulcate; margins irregular; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse olivaceous buff (89) at centre fading into sulphur yellow (15). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins irregular; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins irregular; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins irregular; mycelium sulphur yellow (15) and orange (7); texture floccose;

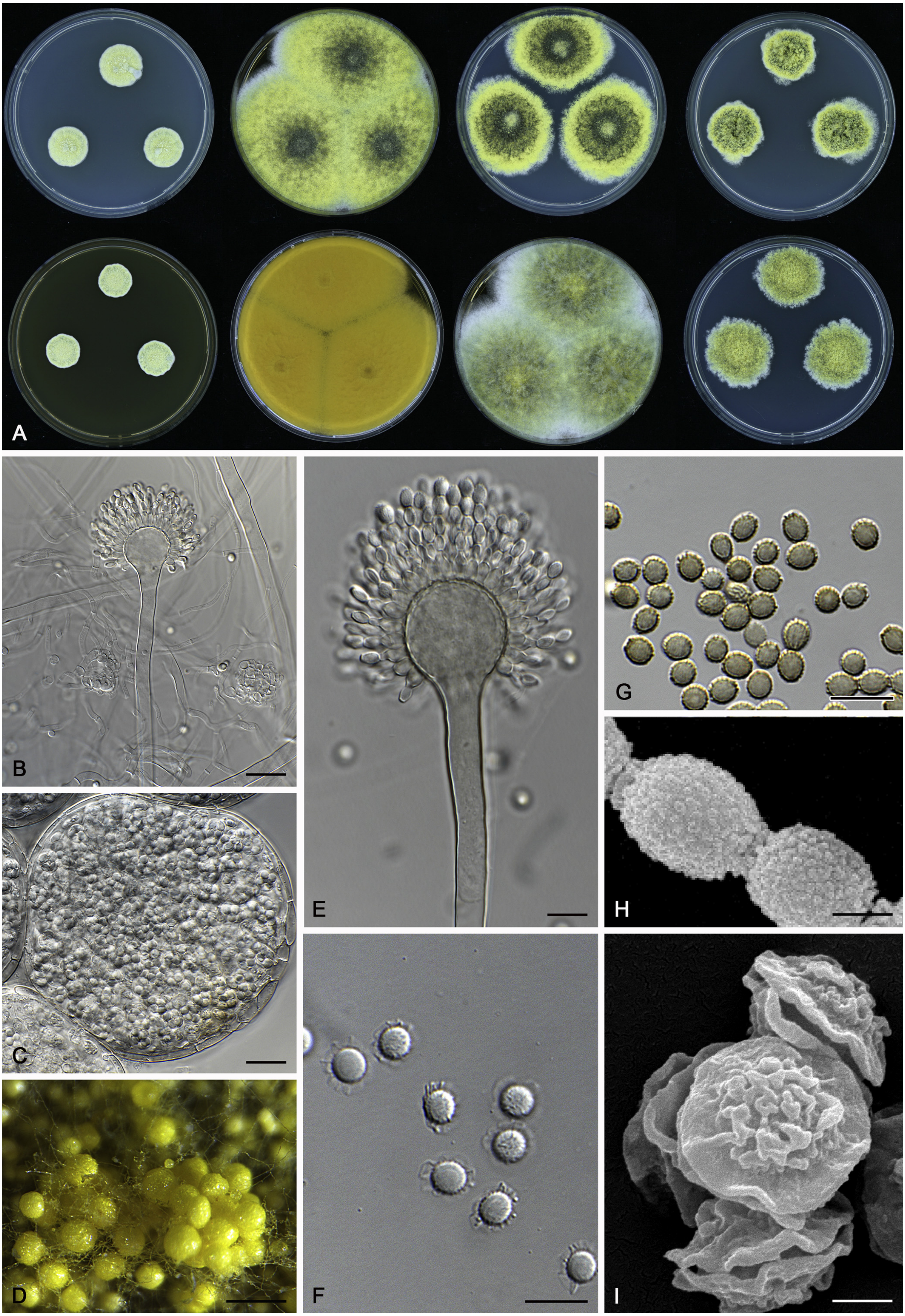


Fig. 26. *Aspergillus cristatus* CBS 123.53^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

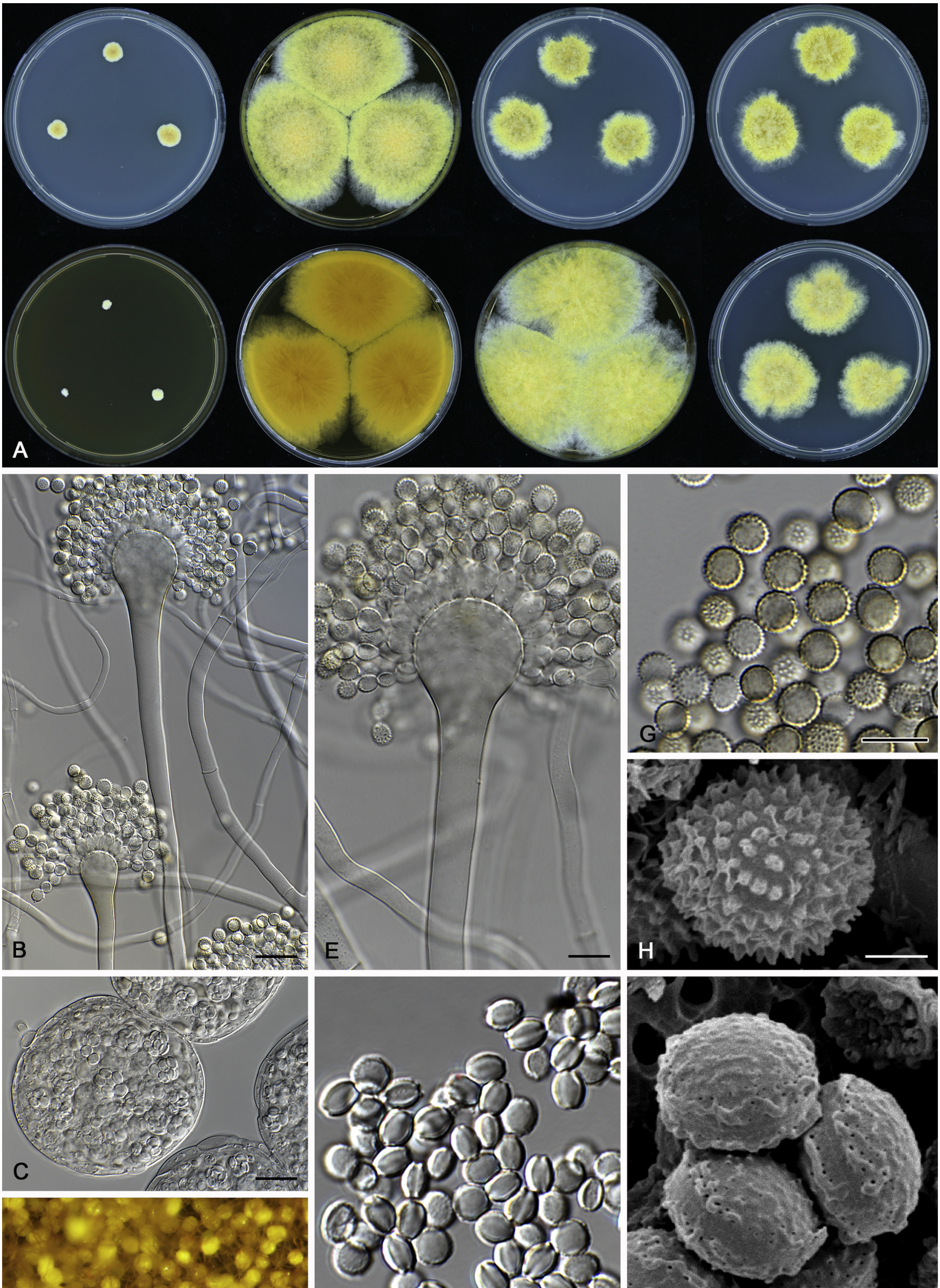


Fig. 27. *Aspergillus cumulatus* KACC 47316^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

sporulation moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins irregular; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse buff (45) or sulphur yellow (15). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15) and orange (7); margins irregular; texture floccose; sporulation moderately dense; conidia *en masse* dark green (21) or yellow-green (71); soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–200 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies slightly rough, 4–6 × 3.5–5 µm, in side view lenticular, furrow pronounced, crests irregular, < 0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 500–1 300 × 7–15 µm. Vesicles globose to subglobose, 32–57 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 7–12 × 4.5–7.5 µm. Conidia globose, tuberculate, 5–8 × 4–7.5 µm.

Distinguishing characters: Phylogenetically *A. cumulatus* belongs to the *A. ruber* clade. The ascospores of *A. cumulatus* are unique by having irregular crests, while remaining species produce non-crested ascospores or ascospores with petaliform crests (*A. appendiculatus* and *A. mallochii*). Morphologically *A. cumulatus* resembles *A. cibarius* and *A. megasporus* in ascospore size and ornamentation, but *A. cibarius* produces subglobose to ellipsoidal conidia, *A. megasporus* produces larger conidia and does not grow on CY20S at 30 °C.

Additional materials examined: **South Korea**, air of a meju fermentation room, KACC 47513 = DTO 303-D8, KACC 47514. **USA**, New York, Bronx, bedroom ceiling, 2015, Ž. Jurjević, EMSL No. 2827 = CCF 5376 = DTO 355-G9.

Aspergillus endophyticus Hubka, A.J. Chen, & Samson, **sp. nov.** MycoBank MB818734. Fig. 28.

Etymology: Name refers to its origin, isolated as endophyte of *Acer pseudoplatanus*.

Diagnosis: Verruculose to rugulose ascospores measuring 4–5.5 × 3–4.5 µm (crests 0.5–1 µm), tuberculate conidia measuring 5.5–8 × 4.5–6 µm.

Typus: **Czech Republic**, Prague, Stromovka park, endophyte of *Acer pseudoplatanus*, 2013, isolated by I. Kelnarová (holotype CBS H-22819, culture ex-type: CBS 141766 = DTO 354-I2 = CCF 5345 = IBT 34511).

ITS barcode: LT670941. (Alternative markers: *BenA* = LT671067; *CaM* = LT671068; *RPB2* = LT671069).

Colony diam, 7 d (mm): CYA 10–12; MEA 10–12; CY20S 24–26; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y 70–75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C 15–17; CYAS 30–35; DG18 35–40; MEA10S 25–35.

Colony characters: CY20S 25 °C, 7 d: Colonies low, plane; margins irregular; mycelium white to straw (46); texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse straw (46). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7) and sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse primrose (66). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse primrose (66). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 120–200 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose to rugulose, 4–5.5 × 3–4.5 µm, in side view lenticular, furrow pronounced, crests 0.5–1 µm. Conidiophores with smooth stipes, hyaline or light brown, 350–800 × 9.5–14 µm. Vesicles globose to subglobose, 32–52 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6–10 × 3.5–5.5 µm. Conidia globose to subglobose, tuberculate to lobate-reticulate, 5.5–8 × 4.5–6 µm.

Distinguishing characters: The phylogenetic position of *A. endophyticus* is not fully resolved, but it has affinity to the *A. ruber* and *A. glaucus* clades (Fig. 1). It does not grow at 30 °C and 37 °C on CY20S similarly to the majority of species from these clades, and it grows at 37 °C on M60Y similarly to *A. pseudoglaucus*, *A. ruber*, *A. tonophilus* and *A. zutongqii* (Table 5). Morphologically it resembles *A. caperatus* in ascospore morphology, but *A. caperatus* produces smaller conidia measuring 3.5–5.5 × 3.5–4.5 µm.

Aspergillus glaucus (L.) Link, Mag. Ges. Naturf. Freunde Berlin 3: 16. 1809. MycoBank MB161735. Fig. 29.

Synonyms: *Mucor glaucus* L., Species Plantarum: 1186. 1753.
Monilia glauca (L.) Pers., Synopsis methodica fungorum: 691. 1801.
Eurotium herbariorum (Weber ex F.H. Wigg.) Link, Magazin der Gesellschaft Naturforschenden Freunde Berlin 3(1): 31. 1809.
Aspergillus herbariorum (F.H. Wigg.) E. Fisch. 1897.
Eurotium herbariorum var. *minor* L. Mangin, Annls Sci. Nat. Bot., Ser. 9: 365. 1909.
Aspergillus minor (L. Mangin) Thom & Raper, Department of Agriculture Miscellaneous Publications 426: 27. 1941.
Aspergillus mangini Thom & Raper, A manual of the Aspergilli: 127. 1945.
Eurotium minus (L. Mangin) Subram., Curr. Sci. 41: 760. 1972.

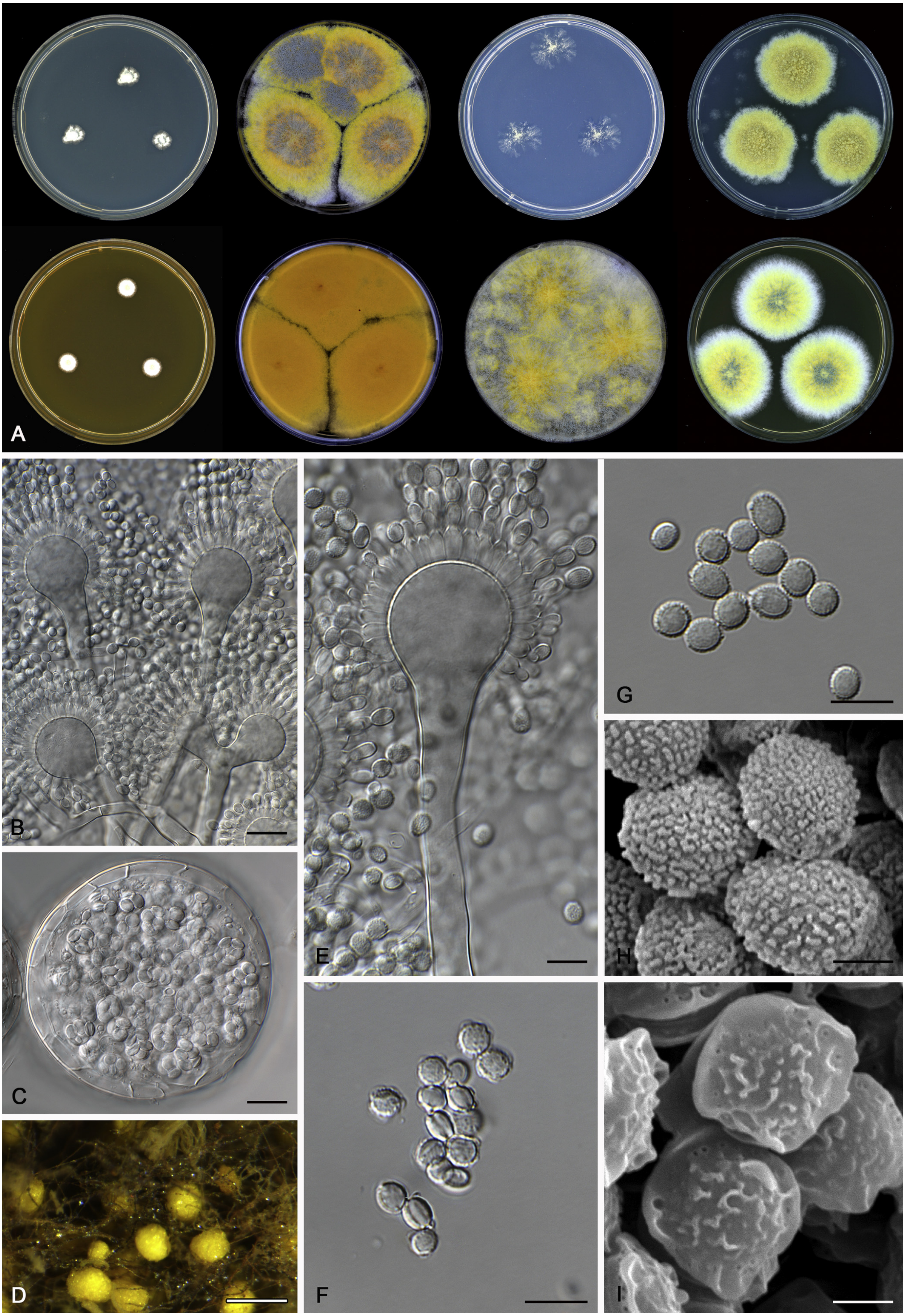


Fig. 28. *Aspergillus endophyticus* CBS 141766^T. **A.** Colonies: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

Aspergillus umbrosus Bainier & Sartory, Bull. Soc. Mycol. France 28 (3): 267. 1912.
Eurotium umbrosum (Bainier & Sartory) Malloch & Cain, Canad. J. Bot. 50 (1): 64. 1972.
Eurotium testaceocolorans Novobr., Novosti Sist. Nizsh. Rast. 9: 173. 1972.
Aspergillus testaceocolorans Novobr., Novosti Sist. Nizsh. Rast. 9: 173. 1972.

Typus: IMI 211383, neotype (Pitt & Samson 2000). Culture ex-type: CBS 516.65 = NRRL 116 = ATCC 16469 = DTO 197-A1 = IBT 32295 = IMI 211383 = LCP 64.1859 = Thom 5629.C = WB 116.

ITS barcode: EF652052. (Alternative markers: *BenA* = EF651887; *CaM* = EF651989; *RPB2* = EF651934).

Colony diam, 7 d (mm): CYA 0–8; MEA 0–6; CY20S 25–30; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C No growth; CYAS 41–49; DG18 48–60; MEA10S 60–66.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) or sulphur yellow (15) or orange (7); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse sulphur yellow (15) or luteous (12). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) or sulphur yellow (15) or orange (7); texture floccose; sporulation moderately dense; conidia *en masse* yellow-green (71) to greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) or sulphur yellow (15) or orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19) to yellow-green (71); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) or sulphur yellow (15) or orange (7); texture floccose; sporulation moderately dense; conidia *en masse* yellow-green (71); soluble pigments absent; exudates absent; reverse straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) or orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse straw (46). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15) and white; margins entire; texture floccose; sporulation moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12) or ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 120–250 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth, 5.5–7.5 × 3.5–6 µm, minute rough along equatorial ridges, in side view lenticular, furrow pronounced, crests irregular, 0.5–1 µm. Conidiophores with smooth stipes, hyaline or light brown, 150–500 × 10–21(–30) µm. Vesicles globose to subglobose, 30–60 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, (8–)12–20 × (4–)5–8.5 µm. Conidia globose, subglobose to ellipsoidal, tuberculate, 6–12.5 × 5.5–9 µm.

Distinguishing characters: Phylogenetically *A. glaucus* is most closely related to *A. proliferans*, *A. aurantiacoflavus* and *A. niveoglaucus*, but *A. proliferans* produces smaller (4–6 × 3–5 µm), non-crested ascospores, ascospores of *A. aurantiacoflavus* are also smaller (4–5.5 × 3–5 µm) and its colonies are orange-yellow. *Aspergillus niveoglaucus* is close to *A. glaucus* morphologically, but the convex surface is roughened makedly in *A. niveoglaucus*.

Notes: Pitt (1985) synonymized *Eurotium herbariorum* var. *minor* and *A. umbrosus* with *A. glaucus*, this was further supported by phylogenetic analyses by Hubka *et al.* (2013a) and our study. *Aspergillus testaceocolorans* was synonymized with *A. glaucus* by Samson (1979), Kozakiewicz (1989) agreed with this treatment on the basis of SEM examination, however, mistakenly synonymized *A. testaceocolorans* with *A. pseudoglaucus* (= *Eurotium repens*). The ex-type culture (CBS 758.74) of *A. testaceocolorans* is contaminated by an *A. appendiculatus* strain, and the position of this species could not be verified in this study.

Additional materials examined: **China**, unknown source, CGMCC 3.01313. **China**, Beijing, unknown source, CGMCC 3.06100. **China**, Shanxi, unknown source, CGMCC 3.06099. **Puerto Rico**, Bayamon, office, air, 2014, isolated by Ž. Jurjević, EMSL No. 2529 = CCF 5381 = DTO 355-H1. **USA**, Washington DC, unpainted board (K.B. Raper's basement), 1938, isolated by K.B. Raper, NRRL 117 = DTO 355-B4 = CCF 5582. **USA**, coffee beans, 1925, isolated by F.A. McCormick, NRRL 120 = 117.46 = CBS 532.65 = CCF 5583. **USA**, New York, Ulster Park, bedroom, settle plates, 2015, isolated by Ž. Jurjević, EMSL No. 3317 = CCF 5382 = DTO 355-H2. Unknown source, NRRL 121 = DTO 355-B5 = CCF 5584.

Aspergillus intermedius Blaser, Sydowia 28: 41. 1975. MycoBank MB309226. Fig. 30.
Synonyms: *Eurotium intermedium* Blaser, Sydowia 28: 44. 1975.
Aspergillus spiculosus Blaser, Sydowia 28: 42. 1975.
Eurotium spiculosum Blaser, Sydowia 28: 42. 1975.

Typus: IMI 89278, neotype (Kozakiewicz 1989). Culture ex-type: CBS 523.65 = NRRL 82 = ATCC 16444 = DSM 2830 = IBT 5677 = IMI 089278ii = IMI 89278 = LSHBBB 107 = LSHTM 107 = QM 7403 = Thom 5612.107 = WB 82.

ITS barcode: EF652074. (Alternative markers: *BenA* = EF651892; *CaM* = EF652012; *RPB2* = EF651958).

Colony diam, 7 d (mm): CYA 18–22; MEA 20–22; CY20S 47–55; CY20S 30 °C 45–55; CY20S 37 °C 27–36; M40Y 72–>75; M60Y 65–>75; M60Y 30 °C 65–75; M60Y 37 °C 70–>75; CYAS 29–34; DG18 39–45; MEA10S 43–54.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense or absent; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12) to sulphur yellow (15). M40Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense or absent; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, slightly

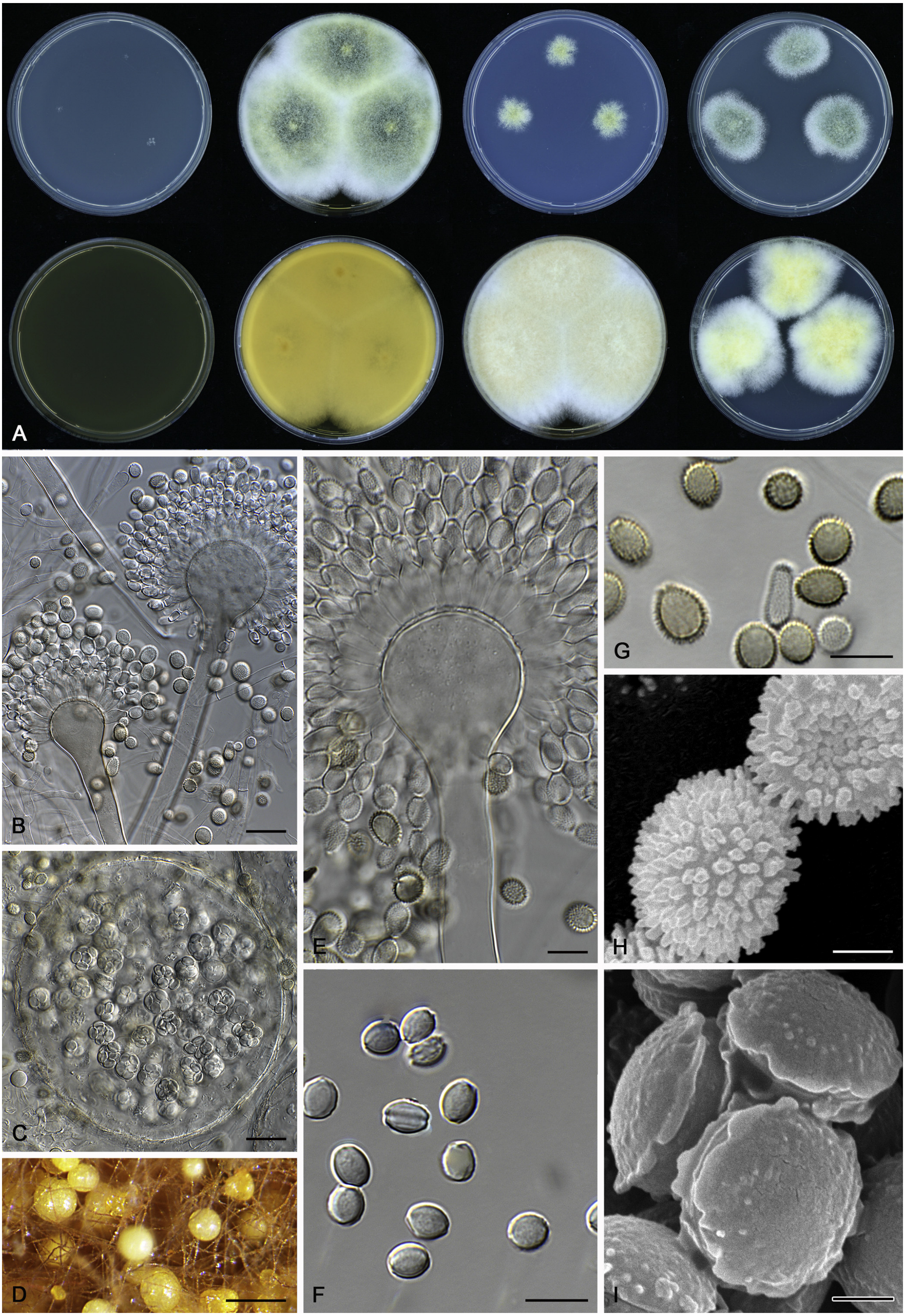


Fig. 29. *Aspergillus glaucus* CBS 516.65^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense or absent; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense or absent; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44) at centre, luteous (12) to sulphur yellow (15) at edge. DG18 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense or absent; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44) to luteous (12) to sulphur yellow (15). MEA10S 25 °C, 7 d: Colonies moderately deep, slightly sulcate; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation moderately dense or absent; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44) to luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–250 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose to rugulose, 3.5–5 × 3–4.5 µm, in side view lenticular, furrow present, crests 0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 250–600 × 7.5–13 µm. Vesicles globose to subglobose, (26–)40–60 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 5.5–7.5(–9) × 3–5.5 µm. Conidia globose to subglobose, microtuberculate, 3–4(–6) × 3–4.5 µm.

Distinguishing characters: Phylogenetically and morphologically *A. intermedius* resembles *A. montevidensis*, *A. porosus* and *A. caperatus*, but can be distinguished by smooth conidia (microtuberculate under SEM) instead of roughened conidia (lobate-reticulate under SEM) in the other species.

Additional materials examined: **China**, unknown source, 1969, CGMCC 3.03968 = DTO 348-D6. **China**, unknown source, CGMCC 3.06138. **China**, Beijing, unknown source, CGMCC 3.01300. **China**, industrial material, 1955, isolated by V. Zánová, CCF 127 = DTO 354-I5. **Croatia**, unknown source, isolated by V. Johanides, CBS 108.55. **Czech Republic**, unknown source, 1956, CGMCC 3.00664 = DTO 348-C1. **Czech Republic**, Prague, sputum of 55-year-old woman, 2013, isolated by P. Lysková, CCF 4681 = DTO 354-I6. **Czech Republic**, Prague, air sampler, surgical operating room, 2014, isolated by A. Ešnerová, CCF 5377 = DTO 355-G5. **Spain**, Badajoz, soil, isolated by P. Blaser, CBS 377.75. **The Netherlands**, fruit jam, 2014, isolated by T. van Doorn, DTO 345-H5. **USA**, IL, Peoria, soy protein, isolated by A.J. Moyer, NRRL 25823. Unknown source, NRRL 84. Unknown country, butter, NRRL 4817 = DTO 355-B9 = IFO 5322 = IMI 313754 = JCM 23051 = CCF 5608.

Aspergillus leucocarpus Hadlok & Stolk, Antonie van Leeuwenhoek 35: 9. 1969. MycoBank MB326642. Fig. 31.
Synonyms: *Eurotium leucocarpum* Hadlok & Stolk, Antonie van Leeuwenhoek 35: 9. 1969.

Typus: CBS 353.68, holotype. Culture ex-type: CBS 353.68 = IBT 5350 = IMI 278375 = NRRL 3497 = PIL 620 = QM 9365 = QM 9707.

ITS barcode: EF652087. (Alternative markers: *BenA* = EF651925; *CaM* = EF652023; *RPB2* = EF651972).

Colony diam, 7 d (mm): CYA 24–31; MEA 21–31; CY20S 68–70; CY20S 30 °C 42–70; CY20S 37 °C No growth; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C 35–58; CYAS 32–40; DG18 43–52; MEA10S 47–50.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture velvety to floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse straw (46). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture floccose; sporulation sparse; conidia *en masse* dark green (21) to greenish olivaceous (90); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture floccose; sporulation sparse; conidia *en masse* dark green (21) to greenish olivaceous (90); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse straw (46). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium straw (46) and white; margins entire; texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, white, globose to subglobose, 80–140 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose, 4.5–5.5 × 3.5–5 µm, in side view lenticular, furrow present, crests 0.8–1.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 800–1 400 × 7.5–12 µm. Vesicles globose to subglobose, 35–60 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 8–11.5 × 3.5–6.5 µm. Conidia globose to subglobose, tuberculate, 5.5–9 × 5–8 µm.

Distinguishing characters: The white ascomata are consistently produced in all available *A. leucocarpus* strains, which can easily distinguish it from other sect. *Aspergillus* species.

Additional materials examined: **Canada**, house dust, 2015, isolated by C.M. Visagie, DTO 357-A2 = KAS7576. **Madagascar**, vanilla sticks, 2012, isolated by J. Houbraken, DTO 174-I5.

Aspergillus levisporus Hubka, A.J. Chen, Jurjević & Samson, **sp. nov.** MycoBank MB818735. Fig. 32.

Etymology: Name refers to its smooth ascospores.

Diagnosis: Smooth ascospores measuring 3–4.5 × 2.5–4 µm.

Typus: **USA**, MO, Saint Louis, bedroom, wood base, 2015, isolated by Ž. Jurjević (holotype: CBS H-22820, culture ex-type: CBS 141767 = DTO 355-G4 = EMSL No.3211 = CCF 5378 = IBT 34512).

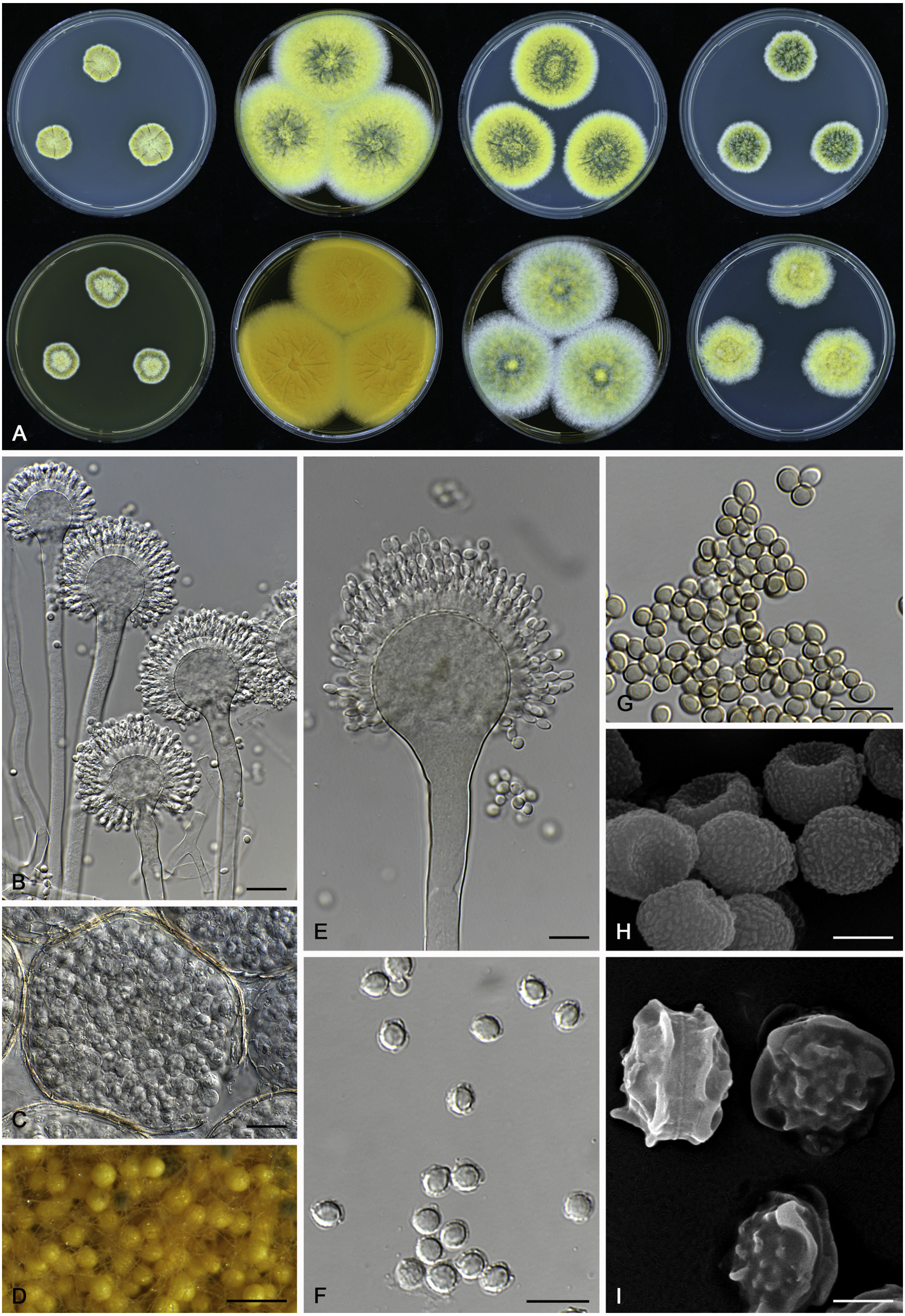


Fig. 30. *Aspergillus intermedius* CBS 523.65^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

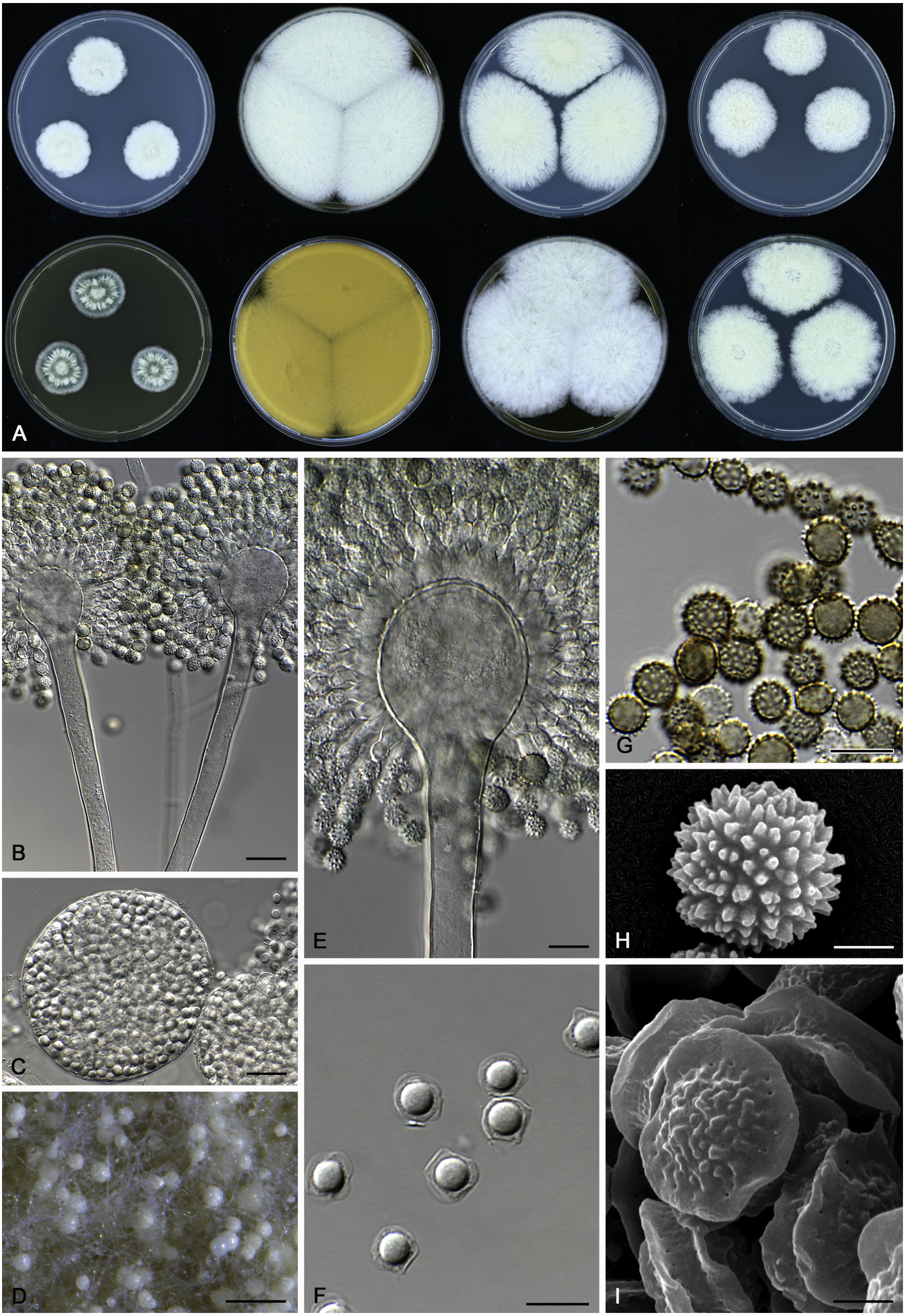


Fig. 31. *Aspergillus leucocarpus* CBS 353.68^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

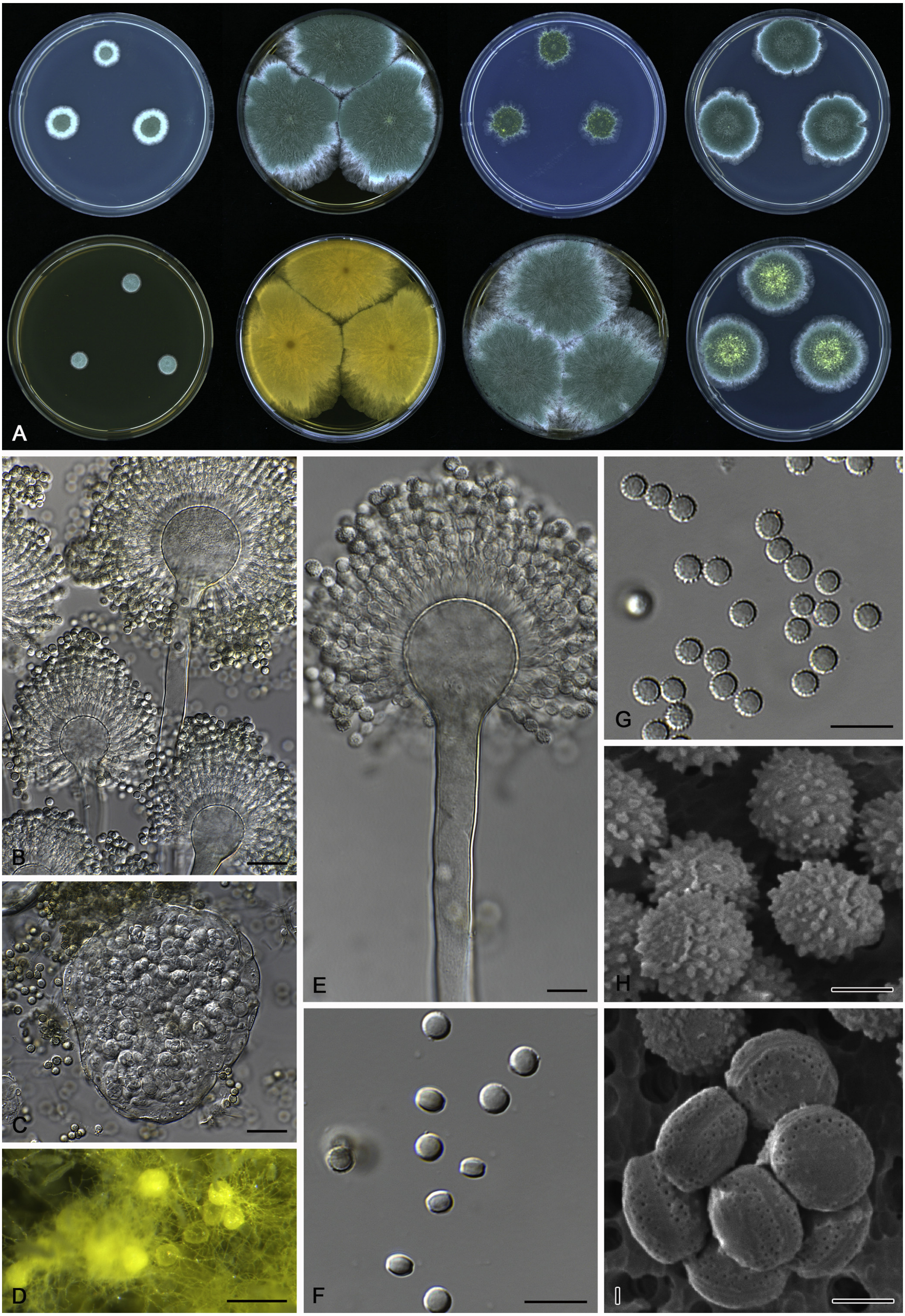


Fig. 32. *Aspergillus levisporus* CBS 141767^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 μm; D = 250 μm; E–G = 10 μm; H, I = 2 μm.

ITS barcode: LT670950. (Alternative markers: *BenA* = LT671094; *CaM* = LT671095; *RPB2* = LT671096).

Colony diam, 7 d (mm): CYA 13–17; MEA 8–10; CY20S 19–20; CY20S 30 °C 18–20; CY20S 37 °C No growth; M40Y 60–65; M60Y 65–67; M60Y 30 °C 70–75; M60Y 37 °C No growth; CYAS 35–37; DG18 35–36; MEA10S 40–41.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins irregular; mycelium sulphur yellow (15); texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse greenish olivaceous (90) at centre, sulphur yellow (15) at edge. M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins irregular; mycelium white; texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins slightly irregular; mycelium white; texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse greenish olivaceous (90) at centre, fading into olivaceous buff (89). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white and sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse sulphur yellow (15) at centre, fading into yellow-green (71). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium white; margins entire; texture floccose; sporulation moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse fulvous (43) at centre, ochreous (44) at edge.

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 70–130 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth, 3–4.5 × 2.5–4 μm, in side view lenticular, furrow present, crests absent. Conidiophores with smooth stipes, hyaline or light brown, 400–600 × 10–14 μm. Vesicles globose to subglobose, 30–44 μm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6–8.5 × 3.5–6 μm. Conidia globose, tuberculate to lobate-reticulate, 3.5–4.5 × 2.5–4 μm.

Distinguishing characters: The non-crested, smooth ascospores of *A. levisporus* resemble those of *A. proliferans*, *A. pseudoglaucus*, *A. ruber* and *A. sloanii*, but the latters all produce larger ascospores, 4–6 × 3–5 μm in *A. proliferans*, 4–6.5 × 3–4.5 μm in *A. pseudoglaucus*, 4–6 × 3.5–5 μm in *A. ruber* and 4–6 × 3–4.5 μm in *A. sloanii*, respectively.

Aspergillus mallochii Visagie, Yilmaz & Seifert, MycoKeys 19: 16. 2017. MycoBank MB819025. Fig. 33.

Typus: DAOM 740296, holotype. Culture ex-type: CBS 141928 = DTO 357-A5 = KAS7618 = DAOMC 146054.

ITS barcode: KX450907. (Alternative markers: *BenA* = KX450889; *CaM* = KX450902; *RPB2* = KX450894).

Colony diam, 7 d (mm): CYA 7–8; MEA 2–3; CY20S 11–12; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y 53–55; M60Y 64–70; M60Y 30 °C 42–47; M60Y 37 °C No growth; CYAS 29–30; DG18 35–38; MEA10S 33–35.

Colony characters: CY20S 25 °C, 7 d: Colonies low, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse sulphur yellow (15). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15), later turn into vinaceous (57) to orange (7); texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse ochreous (44). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse straw (46). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 130–220 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth, minute rough along equatorial ridges, 4–6 × 3–5 μm, in side view lenticular, furrow absent or showing as a trace, crests petaliform, 1–2 μm at high part. Conidiophores with smooth stipes, hyaline or light brown, 600–1 500 × 6–9.5(–12) μm. Vesicles globose to subglobose, 27–43 μm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6.5–9 × 3–5 μm. Conidia subglobose to ellipsoidal, tuberculate, 4.5–7 × 4–5.5 μm.

Distinguishing characters: Phylogenetically and morphologically *A. mallochii* is close to *A. appendiculatus*, but *A. appendiculatus* produces larger ascospores (5–7.5 × 4–5.5 μm) and does not grow on MEA and CYA at 25 °C.

Additional materials examined: **The Netherlands**, chocolat miroir, 2015, CBS 141776 = DTO 343-G3.

Aspergillus megasporus, Visagie, Yilmaz & Seifert, MycoKeys 19: 17. 2017. MycoBank MB819028. Fig. 34.

Typus: DAOM 741781, holotype. Culture ex-type: CBS 141929 = DTO 356-H7 = KAS 6176 = DAOMC 250799.

ITS barcode: KX450910. (Alternative markers: *BenA* = KX450892; *CaM* = KX450905; *RPB2* = KX450897).

Colony diam, 7 d (mm): CYA 10–11; MEA 4–6; CY20S 38–40; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y

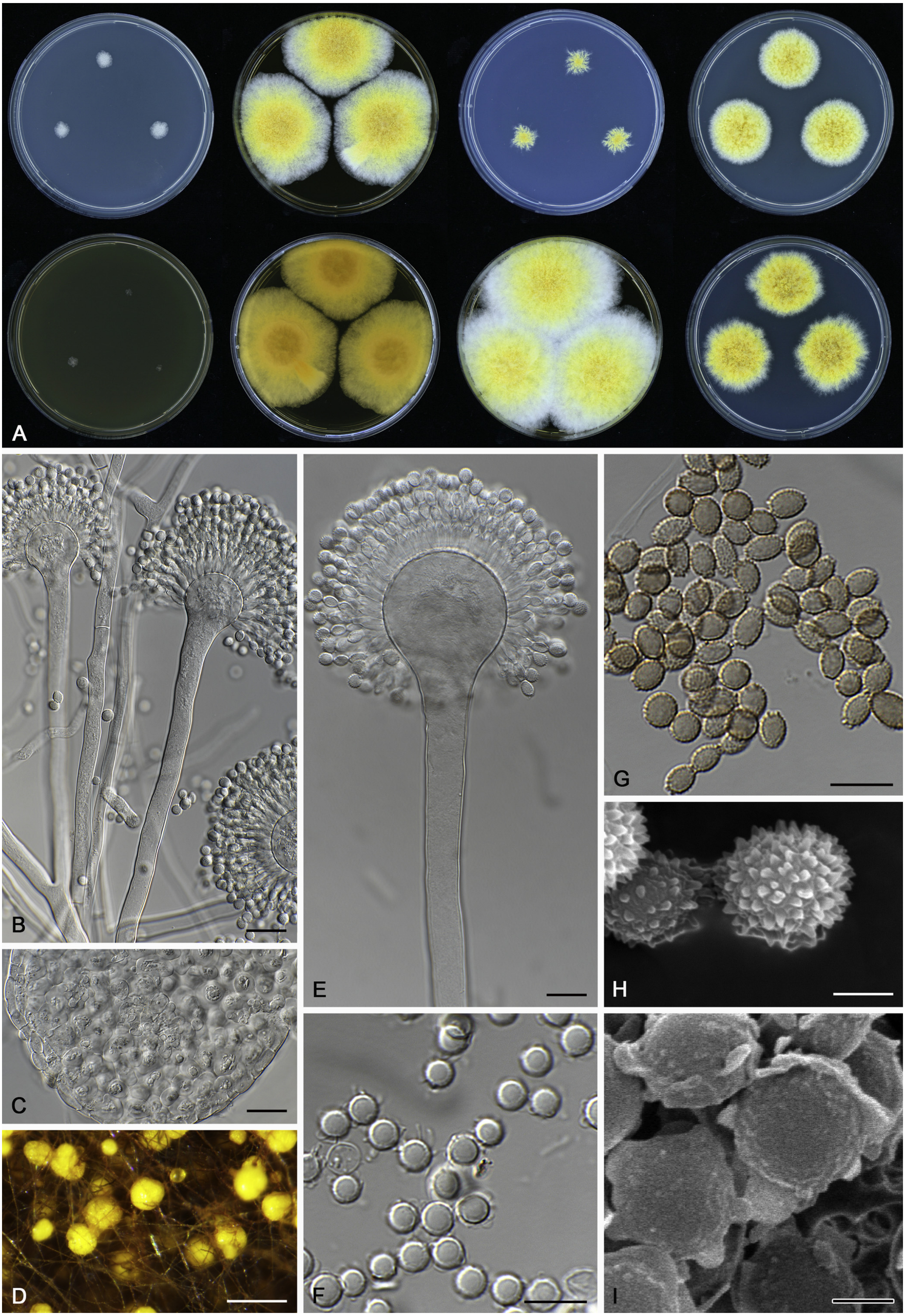


Fig. 33. *Aspergillus mallochii* CBS 141928^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

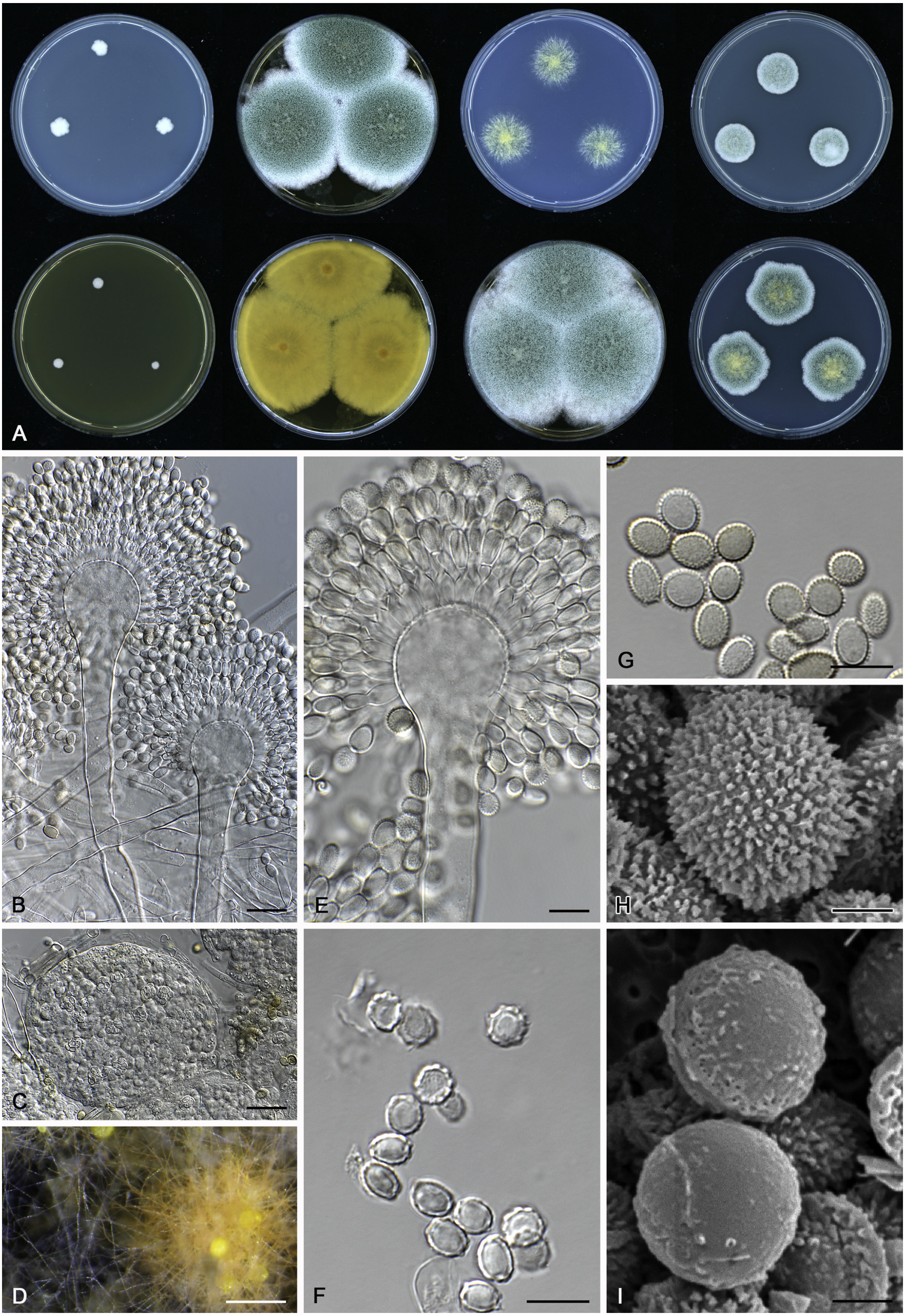


Fig. 34. *Aspergillus megasporus* CBS 141929^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

55–60; M60Y 70–75; M60Y 30 °C 61–64; M60Y 37 °C No growth; CYAS 23–24; DG18 38–40; MEA10S 50–52.

Colony characters: CY20S 25 °C, 7 d: Colonies low, plane; margins entire; mycelium straw (46) to sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse ochreous (44). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation dense; conidia *en masse* greyish green (50) to dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies deep, plane; margins entire; mycelium white; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12) at centre, fading into yellow-green (71). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15) and white; margins entire; texture floccose; sporulation moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 110–300 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth, rough along equatorial ridges, 4–6.5 × 3.5–5.5 μm, in side view lenticular, furrow present, crests absent or indefinite. Conidiophores with smooth stipes, hyaline or light brown, 1 000–1 500 × 6.5–12(–21.5) μm. Vesicles globose to subglobose, 30–54 μm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 7.5–14 × 4–7.5 μm. Conidia subglobose to ellipsoidal, tuberculate, 7–14 × 5–8.5 μm.

Distinguishing characters: *Aspergillus megasporus* belongs to *A. glaucus* clade (Fig. 1). Its ascospore dimensions are similar to those of *A. aurantiacoflavus*, *A. glaucus*, *A. niveoglaucus* and *A. proliferans*. However, *A. aurantiacoflavus*, *A. glaucus* and *A. niveoglaucus* have low, irregular crests in contrast to non-crested ascospores in *A. megasporus* and *A. proliferans*. *Aspergillus proliferans* can be differentiated by smaller conidia.

Additional materials examined: **Canada**, New Brunswick, Little Lepreau, house dust, 2015, isolated by C.M. Visagie, DTO 356-H1 = KAS5973 = DAOMC 250800. **The Netherlands**, Dutch chocolate butter, 2007, isolated by M. Meijer, CBS 141772 = DTO 048-I3.

Aspergillus montevidensis Talice & Mackinnon, Compt. Rend. Soc. Biol. Fr. 108: 1007. 1931. MycoBank MB309231. Fig. 35.

Synonyms: *Eurotium montevidense* (Talice & J.A. Mackinnon) Malloch & Cain, Canad. J. Bot. 50 (1): 64. 1972.
Eurotium amstelodami var. *montevidense* (Talice & J.A. Mackinnon) Kozak., Mycol. Pap. 161: 86. 1989.
Aspergillus vitis var. *montevidensis* Kozak., Mycol. Pap. 161: 86. 1989.
Aspergillus heterocaryoticus C.M. Chr., L.C. López & C.R. Benj., Mycologia 57 (4): 535. 1965.
Eurotium heterocaryoticum C.M. Chr., L.C. López & C.R. Benj., Mycologia 57 (4): 536. 1965.
Aspergillus vitis Novobr., Novosti Sist. Nizsh. Rast. 9: 175. 1972.
Eurotium vitis Novobr., Novosti Sist. Nizsh. Rast. 9: 175. 1972.
Aspergillus hollandicus Samson & W. Gams, Advances in *Penicillium* and *Aspergillus* Systematics: 33. 1985.

Typus: BPI 884202, neotype (Hubka *et al.* 2013a). Culture ex-type: CBS 491.65 = NRRL 108 = ATCC 10077 = IBT 5685 = IHEM 3337 = IMI 172290 = NRRL 109 = QM 7423 = Thom 5290 = Thom 5633.24 = WB 108.

ITS barcode: EF652077. (Alternative markers: *BenA* = EF651898; *CaM* = EF652020; *RPB2* = EF651964).

Colony diam, 7 d (mm): CYA 19–24; MEA 18–23; CY20S 45–61; CY20S 30 °C 25–50; CY20S 37 °C 28–30; M40Y 60–>75; M60Y 60–>75; M60Y 30 °C 60–>75; M60Y 37 °C >75; CYAS 20–47; DG18 38–60; MEA10S 53–65.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, sulcate; margins entire; mycelium sulphur yellow (15) and white; texture velvety to floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50) or white; soluble pigments absent; exudates absent; reverse greenish olivaceous (90) or sulphur yellow (15). M40Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate or plane; margins entire; mycelium sulphur yellow (15) and white; texture velvety to floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50) or white; soluble pigments absent; exudates absent; reverse ochreous (44) or luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and white; texture velvety or floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50) or white; soluble pigments absent; exudates absent; reverse ochreous (44) or luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane or sulcate; margins slightly irregular; mycelium white and sulphur yellow (15); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50) or glaucous (73) or white; soluble pigments absent; exudates absent; reverse greenish olivaceous (90) to salmon (41). DG18 25 °C, 7 d: Colonies moderately deep, plane to slightly sulcate; margins entire; mycelium sulphur yellow (15) and white; texture velvety to floccose; sporulation moderately dense to dense; conidia *en masse* greyish green (50) or white; soluble pigments absent; exudates absent; reverse greenish olivaceous (90) to sulphur yellow (15). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15) and white; margins entire; texture velvety to floccose; sporulation moderately dense or absent; conidia *en masse* greyish green (50) or white; soluble pigments absent; exudates absent; reverse luteous (12) to ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 80–250 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view

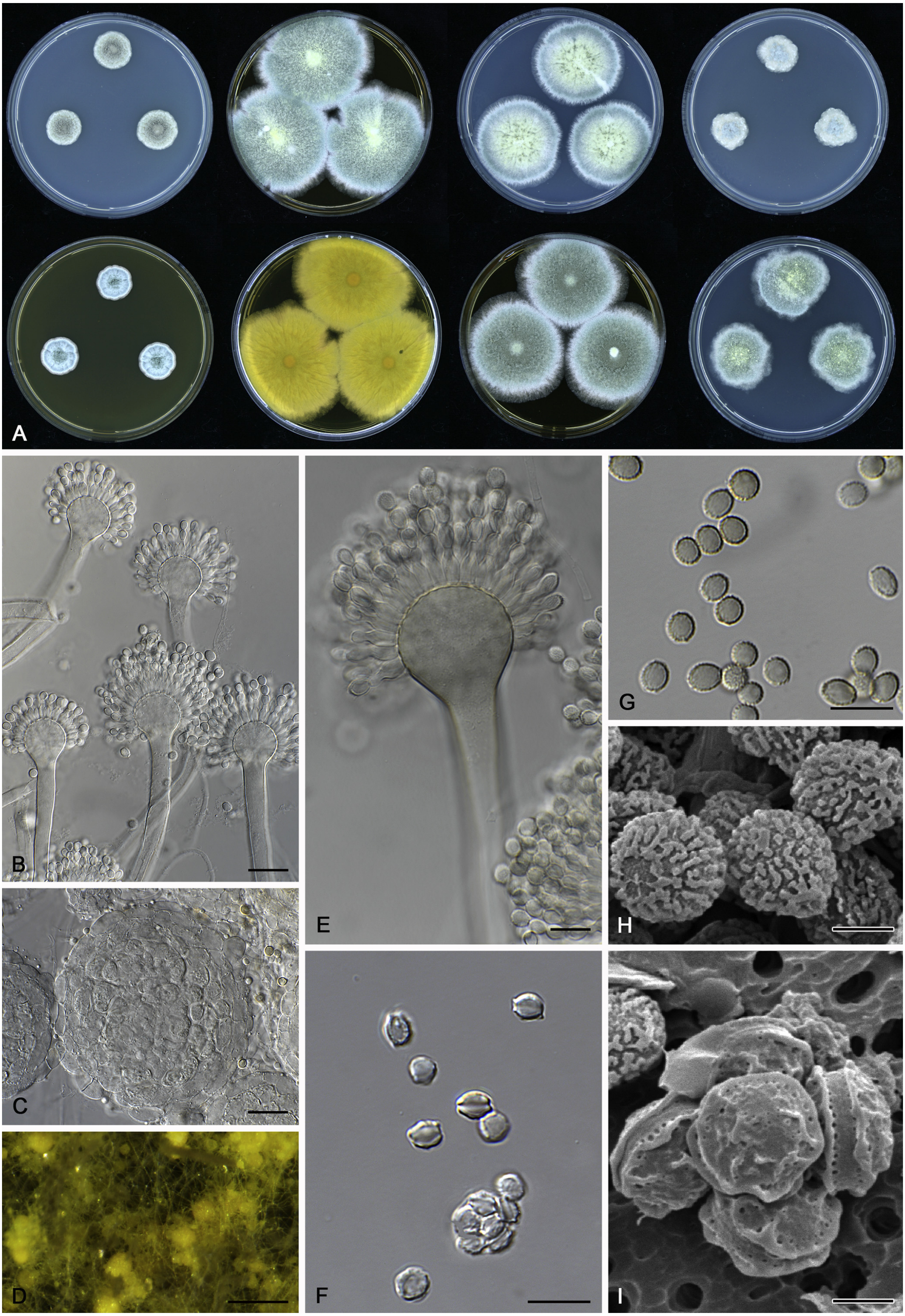


Fig. 35. *Aspergillus montevidensis* CBS 491.65^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

globose to subglobose, spore bodies in most strains rugulose; smooth or slightly rough in atypical strain CCF 4070, tuberculate in atypical strain CCF 4248, 4–6 × 3–4.5 µm, in side view lenticular, furrow pronounced, crests 0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 250–500 × 6–13.5 µm. Vesicles globose to subglobose, 25–35(–50) µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 5–8.5(–11) × 3–6 µm. Conidia globose, subglobose to ellipsoidal, lobate-reticulate, 4–6.5 × 3.5–5 µm.

Distinguishing characters: Morphologically and phylogenetically *A. montevidensis* is close to *A. intermedius*, but *A. intermedius* produces microtuberculate conidia.

Notes: The recent species concept of *A. amstelodami sensu* (Thom & Raper 1941, Raper & Fennell 1965, Blaser 1975) is different from the original description (Mangin 1909). Pitt (1985) speculated that the original strain had been replaced by the species described in Thom & Raper (1941), and recommended *A. montevidensis* as a substitute name for *A. amstelodami*. Hubka *et al.* (2013a) agreed and considered the description of *A. montevidensis* (Talice & Mackinnon 1931) the first valid description of the species consistent with *E. amstelodami sensu* Thom & Raper (1941). *Aspergillus hollandicus* and *A. vitis* were proposed for the anamorphic name of *E. amstelodami* Mangin (Samson & Gams 1985, Kozakiewicz 1989). *Aspergillus heterocaryoticus* was considered to be conspecific with *E. amstelodami* (Blaser 1975, Samson 1979). These three species were synonymized with *A. montevidensis* (Hubka *et al.* 2013a).

Additional materials examined: **China**, mite, 1969, CGMCC 3.03888 = DTO 348-D3. **China**, Ningxia, unknown source, CGMCC 3.06069, CGMCC 3.06072. **China**, unknown source, CGMCC 3.00462, CGMCC 3.01307, CGMCC 3.00771, CGMCC 3.01306, CGMCC 3.01309, CGMCC 3.04462, CGMCC 3.06064, CGMCC 3.03967, CGMCC 3.04059, CGMCC 3.01304, CGMCC 3.01308. **China**, Hebei, unknown source, CGMCC 3.06074. **China**, Neimenggu, unknown source, CGMCC 3.06071, CGMCC 3.06077, CGMCC 3.06078, CGMCC 3.06073. **China**, Hebei, soil, CGMCC 3.06511. **China**, Henan, corn, CGMCC 3.06065. **China**, Ningxia, soil, CGMCC 3.06066. **China**, Hebei, moldy agaric, CGMCC 3.06513. **China**, Yunnan, moldy bean curd, CGMCC 3.06517. **China**, Hebei, straw, CGMCC 3.06512. **China**, moldy sugarcane, CGMCC 3.07157. **China**, Hebei, moldy pine seeds, CGMCC 3.06514. **China**, Xinjiang, soil, CGMCC 3.11413. **China**, Beijing, unknown source, CGMCC 3.06063, CGMCC 3.06075, CGMCC 3.06076. **China**, Hainan, soil, CGMCC 3.06061. **China**, Guizhou, soil, CGMCC 3.06068. **China**, Ningxia, soil, CGMCC 3.06070. **China**, Jiangsu, fabric, CGMCC 3.07178. **China**, Xinjiang, soil, CGMCC 3.11525, CGMCC 3.11410. **China**, Hebei, soil, CGMCC 3.06510. **China**, Hebei, moldy bark, CGMCC 3.06516. **China**, Yunnan, moldy bamboo, CGMCC 3.06518. **China**, Hunan, soil, CGMCC 3.06067. **China**, Hebei, moldy leaves, CGMCC 3.06515. **China**, industrial material, 1955, isolated by V. Zánová, CCF 726. **Czech Republic**, feed, 1984, isolated by V. Neumannová, CCF 1952. **Czech Republic**, Prague, neck skin of 78-year-old woman, 2008, isolated by M. Skořepová, CCF 3998. **Czech Republic**, heel skin of 32-year-old man, Prague, 2007, isolated by M. Skořepová, CCF 4069. **Czech Republic**, fingernail of 32-year-old woman, Prague, 2007, isolated by M. Skořepová, CCF 4070. **Czech Republic**, Prague, thigh and neck skin of 42-year-old woman, 2010, isolated by P. Lysková, CCF 4071. **Czech Republic**, Skrbeň, window sill, 1997, isolated by A. Kubátová, CCF 4248. **Czech Republic**, České Budějovice, sputum of 11-year-old girl, 2010, isolated by N. Mallátová, CCF 4258. **Czech Republic**, Prague, bronchoalveolar lavage of 40-year-old man, 2012, isolated by P. Lysková, CCF 4370. **Czech Republic**, Prague, external auditory canal of 66-year-old man, 2010, isolated by P. Lysková, CCF 4371. **Czech Republic**, Prague, bronchoalveolar lavage fluid of 60-year-old male, 2015, isolated by P. Lysková, PL 378/15. **Czech Republic**, Prague, air sampler – intensive care unit room (haematooncology), 2013, isolated by V. Chrenková, MY1832. **Czech Republic**, Prague, air sampler – paediatric haematooncology unit, 2013, isolated by V. Chrenková, MY2467. **Czech Republic**, Prague, lungs of 43-year-old woman after lung transplantation, 2014, isolated by V. Chrenková, MY4449. **Czech Republic**, Prague, fingernail of 37-year-old man, 2007, isolated by M. Skořepová, SK237. **Czech Republic**, Prague, pigeon dropping, 1991, isolated by K. Prášil and R. Kolínská, CCF 2723. **Czech Republic**, Prague, white Arabic bread (pita), 1999, isolated by A. Kubátová, CCF 3750. **Czech Republic**, Veleliby near Nymburk, seeds of *Papaver somniferum*, 1999, isolated by J. Hubert, CCF 3135. **Denmark**, straw, 2012, isolated by J. Houbraken, DTO 212-D3. **Germany**, bakery, 2010, isolated by T. Hoogenhuijzen, DTO 121-G7. **Hungary**, table, 2009, isolated by van Mil, DTO 101-F5. **Hungary**, indoor air, 2014, isolated by M. Meijer, DTO 147-I4. **Kazakhstan**, Alma-Ata, ex grapes, 1968, isolated by L.A. Beljakova, CBS 651.74 = ATCC 24717 = IMI 174724 = VKM F-1760. **Mexico**, Oryza sativa kernel, 1963, isolated by C.R. Benjamin, NRRL A-13891 = CBS 410.65. **Spain**, Cantabria, Altamira Cave, cave sediment, 2008, isolated by A. Nováková, S14. **Suriname**, plywood, isolated by M.B. Schol-Schwarz, CBS 111.52 = DTO 351-C9. **The Netherlands**, cake, 2015, isolated by M. Meijer, DTO 334-A3. **The Netherlands**, corn kernels (imported), 2014, isolated by J. Houbraken, DTO 300-E3. **The Netherlands**, sesame seed (imported), 2013, isolated by J. Houbraken, DTO 253-H7. **USA**, unknown source, ~1910, NRRL 90 = CBS 518.65. **USA**, Missouri, Columbia, candied grapefruit rind, isolated by D.I. Fennell, NRRL 4716. **USA**, IL, Peoria, refrigerated bread dough, isolated by R. Graves, NRRL 25850. **USA**, IL, Chicago, nasal swab, NRRL 35697. **USA**, PA, Mahanoy City, bedroom, settle plates, 2015, isolated by Ž. Jurjević, EMSL No. 2934 = CCF 5379 = DTO 355-H3. **USA**, Delaware, green house, air, 2011, isolated by Ž. Jurjević, EMSL No. 1589. **USA**, FL, Loxahatchee, Home, Kitchen cabinet, 2013, isolated by Ž. Jurjević, EMSL No. 2187. **USA**, IL, Chicago, bathroom, settle plates, 2015, isolated by Ž. Jurjević, EMSL No. 2790. Unknown source, NRRL 89.

Aspergillus neocarnoyi Kozak., Mycol. Pap. 161: 63. 1989. MycoBank MB127756. Fig. 36.

Synonyms: *Aspergillus carnoyi* (Biourge) Thom & Raper, Misc. Publ. U.S. Dept. Agric.: 34. 1941, nom. inval. [Art. 39.1 McNeill *et al.* 2012]

Eurotium carnoyi Malloch & Cain, Canad. J. Bot. 50 (1): 63. 1972.

Typus: IMI 172279, holotype. Culture ex-type: CBS 471.65 = NRRL 126 = ATCC 16924 = IBT 6016 = IMI 172279 = LSHTM A32 = QM 7402 = Thom 5612.A32 = WB 126 = DTO 196-H6.

ITS barcode: EF652057. (Alternative markers: *BenA* = EF651903; *CaM* = EF651985; *RPB2* = EF651942).

Colony diam, 7 d (mm): CYA No growth; MEA No growth; CY20S 3–5; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y 20–25; M60Y 53–65; M60Y 30 °C 15–18; M60Y 37 °C No growth; CYAS 18–20; DG18 32–42; MEA10S 35–38.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse straw (46). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7) at centre, white at edge; texture floccose; sporulation sparse; conidia *en masse* green (20); soluble pigments absent; exudates absent; reverse luteous (12) fading into saffron (10). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium orange (7) at centre, white at edge; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) fading into straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium fulvous (43) at centre, white at edge; texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent;

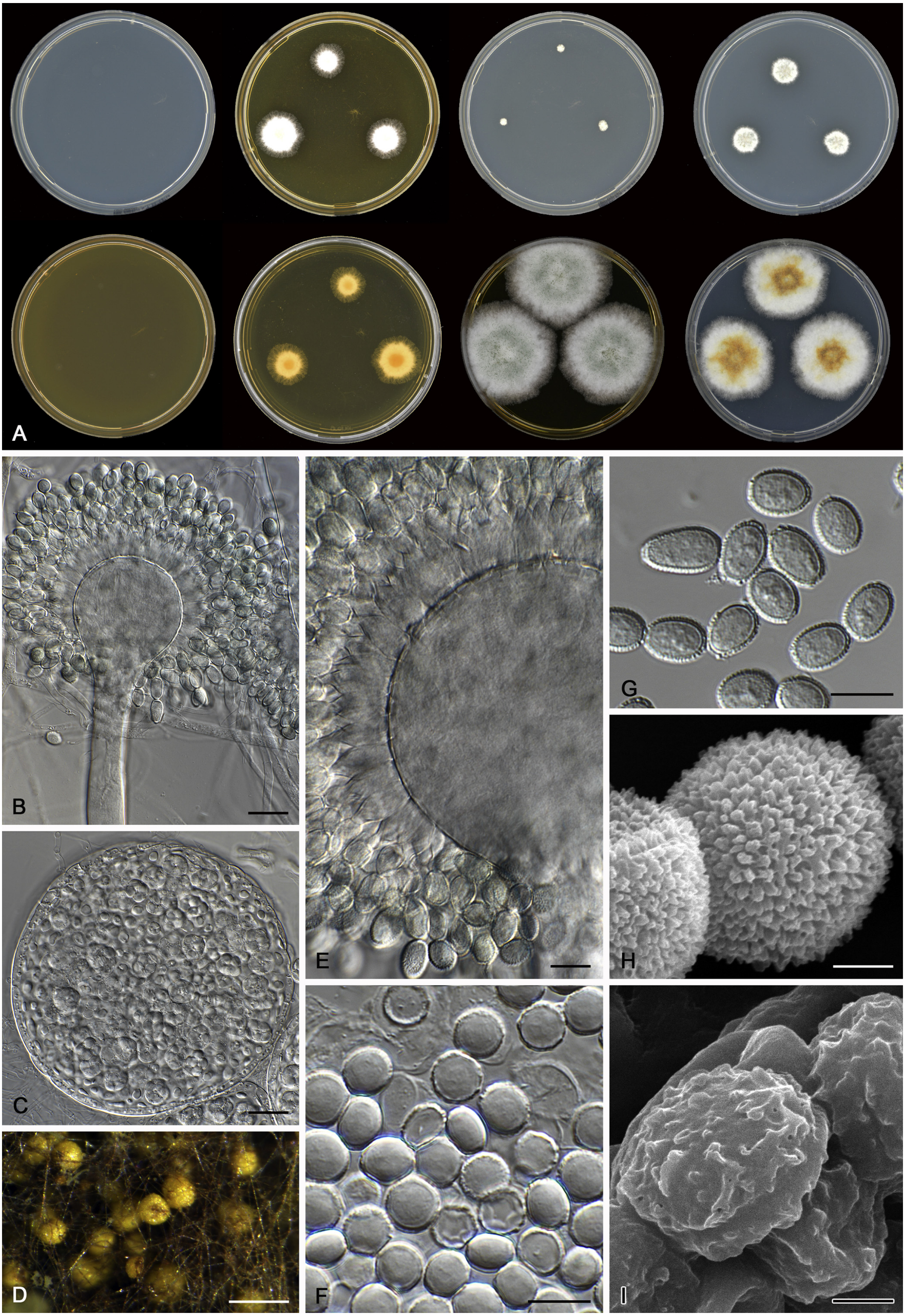


Fig. 36. *Aspergillus neocarnoyi* CBS 471.65^T. **A.** Colonies: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

reverse luteous (12) fading into straw (46). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium saffron (10) at centre, white at edge; margins entire; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse rust (39) at centre, fading into saffron (10).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 120–230 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose to rugulose, 6.5–9 × 4.5–7 µm, in side view lenticular, furrow present, crests absent or indefinite. Conidiophores with smooth stipes, hyaline or light brown, 1 000–2 000 × (9–)12–23 µm. Vesicles globose to subglobose, (32–)50–92 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 12–21 × 6–9 µm. Conidia ellipsoidal, tuberculate, 8–15.5 × 6–10 µm.

Distinguishing characters: Phylogenetically *A. neocarnoyi* is closely related to *A. brunneus* and *A. niveoglaucus*, but *A. brunneus* produces mainly globose conidia, while *A. niveoglaucus* produces smaller ascospores. The large ascospores of *A. neocarnoyi* also resemble those of *A. osmophilus*, but *A. osmophilus* produces smaller conidia and ascospores with thick crests.

Additional materials examined: **Slovenia**, Ljubljana, Slovene Ethnographic museum, air at the sampling of shaman statue originating from Mali, 2016, isolated by P. Zalar, EXF-10029 = DTO 357-E2.

Aspergillus niveoglaucus Thom & Raper, U.S.D.A. Misc. Pub. 426: 35. 1941. MycoBank MB120985. Fig. 37.
Synonyms: *Eurotium niveoglaucum* (Thom & Raper) Malloch & Cain, Canad. J. Bot. 50 (1): 64. 1972.
Aspergillus glauconiveus Samson & W. Gams, Advances in *Penicillium* and *Aspergillus* Systematics: 45. 1985.
Aspergillus parviverruculosus H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14 (1): 12. 1995.
Eurotium parviverruculosum H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14 (1): 12. 1995.

Typus: IMI 32050ii, neotype (Samson & Gams 1985). Culture ex-type: CBS 114.27 = CBS 517.65 = NRRL 127 = ATCC 10075 = BCRC 33096 = CGMCC 3.4374 = FRR 927 = IBT 5356 = IMI 32050 = JCM 1578 = LSHBA 16 = NRRL 129 = NRRL 130 = QM 1977 = Thom 5612.A16 = Thom 5633 = Thom 5633.7 = Thom 7053.2 = UAMH 6591 = WB 127 = WB 130.

ITS barcode: EF652058. (Alternative markers: *BenA* = EF651905; *CaM* = EF651993; *RPB2* = EF651943).

Colony diam, 7 d (mm): CYA 2–8; MEA 0–5; CY20S 12–30; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y >75; M60Y >75; M60Y 30 °C 65–>75; M60Y 37 °C No growth; CYAS 32–37; DG18 34–42; MEA10S 40–45.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) or white; texture floccose; sporulation sparse; conidia *en masse* white or pale green (19); soluble pigments absent; exudates absent; reverse straw (46). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium rosy buff (61) or straw (46) or white; texture floccose; sporulation sparse; conidia *en masse* pale green (19) or white; soluble pigments absent; exudates absent; reverse apricot (42). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) or white; texture floccose; sporulation sparse; conidia *en masse* white or pale green (19); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) or white; texture floccose; sporulation moderately dense; conidia *en masse* white or pale green (19); soluble pigments absent; exudates absent; reverse straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) or white; texture floccose; sporulation moderately dense; conidia *en masse* white or pale green (19); soluble pigments absent; exudates absent; reverse straw (46). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium straw (46) or white; margins entire; texture floccose; sporulation moderately dense; conidia *en masse* white or pale green (19); soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 90–240 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies rough along equatorial ridges or verruculose to rugulose, (4.5–)5.5–7.5 × (3–)5–6 µm, in side view lenticular, furrow present, crests irregular, < 0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 1 000–1 500 × (7.5)–10–23 µm. Vesicles globose to subglobose, (31–)55–85 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 8–14(–20) × 4–7(–11) µm. Conidia subglobose to ellipsoidal, tuberculate, (6–)8–13.5 × 4–9 µm.

Distinguishing characters: Phylogenetically *A. niveoglaucus* is closely related to *A. brunneus* and *A. neocarnoyi*, but these two species produce larger ascospores, 7–10 × 6–8 µm in *A. brunneus* and 6.5–9 × 4.5–7 µm in *A. neocarnoyi*. Morphologically, it resembles *A. glaucus* in ascospore size and ornamentation, but the convex surface is less roughened in ascospores of *A. glaucus*.

Additional materials examined: **Belgium**, Namur, indoor air, 1983, IHEM 1811 = DTO 355-C3. **Brazil**, corn kernels, 2008, isolated by J. Houbraken, DTO 060-I3. **Canada**, Manitoba, Barley feed, isolated by M. Desjardins, CBS 117311. **China**, Hebei, soil, CBS 101750 = CGMCC 3.04665 (AS 3.4665) = DTO 197-B4. **China**, Guangdong, cashew Kernel, 2001, CGMCC 3.06092 = DTO 348-F3. **China**, Yunnan, moldy corn leaves, CGMCC 3.06496. **China**, Neimenggu, soil, CGMCC 3.07854. **China**, Guizhou, unknown source, CGMCC 3.06102. **China**, unknown source, CGMCC 3.01312, CGMCC 3.01294. **Czech Republic**, garlic, isolated by L. Marvanová, CCM F-530 = CCF 4038. **Czech Republic**, Prague, cereals, 1993, isolated by A. Kubátová, CCF 4388. **South Korea**, soybeans, 2012, isolated by D.H. Kim, CCF 4787 = KACC 47144 = DTO 355-C4, CCF 4790 = KACC 47147 = DTO 355-C5. **Spain**, Andalusia, Málaga, Cueva del Tesoro, cave sediment from the cave wall, 2010, A. Nováková, CCF 4191 = DTO 355-C1. **The Netherlands**, apricot paste, 2014, isolated by M. Meijer, DTO 308-B9. **The Netherlands**, animal feed kernels, 2016, isolated by J. Dijksterhuis, DTO 346-B4. **The Netherlands**, spoiled starch, isolated by J. Houbraken, DTO 193-B6. **USA**, Montana, Great Falls, air of bathroom, 2013, isolated by Ž. Jurjević, EMSL No. 2211 = CCF 5380 = DTO 355-H8. Unknown source, isolated by G. Smith, NRRL 128, NRRL 136, NRRL 137.

Aspergillus osmophilus Asgari & Zare, Mycoscience 55: 58. 2013. MycoBank MB803278. Fig. 38.

Typus: IRAN 16110 F, holotype. Culture ex-type: CBS 134258 = IRAN 2090C = DTO 354-C1.

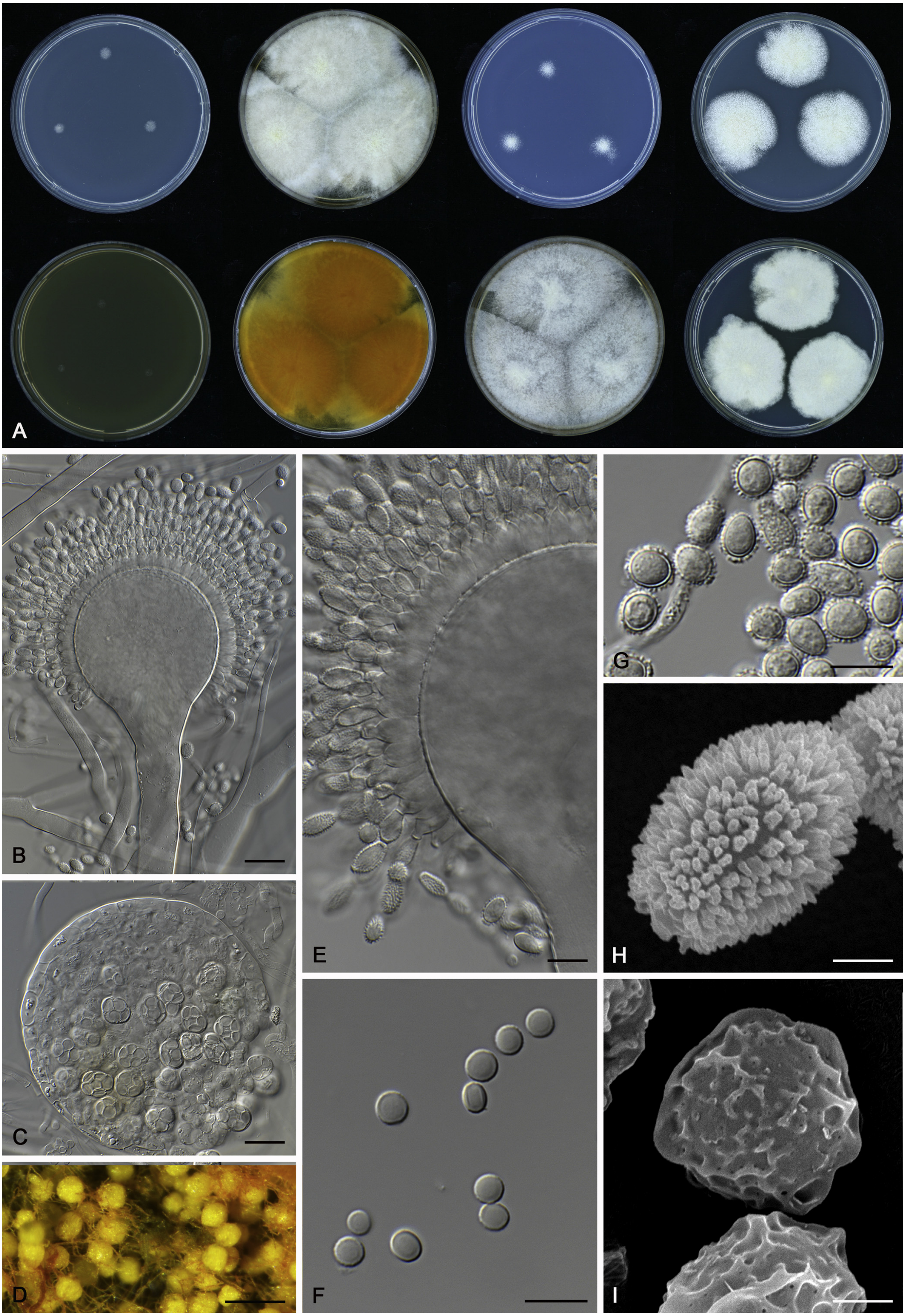


Fig. 37. *Aspergillus niveoglaucus* CBS 114.27^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

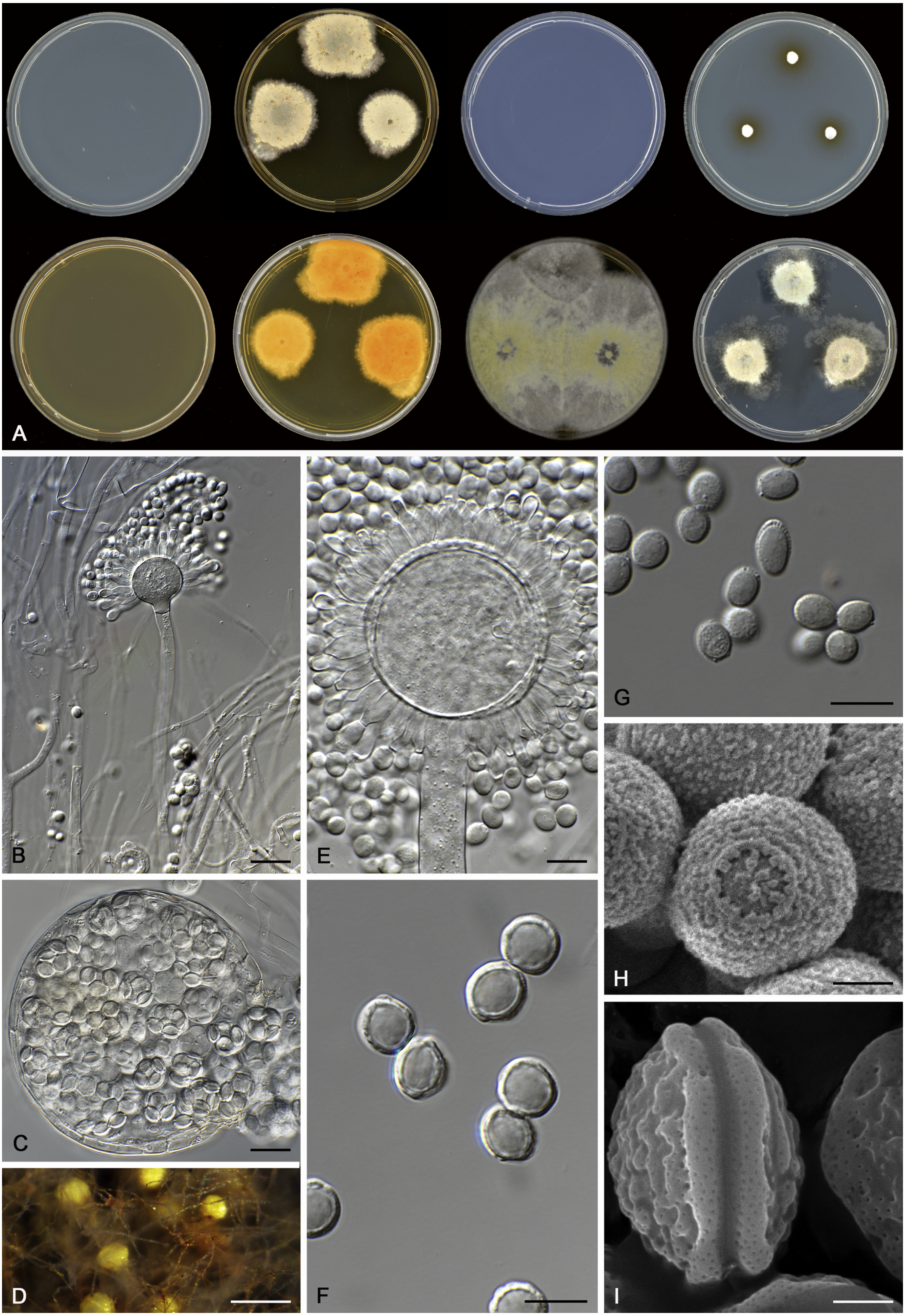


Fig. 38. *Aspergillus osmophilus* CBS 134258^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

ITS barcode: KC473921. (Alternative markers: *BenA* = LT671127; *CaM* = LT671128; *RPB2* = LT671129).

Colony diam, 7 d (mm): CYA No growth; MEA No growth; CY20S No growth; CY20S 30 °C 2–3; CY20S 37 °C No growth; M40Y 30–41; M60Y >75; M60Y 30 °C >75; M60Y 37 °C 63–65; CYAS 6–7; DG18 43–45; MEA10S 54–60.

Colony characters: M40Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium salmon (41); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates light yellow droplets; reverse fulvous (43). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium primrose (66); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates light yellow droplets; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium primrose (66); texture floccose; sporulation absent; soluble pigments light brown; exudates absent; reverse orange (7) at centre, saffron (10) at edge. DG18 25 °C, 7 d: Colonies moderately deep, plane; margins irregular; mycelium salmon (41); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates light yellow droplets; reverse fulvous (43). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium primrose (66); margins entire; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–350 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose, 7–9 × 6–7.5 µm, in side view lenticular, furrow pronounced, crests 0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 300–1 000 × 7.5–12 µm. Vesicles globose to subglobose, 28–46 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 9–12 × 4.5–7 µm. Conidia subglobose to ellipsoidal, microtuberculate to tuberculate, 6–8.5 × 5.5–7.5 µm.

Distinguishing characters: Phylogenetically *A. osmophilus* is closely related to *A. xerophilus*, but *A. xerophilus* produces smaller ascospores (4.5–6.5 × 3.5–5 µm) and does not grow on M60Y at 37 °C. The large ascospores of *A. osmophilus* resemble those of *A. brunneus* and *A. neocarnoyi*, but *A. brunneus* can grow on CYA and MEA, *A. neocarnoyi* produces larger conidia measuring 8–15.5 × 6–10 µm.

Aspergillus porosus A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB818736. Fig. 39.

Etymology: Name refers to small holes on the ascospores.

Diagnosis: Small, pitted ascospores (3.5–5.5 × 3–4.5 µm), lobate-reticulate conidia (3.5–5.5 × 2.5–4.5 µm).

Typus: **Turkey**, soil, 2013, isolated by Canan Unal (holotype: CBS H-22822, culture ex-type: CBS 141770 = DTO 262-D7 = IBT 34443).

ITS barcode: LT670961. (Alternative markers: *BenA* = LT671130; *CaM* = LT671131; *RPB2* = LT671132).

Colony diam, 7 d (mm): CYA 21–23; MEA 18–19; CY20S 58–60; CY20S 30 °C 37–58; CY20S 37 °C 31–33; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C >75; CYAS 35–41; DG18 45–50; MEA10S 62–63.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, sulcate; margins entire; mycelium sulphur yellow (15); texture velvety; sporulation moderately dense or absent; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12) to ochreous (44). M40Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation absent to sparse; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse ochreous (44) fading into sulphur yellow (15). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse to moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12) to sulphur yellow (15). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation sparse to moderately dense; conidia *en masse* dark green (21); soluble pigments absent; exudates absent; reverse luteous (12) to ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 80–230 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies rugulose, pitted, 3.5–5.5 × 3–4.5 µm, in side view lenticular, furrow pronounced, crests 0.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 250–600 × 5–12.5 µm. Vesicles globose to subglobose, 24–58 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 5–10 × 2.5–5 µm. Conidia globose to subglobose, lobate-reticulate, 3.5–5.5 × 2.5–4.5 µm.

Distinguishing characters: Under SEM, the entire surface of ascospores of *A. porosus* is pitted, in contrast most sect. *Aspergillus* species have holes along equatorial ridges. Phylogenetically *A. porosus* is related to *A. caperatus*, *A. intermedius* and *A. montevidensis*, but *A. intermedius* can be distinguished by smooth conidia (microtuberculate under SEM), *A. caperatus* does not grow on CY20S at 37 °C, and *A. montevidensis* produces slightly larger conidia (4–6.5 × 3.5–5 µm).

Additional materials examined: **Israel**, Arachis hypogaea fruit, isolated by P. Blaser, CBS 375.75 = DTO 197-C4. **South Africa**, Robben Island, soil, 2015, isolated by M. Meijer, DTO 338-A7. **Turkey**, soil, 2014, isolated by R. Demirel, DTO 308-D1. **Turkey**, soil, 2013, isolated by A. Yoltas, DTO 262-D4, DTO 262-D2.

Aspergillus proliferans G. Sm., Trans. Brit. Mycol. Soc. 26: 26. 1943. MycoBank MB284312. Figs 40, 41.

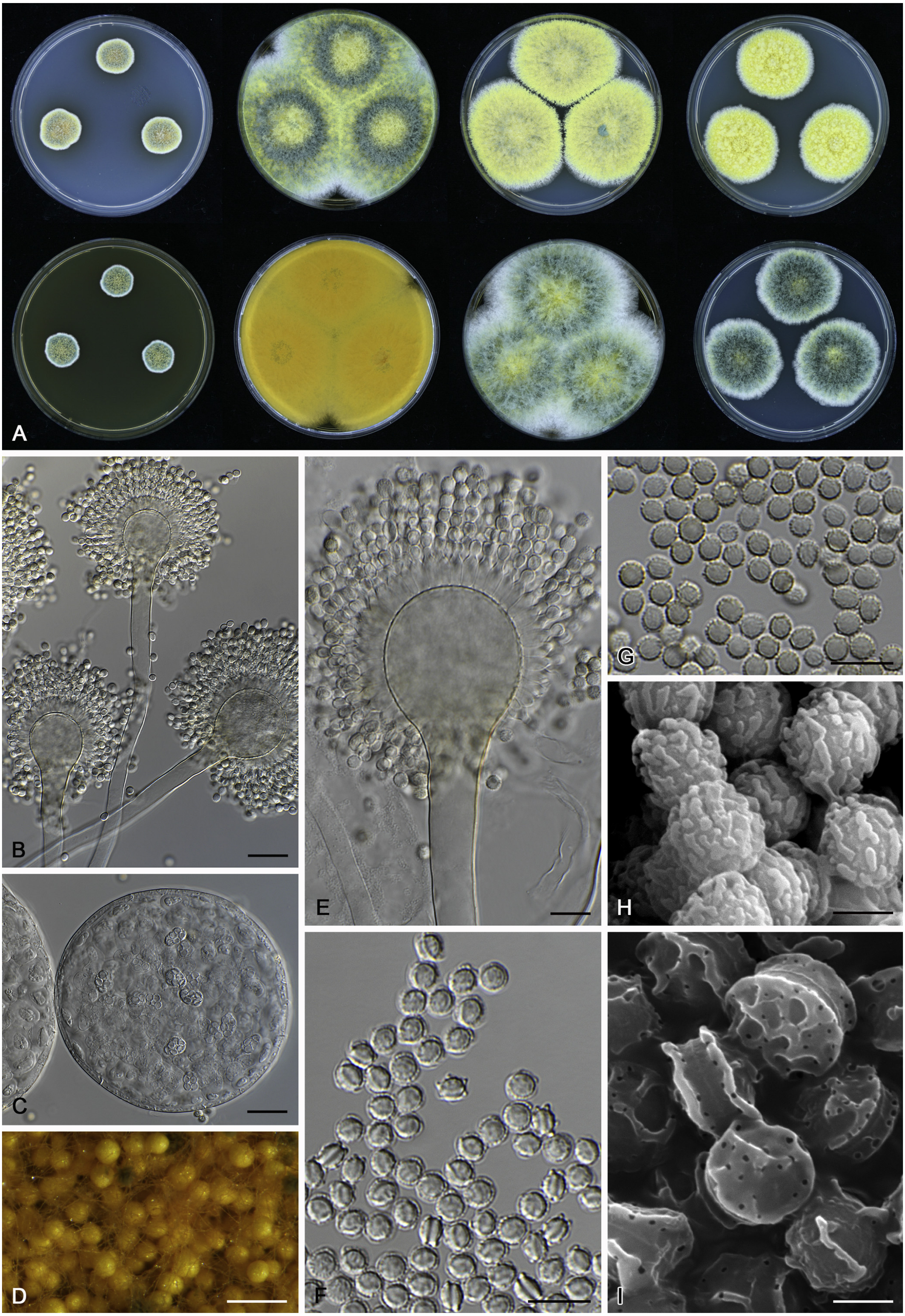


Fig. 39. *Aspergillus porosus* CBS 141770^{T}. **A.** Colonies: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 μm; D = 250 μm; E–G = 10 μm; H, I = 2 μm.

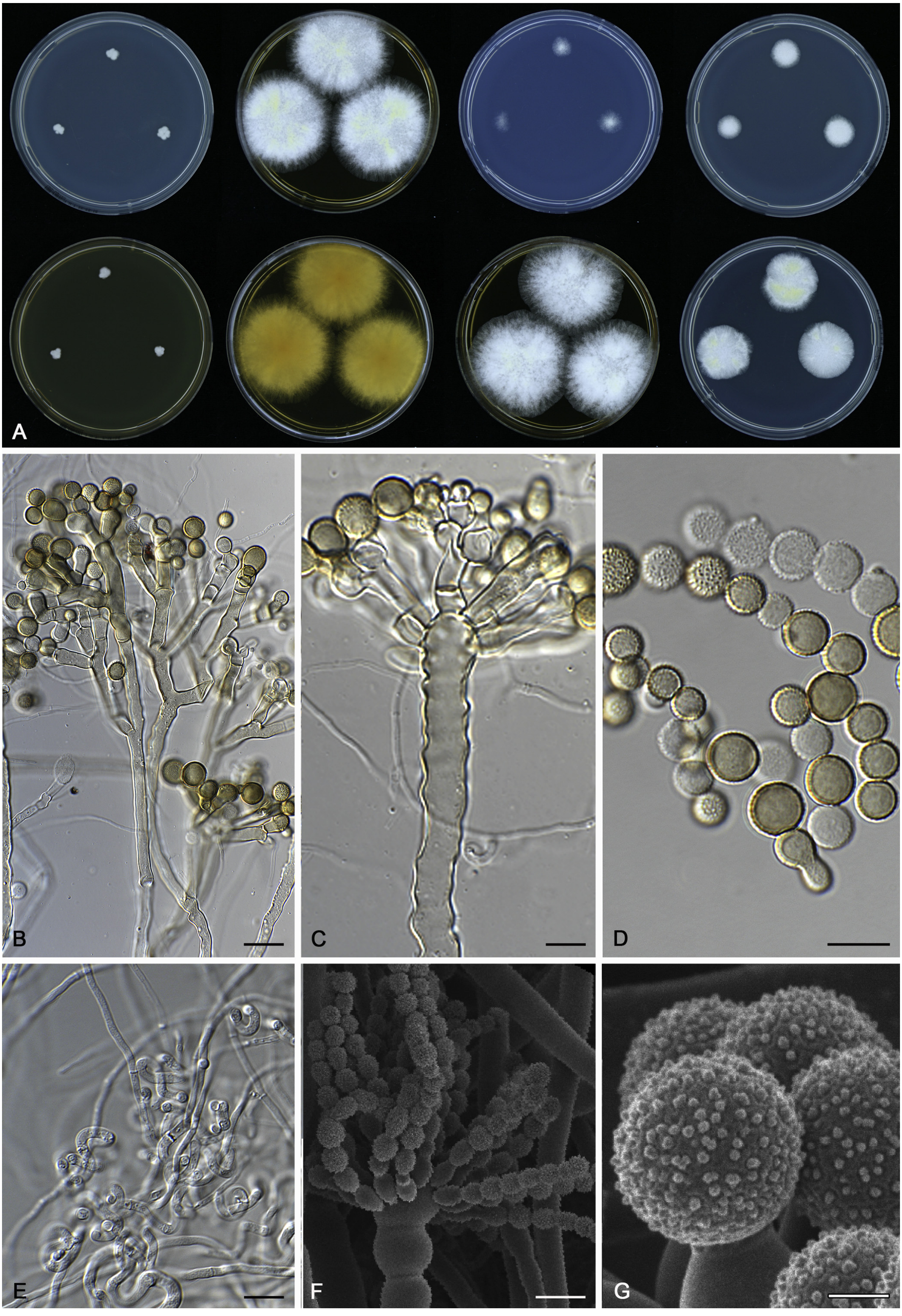


Fig. 40. *Aspergillus proliferans* CBS 121.45^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, C, F.** Conidiophores. **D, G.** Conidia. **E.** Ascomata initials. Scale bars: B = 20 µm; C–E = 10 µm; F = 20 µm; G = 2 µm.

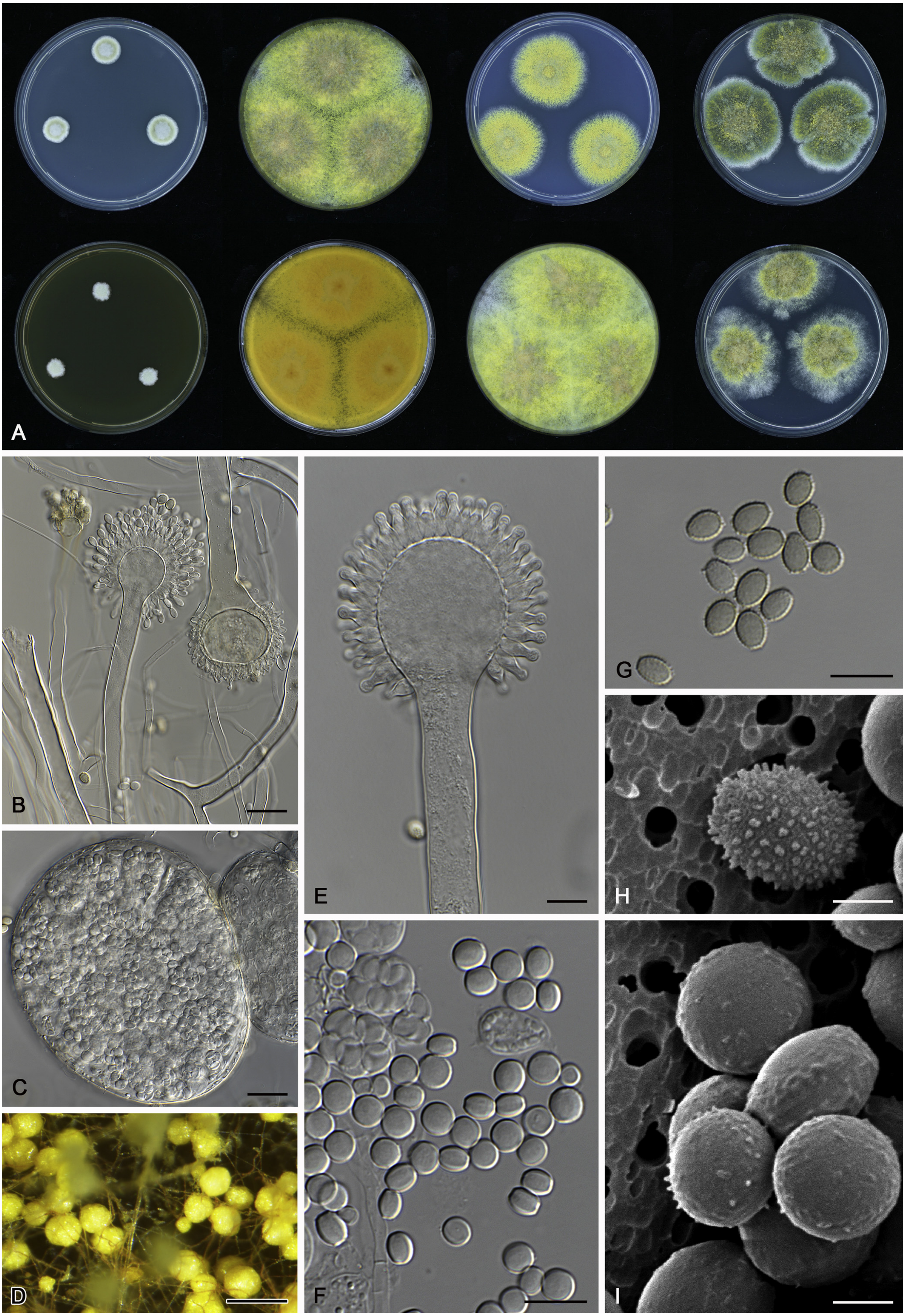


Fig. 41. *Aspergillus proliferans* DTO 322-A2. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

Synonyms: *Aspergillus acutus* Blaser, Sydowia 28: 33. 1975.
Eurotium acutum Blaser, Sydowia 28: 33. 1975.

Typus: IMI 016105iii, lectotype (Samson & Gams 1985). Culture ex-type: CBS 121.45 = NRRL 1908 = IBT 6213 = IMI 016105ii = IMI 016105iii = IMI 016105 = LSHB BB.82 = MUCL 15625 = NCTC 6546 = QM 7462 = UC 4303 = WB 1908.

ITS barcode: EF652064. (Alternative markers: *BenA* = EF651891; *CaM* = EF651988; *RPB2* = EF651941).

Colony diam, 7 d (mm): CYA 5–20; MEA 5–20; CY20S 10–26; CY20S 30 °C 0–20; CY20S 37 °C No growth; M40Y 48–70; M60Y 48–>75; M60Y 30 °C 44–>75; M60Y 37 °C No growth; CYAS 11–55; DG18 25–44; MEA10S 18–50.

Colony characters: CY20S 25 °C, 7 d: Colonies low to moderately deep, plane; margins entire; mycelium white or sulphur yellow (15) or orange (7); texture floccose; sporulation absent to sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white and sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12) or orange (7). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white and sulphur yellow (15); texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white; texture floccose; sporulation absent to moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse primrose (66) to luteous (12). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white and sulphur yellow (15) or orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse primrose (66) or luteous (12). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium white or sulphur yellow (15) or orange (7); margins entire; texture floccose; sporulation absent to moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse primrose (66) or luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–240 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth or slightly verruculose or rough along equatorial ridges, 4–6 × 3–5 µm, in side view lenticular, furrow present or pronounced, crests absent. Conidiophores with smooth stipes, hyaline or light brown, 250–1000 × 8–16.5 µm. Vesicles globose to subglobose, 20–50 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6–12 × 3–5.5 µm. Conidia globose, subglobose to ellipsoidal, tuberculate, 5–7.5(–10) × 4–6(–7) µm. In culture ex-type (CBS 121.45) ascomata are absent, irregular proliferating conidiophores and phialides are produced, conidia measuring 9–17.5 × 7–13 µm.

Distinguishing characters: Phylogenetically *A. proliferans* is closely related to *A. glaucus* and *A. aurantiacoflavus*, but *A. glaucus* produces larger ascospores (5.5–7.5 × 3.5–6 µm) with irregular crests, *A. aurantiacoflavus* produces verruculose ascospores and has orange and yellow colony. The non-crested ascospores of *A. proliferans* resemble those of *A. pseudoglaucus* and *A. ruber*, but the latter two species grow well on M60Y at 37 °C, while *A. proliferans* does not grow under the same conditions.

Notes: *Aspergillus proliferans* was listed as the only anamorphic species in *Aspergillus* sect. *Aspergillus* by Thom & Raper (1945) and they observed the presence of cleistothecial initials (Fig. 40) which indicated some deficiency in the sexual cycle. The sexual strains were connected to this species by molecular data (Hubka *et al.* 2013a, Asgari *et al.* 2014), and are also confirmed by this study.

Additional materials examined: **China**, Tibet, Yak dung, CGMCC 3.04666. **China**, unknown source, CGMCC 3.04667, CGMCC 3.03971. **China**, Tibet, donkey dung, CGMCC 3.04668. **China**, Tibet, soil, CGMCC 3.04671. **China**, Hebei, soil, CGMCC 3.06523. **China**, Xinjiang, soil, CGMCC 3.10130. **China**, Yunnan, soil, CGMCC 3.06095. **China**, Yunnan, moldy wood, CGMCC 3.06495. **China**, Hebei, corn, CGMCC 3.04670. **China**, Hebei, unknown source, CGMCC 3.06097. **Czech Republic**, Prague, palm skin, 28-year-old woman, 2008, isolated by M. Skořepová, CCF 4096 = NRRL 62482 = DTO 355-C8. **Czech Republic**, Prague, toenail of 64-year-old man, 2010, isolated by P. Lysková, CCF 4115 = NRRL 62497 = DTO 355-C9. **Czech Republic**, Prague, toenail of 48-year-old man, 2011, isolated by P. Lysková, CCF 4146 = NRRL 62494 = DTO 355-D1. **Czech Republic**, Opava, stuffed bird, 2010, isolated by M. Polásek, CCF 4232. **Czech Republic**, Prague, toenail of 66-year-old man, 2011, isolated by P. Lysková, CCF 4263. **South Korea**, soybeans, 2012, isolated by D.H. Kim, CCF 4789 = KACC 47146 = DTO 355-D3. **Spain**, Andalusia, Aracena, Gruta de la Maravillas, cave sediment, 2010, isolated by A. Nováková , CCF 4192 = DTO 355-C6. **The Netherlands**, egg waffles, 2014, isolated by M. Meijer, DTO 322-A2. **USA**, Massachusetts, unknown source, NRRL 114 = DTO 355-C7 = CCF 5579. **USA**, Louisiana, library, inside the book, 2012, isolated by Ž. Jurjević, EMSL No. 1814. **USA**, Maryland, leafhoppers, isolated by V.K. Charles, NRRL 71 = DTO 355-D2 = CCF 5578. **USA**, Pennsylvania, Yardley, air of living room, 2013, isolated by Ž. Jurjević, EMSL No. 2207 = CCF 5395 = DTO 355-H5. **USA**, New York, Troy, basement, settle plates, 2015, isolated by Ž. Jurjević, EMSL No. 2791 = CCF 5392 = DTO 355-H6.

Aspergillus pseudoglaucus Blochwitz, Ann. Mycol. 27: 207. 1929. MycoBank MB275429. Fig. 42.

Synonyms: *Eurotium pseudoglaucum* Malloch & Cain, Canad. J. Bot. 50: 64. 1972.
Aspergillus glaucoaffinis Samson & W. Gams, Advances in *Penicillium* and *Aspergillus* Systematics: 47. 1985.
Eurotium repens var. *pseudoglaucum* (Blochwitz) Kozak., Mycol. Pap. 161: 76. 1989.
Eurotium repens de Bary, Hedwigia: 52. 1870.
Aspergillus reptans Samson & W. Gams, Advances in *Penicillium* and *Aspergillus* Systematics: 48. 1985.
Aspergillus glaber Blaser, Sydowia 28: 35. 1975.
Eurotium glabrum Blaser, Sydowia 28: 35. 1975.
Aspergillus fimicola H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14 (2): 86. 1995.
Eurotium fimicola H.Z. Kong & Z.T. Qi, Acta Mycol. Sin. 14 (2): 86. 1995.

Typus: IMI 016122ii, lectotype (Samson & Gams 1985). Culture ex-type: CBS 123.28 = NRRL 40 = ATCC 10066 = IBT 5353 = IMI 016122 = IMI 016122ii = LSHBA 19 = MUCL 15624 = QM 7463 = Tom 5343 = WB 40.

ITS barcode: EF652050. (Alternative markers: *BenA* = EF651917; *CaM* = EF652007; *RPB2* = EF651952).

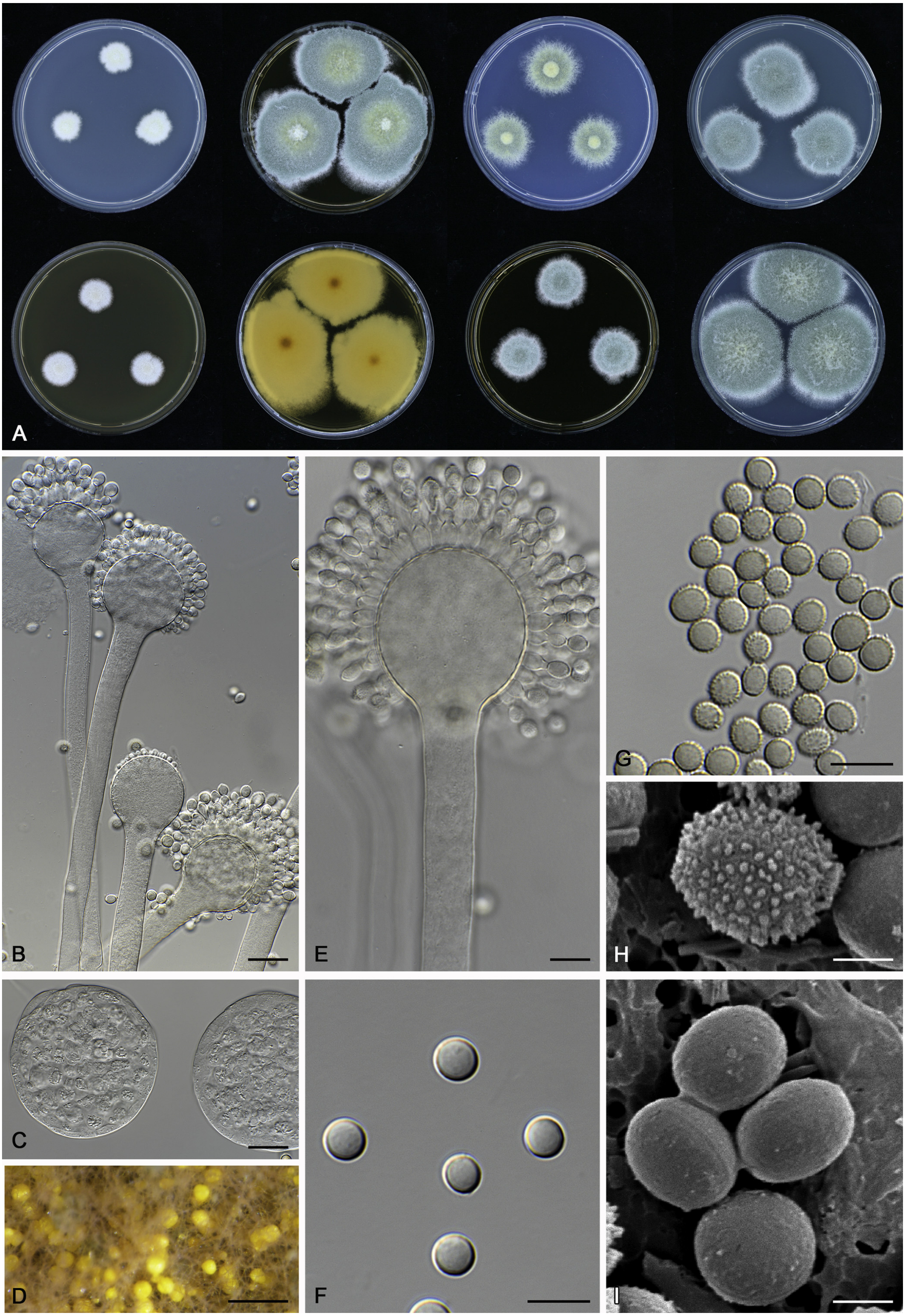


Fig. 42. *Aspergillus pseudoglaucus* CBS 101747. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. G, H. Conidia. Scale bars: B, C = 20 μm; D = 250 μm; E–G = 10 μm; H, I = 2 μm.

Colony diam, 7 d (mm): CYA 20–35; MEA 19–26; CY20S 38–60; CY20S 30 °C 36–53; CY20S 37 °C No growth; M40Y 65–>75; M60Y 35–>75; M60Y 30 °C 53–>75; M60Y 37 °C 35–>75; CYAS 60–72; DG18 52–>75; MEA10S 50–65.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) or orange (7) and white; texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19) to yellow-green (71); soluble pigments absent; exudates absent; reverse straw (46), greenish olivaceous (90) or luteous (12). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) or orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12) or fulvous (43). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse to moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white or sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greenish olivaceous (90); soluble pigments absent; exudates absent; reverse grey olivaceous (107) at centre, fading into light grey olivaceous (107). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium white and sulphur yellow (15) or orange (7); texture floccose; sporulation sparse or moderately dense; conidia *en masse* pale green (19) to dark greenish olivaceous (90); soluble pigments absent; exudates absent; reverse sulphur yellow (15) or ochreous (44). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium white or sulphur yellow (15) or orange (7); margins entire; texture floccose; sporulation sparse or moderately dense; conidia *en masse* pale green (19) to dark greenish olivaceous (90); soluble pigments absent; exudates absent; reverse ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 75–200 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth or slightly rough, 4–6.5 × 3–4.5 µm, in side view lenticular, furrow absent or showing as a trace, crests absent. Conidiophores with smooth stipes, hyaline or light brown, 500–1 000 × (7–)11–22 µm. Vesicles globose to subglobose, (26–)37–65 µm wide (degenerated smaller vesicles measuring 11–21 µm were observed in ex-type CBS 123.28), fertile over two thirds to entire surface. Phialides flask-shaped, 6–11 × 4–6.5 µm. Conidia globose to subglobose, in most strains tuberculate; microtuberculate in atypical strain CBS 379.75, (3.5)–6–9 × (3–)5.5–7.5 µm.

Distinguishing characters: Morphologically *A. pseudoglaucus* resembles *A. proliferans* and *A. ruber* in ascospore size and ornamentation, however the ascospores of *A. pseudoglaucus* do not have or have indefinite furrow, while *A. proliferans* and *A. ruber* have more pronounced furrow on ascospores. The growth profile characters on M60Y at 37 °C can be used to distinguish *A. pseudoglaucus* and *A. proliferans*, the latter species cannot grow under this condition (Table 5). *Aspergillus pseudoglaucus* belongs to the *A. ruber* clade (Fig. 1). Other species in the *A. ruber* clade such as *A. cumulatus*, *A. appendiculatus* and *A. mallochii* can be differentiated by presence of crests, while *A. tonophilus* and *A. sloanii* do not grow on MEA and CYA at 25 °C and *A. zutongqii* has larger ascospores measuring 6–7.5 × 4.5–6 µm.

Notes: *Aspergillus repens* (de Bary) Fischer is a later homonym of *Aspergillus repens* (Corda) Sacc. 1882 pertaining to a different species, and *A. pseudoglaucus* is considered the correct name for *Eurotium repens* (Hubka *et al.* 2013a), we concur with this.

Additional materials examined: **Canada**, Quebec, cake, collected by A. Lafond, CBS 117314 = CCFC 008006 = DAOM 221134. **China**, Tibet, animal dung, CBS 101747 = CGMCC 3.04674 (AS 3.4674). **China**, tea, 1952, CGMCC 3.00460 = DTO 348-B9. **China**, Xinjiang, nest, CGMCC 3.06123. **China**, unknown source, CGMCC 3.01292, CGMCC 3.00452, CGMCC 3.00107, CGMCC 3.00472, CGMCC 3.03976, CGMCC 3.00456, CGMCC 3.01231, CGMCC 3.01070, CGMCC 3.03959, CGMCC 3.04063, CGMCC 3.00455, CGMCC 3.00461, CGMCC 3.00666, CGMCC 3.03565, CGMCC 3.03978, CGMCC 3.00133, CGMCC 3.01293. **China**, Sichuan, soil, CGMCC 3.06120. **China**, Hebei, unknown source, CGMCC 3.06112. **China**, Guangxi, earthworm faeces, CGMCC 3.06111. **China**, Yunnan, unknown source, CGMCC 3.06121. **China**, Zhejiang, soil, CGMCC 3.06110. **China**, Shandong, unknown source, CGMCC 3.06101. **China**, Yunnan, dry locust, CGMCC 3.06488. **China**, Yunnan, moldy noodles, CGMCC 3.06508. **China**, Shanxi, soil, CGMCC 3.06107. **China**, Heilongjiang, soil, CGMCC 3.06094. **China**, Fujiang, leaf, CGMCC 3.06105. **China**, Ningxia, soil, CGMCC 3.06079. **China**, Tibet, soil, CGMCC 3.06119. **China**, Neimenggu, unknown source, CGMCC 3.06117. **China**, Hebei, moldy mushroom, CGMCC 3.06505. **China**, Hebei, dung, CGMCC 3.06500. **China**, Yunnan, moldy herbs, CGMCC 3.06509. **China**, Guangdong, soil, CGMCC 3.06093. **China**, Hainan, coccid, CGMCC 3.06106. **China**, Hebei, soil, CGMCC 3.06502. **China**, Hebei, straw, CGMCC 3.06504. **China**, Beijing, unknown source, CGMCC 3.06115, CGMCC 3.06113, CGMCC 3.06114. **China**, Beijing, herbs, CGMCC 3.06080. **Czech Republic**, Prague, 2002, isolated by A. Kubátová, CCF 3283. **Czech Republic**, Prague, back skin of 39-year-old woman, 2008, isolated by M. Skořepová, CCF 4011. **Czech Republic**, Říčany, trunk skin of 39-year-old woman, 2009, isolated by P. Lysková and Z. Kolací, CCF 4072. **Czech Republic**, Prague, toenail of 57-year-old woman, 2011, isolated by P. Lysková and L. Jelínková, CCF 4372. **Czech Republic**, Prague, fingernail of 37-year-old man, 2011, isolated by P. Lysková and H.A. Macková, CCF 4373. **Czech Republic**, Prague, toenail of 31-year-old woman, 2007, isolated by M. Skořepová, CCF 4374. **Czech Republic**, near Mladeč Caves, outdoor air, 2012, isolated by A. Nováková, S86. **France**, Prunus domestica, isolated by da Fonseca, NRRL 13 = CBS 529.65. **France**, unknown source, isolated by A. Sartory, CBS 114.30. **Hungary**, indoor air, 2010, DTO 147-G3. **Indonesia**, Bali, tea, DTO 055-B3. **Indonesia**, *Melastome*, isolated by J. Houbraken, DTO 164-E5. **Japan**, Tokyo, unknown source, isolated by T. Ohtsuki, NRRL 25865. **Nepal**, Himalaya, soil, 1972, isolated by V. Janečková, CCF 1454. **Portugal**, unknown source, CBS 126221. **Romania**, Movile cave, Lake Room, *Trachelipus troglobius* faeces, 2011, isolated by A. Nováková, CCF 4950. **Slovakia**, Silická ladnica Cave, Archeological Dome, cave sediment, 2012, isolated by A. Nováková, S75. **Spain**, Madrid, chocolate, isolated by J. Varga, DTO 043-D3. **Switzerland**, Zuoz, *Vaccinium myrtillus* leaf, isolated by P. Blaser, CBS 379.75. **Turkey**, keratitis patient, isolated by M. Ilkit, DTO 244-D2. **USA**, wrist skin, NRRL 17. **USA**, Pennsylvania, floor swab, 2012, isolated by Ž. Jurjević, EMSL No. 1780 = CCF 5388 = DTO 355-I2. **USA**, Florida, Melbourne, vent, settle plates, 2015, isolated by Ž. Jurjević, EMSL No. 2779 = CCF 5389 = DTO 355-I3. **USA**, New York, Endicott, office, settle plates, 2015, isolated by Ž. Jurjević, EMSL No. 2809 = CCF 5386. **USA**, New Jersey, Piscataway, air, basement, 2014, isolated by Ž. Jurjević, EMSL No. 2474 = CCF 5387 = DTO 355-I4. **USA**, Missouri, St. Louis, cheddar cheese, 2015, isolated by Ž. Jurjević, EMSL No. 2853 = CCF 5390 = DTO 355-I5. **The Netherlands**, parmezan cheese, isolated by J. Houbraken, CBS 108961 = DTO 351-D2. **USA**, NY, Elmsford, swab, wallet drawer, 2014, isolated by Ž. Jurjević, EMSL No. 2643. **USA**, IL, Chicago, rubber toy import from China, 2015, isolated by Ž. Jurjević, EMSL No. 2695. **USA**, NY, Orangeburg, plastic bottle, 2015, isolated by Ž. Jurjević, EMSL No. 2789. **USA**, NY, Hempstead, living room, rug, 2013, isolated by Ž. Jurjević, EMSL No. 2190. **USA**, KY, Bowling Green, living room, air, 2015, isolated by Ž. Jurjević, EMSL No. 2862. Unknown country, milk powder, DTO 278-D5; quail egg, DTO 315-E8, DTO 315-E7; dolphin bones, 2010, isolated by T. Hoogenhuijzen, DTO 128-E8; gingerbread, DTO 235-B3.

Aspergillus ruber (Jos. König *et al.*) Thom & Church, *Aspergillus*: 112. 1926. MycoBank MB490579. Fig. 43.

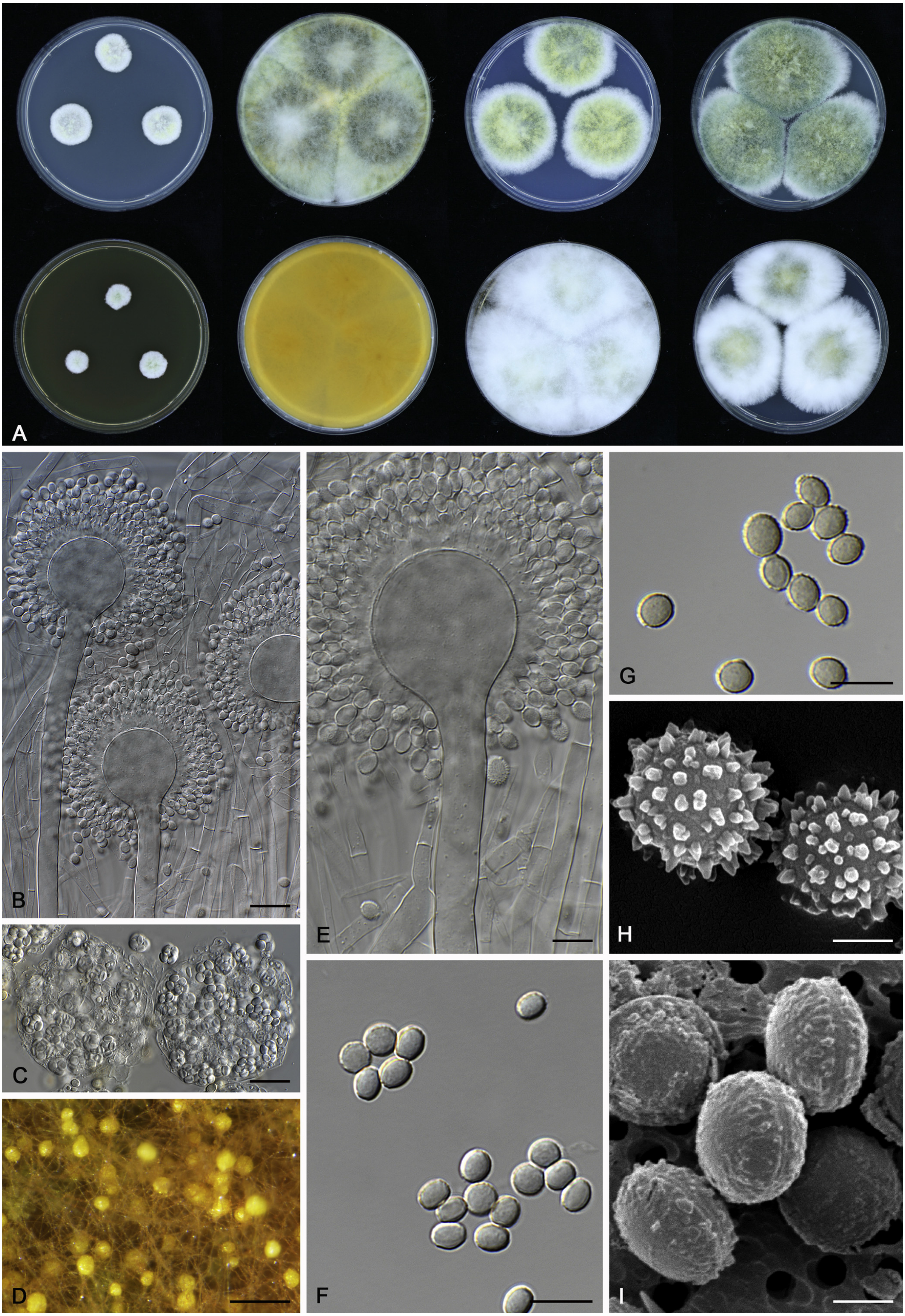


Fig. 43. *Aspergillus ruber* CBS 530.65^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

Synonyms: *Eurotium rubrum* J. König, Spieck. & W. Bremer, Z. Untersuch. Nahr. u. Genussm. 4: 726. 1901.
Aspergillus rubrobrunneus Samson & W. Gams, Advances in *Penicillium* and *Aspergillus* Systematics: 49. 1985.
Aspergillus athecius Raper & Fennell, The Genus *Aspergillus*: 183. 1965.
Gymnoeurotium athecium (Raper & Fennell) Malloch & Cain, Canad. J. Bot. 50 (12): 2619. 1972.
Edyuillia athecia (Raper & Fennell) Subram., Curr. Sci. 41: 756. 1972.
Eurotium athecium (Raper & Fennell) Arx, The genera of fungi sporulating in pure culture: 91. 1974.
Aspergillus atheciellus Samson & W. Gams, Advances in *Penicillium* and *Aspergillus* Systematics: 34. 1985.
Aspergillus tuberculatus Z.T. Qi & Z.M. Sun, Acta Mycol. Sin. 13: 86. 1994.
Eurotium tuberculatum Z.T. Qi & Z.M., Acta Mycol. Sin. 13: 86. 1994.

Typus: CBS 530.65, neotype (Samson & Gams 1985). Culture ex-type: CBS 530.65 = NRRL 52 = ATCC 16441 = IBT 5453 = IMI 211380 = JCM 22942 = QM 1973 = Thom 5599B = WB 52.

ITS barcode: EF652066. (Alternative markers: *BenA* = EF651920; *CaM* = EF652009; *RPB2* = EF651947).

Colony diam, 7 d (mm): CYA 21–22; MEA 15–16; CY20S 51–52; CY20S 30 °C 18–30; CY20S 37 °C No growth; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C >75; CYAS 65–66; DG18 >75; MEA10S 65–67.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* green (20) or vinaceous buff (86); soluble pigments absent; exudates absent; reverse sulphur yellow (15) at centre, pale green (20) at edge. M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) later turning orange (7); texture floccose; sporulation moderately dense; conidia *en masse* green (20) or vinaceous buff (86); soluble pigments absent; exudates absent; reverse ochreous (44). M60Y 25 °C, 7 d: Colonies deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* greyish green (50) or vinaceous buff (86); soluble pigments absent; exudates absent; reverse ochreous (44). CYAS 25 °C, 7 d: Colonies deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation dense; conidia *en masse* greyish green (50) or vinaceous buff (86); soluble pigments absent; exudates absent; reverse buff (45). DG18 25 °C, 7 d: Colonies deep, plane; margins entire; mycelium white and sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50) or vinaceous buff (86); soluble pigments absent; exudates absent; reverse amber (47). MEA10S 25 °C, 7 d: Colonies deep, plane; mycelium white and sulphur yellow (15); margins entire; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50) or vinaceous buff (86); soluble pigments absent; exudates absent; reverse ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 50–175 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies in most strains smooth or minute rough along equatorial ridges, tuberculate in atypical strain CBS 101748, 4–6 × 3.5–5 µm, in side view lenticular, furrow present or pronounced, crests absent. Conidiophores with smooth stipes, hyaline or light brown, 500–750 × 7–13.5 µm. Vesicles globose to subglobose, 25–48 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 7–9(–12) × 3.5–6 µm. Conidia subglobose to ellipsoidal, tuberculate, (4.5–)7–9(–12) × 4–6(–8) µm.

Distinguishing characters: Phylogenetically, *Aspergillus ruber* is closely related to *A. zutongqii*, but *A. zutongqii* produces larger ascospores measuring 6–7.5 × 4.5–6 µm. Morphologically, *A. ruber* resembles *A. proliferans* in ascospore and conidia morphology, but *A. proliferans* cannot grow on M60Y at 37 °C.

Additional materials examined: **Argentina**, Buenos Aires Prov., San Martin, honey sample, 2007, isolated by M.C. Hostench, CBS 123575. **Brazil**, Corn kernels, 2008, isolated by J. Houbraken, DTO 060-I9. **Canada**, British Columbia, hay, collected by V. Chang, CBS 117310. **China**, Shanxi, soil, CBS 101748 = CGMCC 3.04632 (AS 3.4632). **China**, tea, 1952, CGMCC 3.00457 = DTO 348-B6. **China**, tea, CGMCC 3.00458. **China**, unknown source CGMCC3.02577, CGMCC 3.02573, CGMCC 3.00459, CGMCC 3.03957, CGMCC 3.01296, CGMCC 3.00401, CGMCC 3.01298, CGMCC 3.01297, CGMCC 3.01069, CGMCC 3.00439, CGMCC 3.00388, CGMCC 3.04318, CGMCC 3.04315, CGMCC 3.04061, CGMCC 3.00298, CGMCC 3. 01295. **China**, Beijing, medicinal herb, CGMCC 3.06125. **China**, Beijing, beverage, CGMCC 3.09054. **China**, Beijing, unknown source, CGMCC 3.06130, CGMCC 3.06127, CGMCC 3.06129. **China**, Shanxi, Wugong, soil, CGMCC 3.06137. **China**, Henan, unknown source, CGMCC 3.06124. **China**, pig hair, CGMCC 3.03551. **China**, Hebei, soil, CGMCC 3.06497. **China**, Hainan, resin, CGMCC 3.06118. **China**, Xinjiang, nest, CGMCC 3.06122. **China**, Hunan, unknown source, CGMCC 3.06098. **China**, Hebei, straw, CGMCC 3.06499. **China**, Shanxi, Wugong, soil, CGMCC 3.04632. **China**, Pu'er tea, isolated by J. Houbraken, DTO 257-G7. **Czech Republic**, Nymburk, malt dust, 1993, isolated by A. Kubátová, CCF 2920. **Czech Republic**, Prague, toenail of 60-year-old woman, 2011, isolated by P. Lysková, CCF 4377. **Czech Republic**, Prague, Coptish textile (Museum of Decorative Arts), 1999, A. Kubátová, CCF 3464. **Czech Republic**, white pepper, isolated by L. Marvanová, CCM F-438. **Czech Republic**, Prague, toenail of 32-year-old man, 2010, isolated by P. Lysková, CCF 4104. **Germany**, archive, 2009, isolated by J. Houbraken, DTO 088-E3. **Indonesia**, peanuts, 2008, isolated by J. Houbraken, DTO 062-I5, DTO 062-I9, DTO 063-A2. **Indonesia**, Geography Library (stacks), 2012, isolated by Rahmawati, from air in Yogyakarta, DTO 238-C4. **Thailand**, coffee beans, 2006, isolated by P. Noonim, DTO 287-A1, DTO 287-A2, DTO 289-A6, DTO 286-E5. **UK**, coffee beans, 1965, isolated by E. Yuill, NRRL 5000 = CBS 464.65. **Zaire**, leaf, isolated by J. Houbraken, DTO 257-F8. Unknown source, isolated by G. Pollacci, CBS 110.31. Unknown country, tobacco, isolated by M. Meijer, DTO 220-A9. Unknown source, isolated by G. Smith, NRRL 76. Unknown source, 1918, isolated by O. Goethals, CBS 104.18 = DTO 351-C4.

Aspergillus sloanii Visagie, Hirooka & Samson, Stud. Mycol. 78: 108. 2014. MycoBank MB809194. Fig. 44.

Typus: CBS H-21811, holotype. Culture ex-type: CBS 138177 = DTO 245-A1 = IBT 34509.

ITS barcode: KJ775540. (Alternative markers: *BenA* = KJ775074; *CaM* = KJ775309; *RPB2* = KX463365).

Colony diam, 7 d (mm): CYA 2–4; MEA No growth; CY20S 9–15; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y 46–67; M60Y 55–>75; M60Y 30 °C 47–61; M60Y 37 °C No growth; CYAS 17–27; DG18 28–55; MEA10S 40–55.

Colony characters: CY20S 25 °C, 7 d: Colonies low, plane; margins entire; mycelium white and straw (46); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse white. M40Y 25 °C,

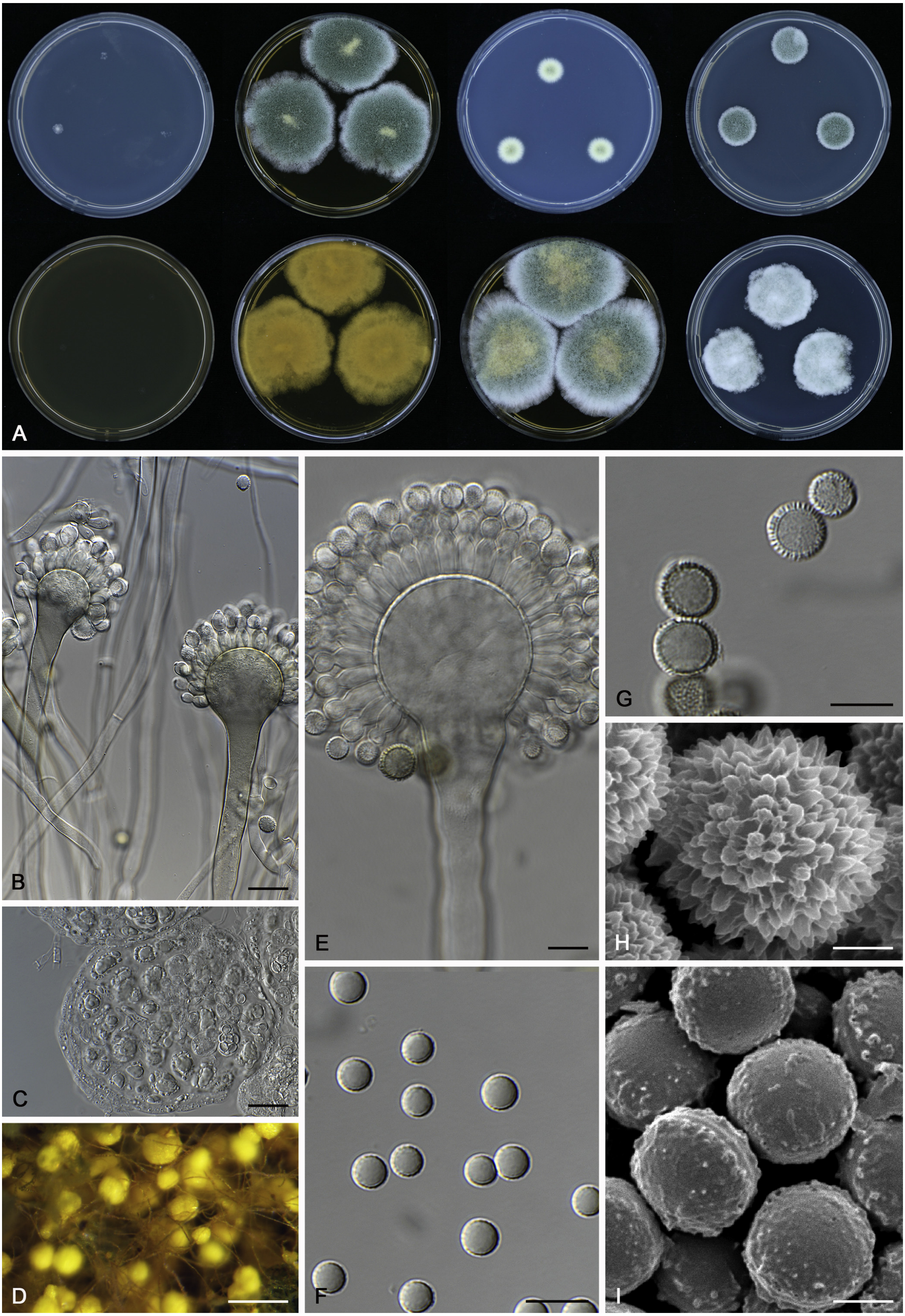


Fig. 44. *Aspergillus sloanii* CBS 138177^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and white; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and white; texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and white; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and white; texture floccose; sporulation sparse; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse sulphur yellow (15). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15) and white; margins entire; texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 60–205 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies smooth, minute rough along equatorial ridges, 4–6 × 3–4.5 µm, in side view lenticular, furrow present, crests absent. Conidiophores with smooth stipes, hyaline or light brown, 160–900 × 7.5–16 µm. Vesicles globose to subglobose, (10–)34–53 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, (7.5–)9–13.5(–18) × (5–)7–9.5 µm. Conidia globose, tuberculate, 5.5–9.5 × 5.5–9 µm.

Distinguishing characters: *Aspergillus sloanii* resembles *A. ruber*, *A. proliferans* and *A. pseudoglaucus* in ascospore morphology, *A. sloanii* does not grow or grows very restrictedly on CYA and MEA. Good growth occurs on M40Y and M60Y.

Additional materials examined: **UK**, Middlesex, house dust, 2010, isolated by E. Whitfield & K. Mwange, CBS 138176 = DTO 244-I8 = CCF 4926, CBS 138231 = DTO 245-A6, CBS 138178 = DTO 245-A8, CBS 138179 = DTO 245-A9.

Aspergillus tamarindosoli A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB818737. Fig. 45.

Etymology: Name refers to its origin, isolated from soil under tamarind.

Diagnosis: Verruculose ascospores with 0.5–1 µm crests, wide vesicles measuring 40–72 µm, lobate-reticulate conidia measuring 4–7 × 3–4.5 µm.

Typus: **Thailand**, Hua Hin, soil under tamarind, 2007, isolated by R. Samson & J. Houbraken (holotype CBS H-22826, culture ex-type: CBS 141775 = DTO 054-A8 = IBT 34432).

ITS barcode: LT670981. (Alternative markers: *BenA* = LT671191; *CaM* = LT671192; *RPB2* = LT671193).

Colony diam, 7 d (mm): CYA 16–17; MEA 13–15; CY20S 40–43; CY20S 30 °C 14–16; CY20S 37 °C No growth; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C 40–45; CYAS 40–42; DG18 35–36; MEA10S 46–48.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse sulphur yellow (15). M40Y 25 °C, 7 d: Colonies moderately deep, slightly sulcate; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse primrose (66). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) at centre, fading into yellow-green (71). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium white; margins entire; texture floccose; sporulation dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 130–240 µm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose, 3.5–5 × 3–4 µm, in side view lenticular, furrow present, crests irregular, 0.5–1.5 µm. Conidiophores with smooth stipes, hyaline or light brown, 700–1 000 × 10–15 µm. Vesicles globose to subglobose, 40–72 µm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6.5–12 × 4–5.5 µm. Conidia subglobose to ellipsoidal, lobate-reticulate, 4–7 × 3–4.5 µm.

Distinguishing characters: *Aspergillus tamarindosoli* resembles *A. chevalieri* in ascospore morphology, but *A. chevalieri* produces smaller conidia measuring 3–4(–6) × 2.5–3.5(–5) µm and narrower vesicles measuring 23–47 µm.

Aspergillus teporis A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB818738. Fig. 46.

Etymology: Name refers to its origin, isolated from heat treated corn kernels.

Diagnosis: Protuberance presented on ascospore convex and furrow.

Typus: **The Netherlands**, heat treated corn kernels, 2008, isolated by M. Meijer (holotype CBS H-22821, culture ex-type: CBS 141768 = DTO 058-E5 = IBT 34513).

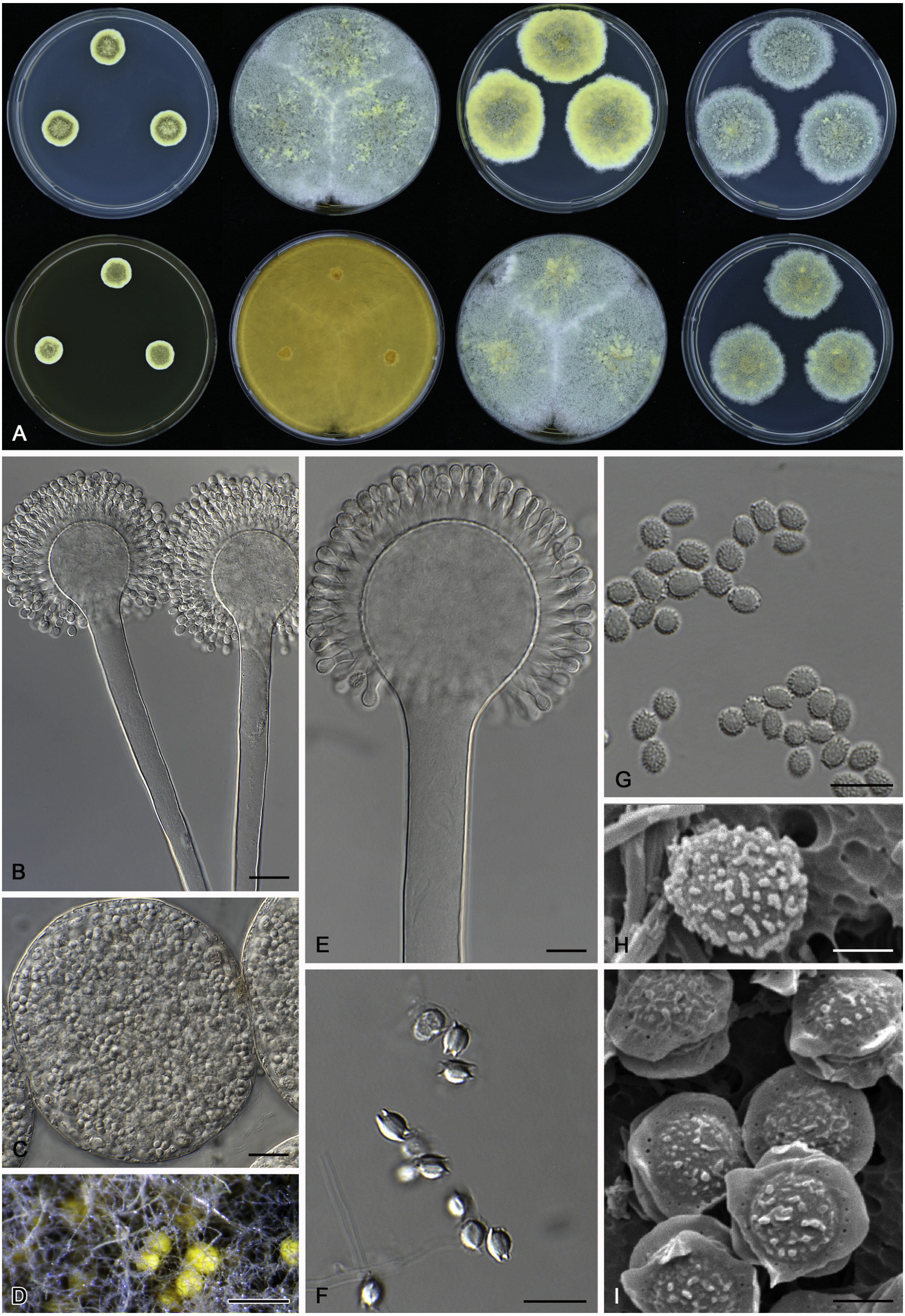


Fig. 45. *Aspergillus tamarindosoli* CBS 141775^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

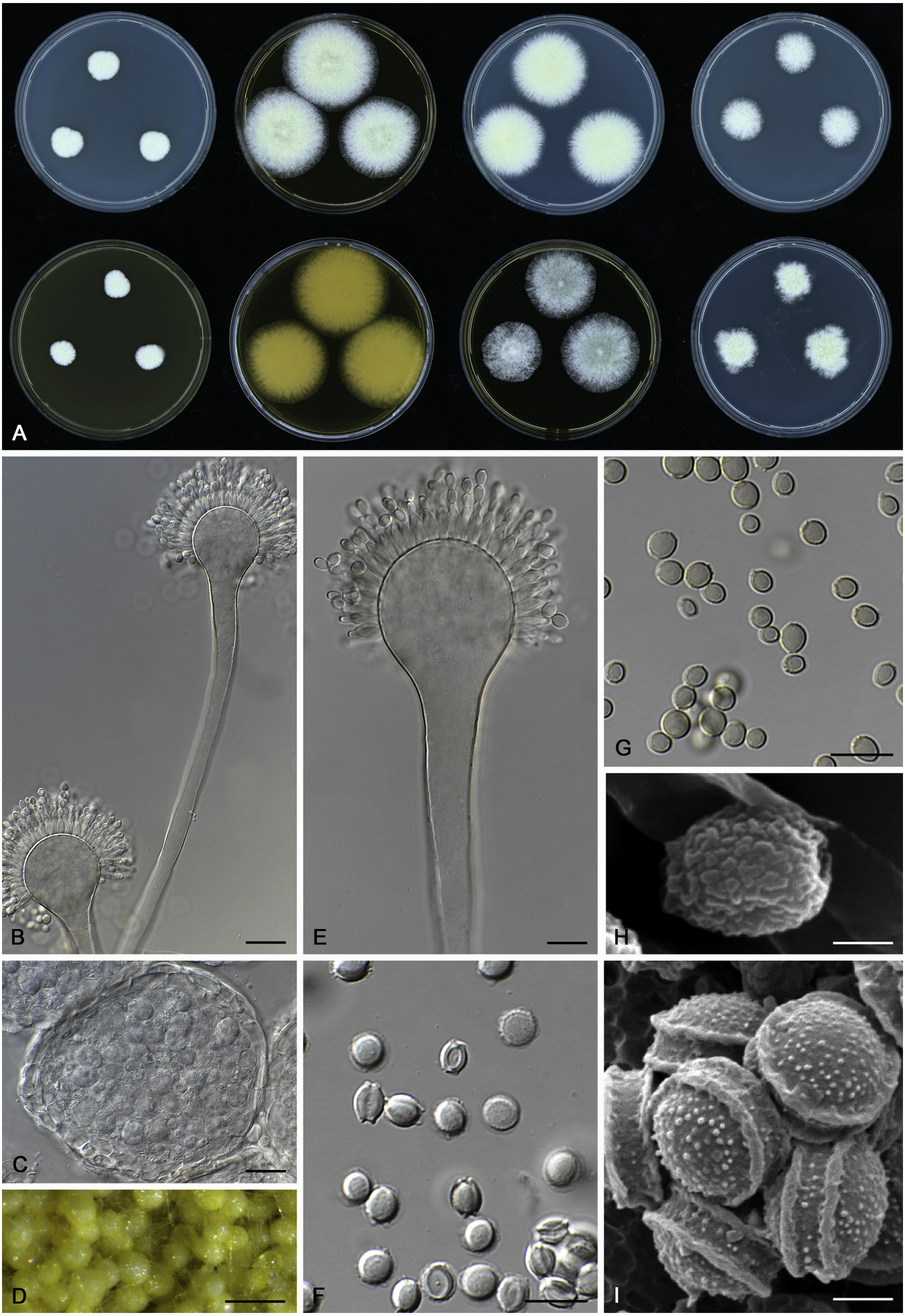


Fig. 46. *Aspergillus teporis* CBS 141768^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

ITS barcode: LT670982. (Alternative markers: *BenA* = LT671194; *CaM* = LT671195; *RPB2* = LT671196).

Colony diam, 7 d (mm): CYA 19–20; MEA 16–18; CY20S 46–47; CY20S 30 °C 48–50; CY20S 37 °C 49–50; M40Y 53–56; M60Y 50–54; M60Y 30 °C 55–63; M60Y 37 °C >75; CYAS 28–29; DG18 30–37; MEA10S 35–40.

Colony characters: CY20S 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46); texture floccose; sporulation sparse; conidia *en masse* pale green (19) to greyish green (50); soluble pigments absent; exudates absent; reverse straw (46). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46); texture floccose; sporulation sparse; conidia *en masse* greyish green (50) to dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture floccose; sporulation sparse; conidia *en masse* greyish green (50) to dark green (21); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse straw (46). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46); texture floccose; sporulation sparse; conidia *en masse* greyish green (50) to dark green (21); soluble pigments absent; exudates absent; reverse straw (46). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium straw (46); margins entire; texture floccose; sporulation sparse; conidia *en masse* greyish green (50) to dark green (21); soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, cream yellow, globose to subglobose, 120–180 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies slightly verruculose, 5–6.5 × 4–5.5 μm, in side view lenticular, furrow pronounced, with scattered protuberance, crests 0.5 μm. Conidiophores with smooth stipes, hyaline or light brown, 800–1 200 × 8–19 μm. Vesicles globose to subglobose, 33–53 μm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 7–12 × 3.5–5 μm. Conidia globose, subglobose to ellipsoidal, lobate-reticulate, 3.5–6 × 3–4.5 μm.

Distinguishing characters: *Aspergillus teporis* is a representative of the basal clades of sect. *Aspergillus*. It is closely related to *A. leucocarpus*, which produces white ascomata and larger conidia (5.5–9 × 5–8 μm). Under the SEM, the protuberance present on the ascospore convex and furrow can distinguish *A. teporis* from other taxa in this section.

Aspergillus tonophilus Ohtsuki, Bot. Mag. (Tokyo) 75: 438. 1962. MycoBank MB326663. Fig. 47.
Synonyms: *Eurotium tonophilum* Ohtsuki, Bot. Mag. (Tokyo) 75: 438. 1962.

Typus: IMI 108299, neotype (Samson & Gams 1985). Culture ex-type: CBS 405.65 = NRRL 5124 = ATCC 16440 = ATCC 36504 = IBT 21230 = IMI 108299 = QM 8599 = WB 5124.

ITS barcode: EF652081. (Alternative markers: *BenA* = EF651919; *CaM* = EF652000; *RPB2* = EF651969).

Colony diam, 7 d (mm): CYA No growth; MEA No growth; CY20S 24–25; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C 8–9; CYAS 49–53; DG18 56–58; MEA10S 56–58.

Colony characters: CY20S 25 °C, 7 d: Colonies low, plane; margins entire; mycelium sulphur yellow (15) and white; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse white. M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation sparse; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse luteous (12) fading to sulphur yellow (15). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15); texture floccose; sporulation moderately dense; conidia *en masse* pale green (19); soluble pigments absent; exudates absent; reverse sulphur yellow (15). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse luteous (12).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 100–235 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose, 4–6 × 3–4.5 μm, in side view lenticular, furrow present, crests absent. Conidiophores with smooth stipes, hyaline or light brown, 120–500 × 7–12.5 μm. Vesicles globose to subglobose, 25–44 μm wide (degenerated, smaller vesicles measuring 8–16 μm were observed in ex-type CBS 405.65), fertile over two thirds to entire surface. Phialides flask-shaped, 6–11 × 3–5 μm. Conidia globose to subglobose, tuberculate to lobate-reticulate, 5–7.5 × 3.5–6 μm.

Distinguishing characters: *Aspergillus tonophilus* is a member of *A. ruber* clade (Fig. 1). The colonies of *A. tonophilus* remain brightly yellow even after two weeks of cultivation in contrast to other species from the *A. ruber* clade. The ascospores of *A. tonophilus* resemble those of *A. aurantiacoflavus*, however, *A. aurantiacoflavus* produces orange and yellow colonies and slightly larger conidia measuring 5–9 × 4–7 μm.

Additional materials examined: **Canada**, house dust, 2015, isolated by C.M. Visagie, DTO 356-H6 = KAS6175. **South Korea**, meju, 2012, isolated by S.B. Hong, KACC 45365 = CCF 4785 = DTO 355-A2. **South Korea**, soybeans, 2012, isolated by D.H. Kim, KACC 47150 = CCF 4786 = DTO 355-A1.

Aspergillus xerophilus Samson & Mouch., Antonie van Leeuwenhoek 41: 348. 1975. MycoBank MB309251. Fig. 48.

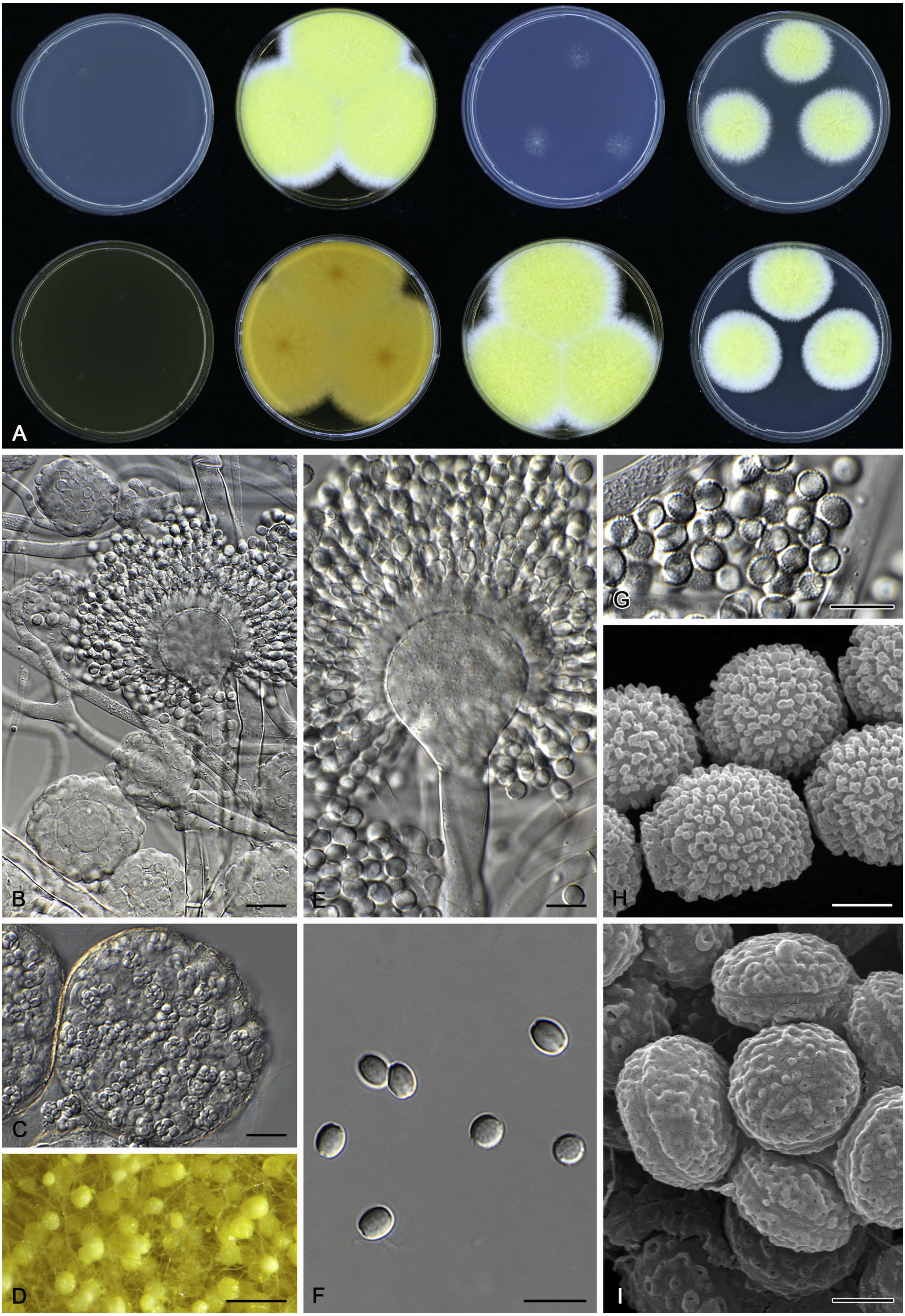


Fig. 47. *Aspergillus tonophilus* KACC 47150. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

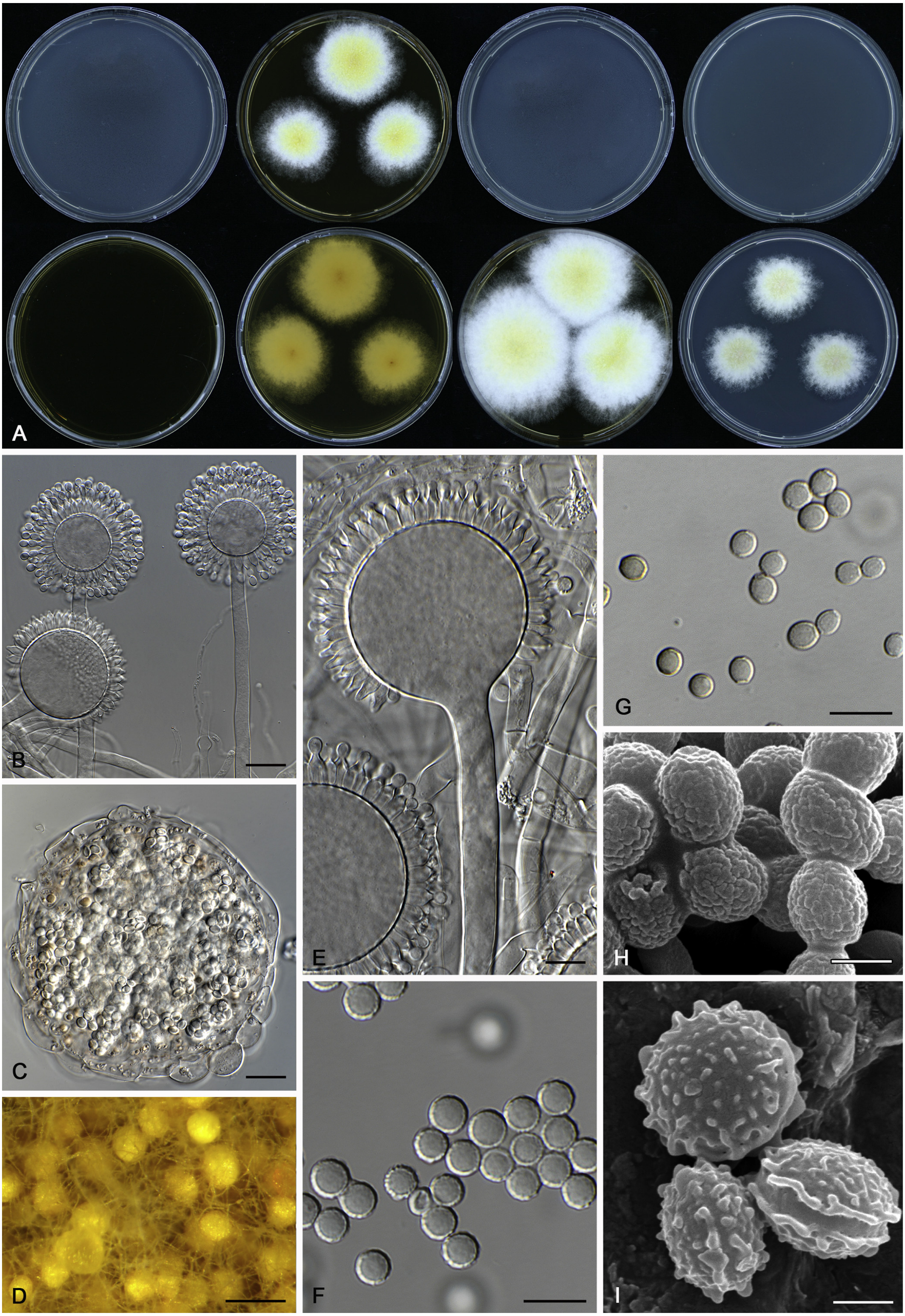


Fig. 48. *Aspergillus xerophilus* CBS 938.73^{T}. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

Synonyms: *Eurotium xerophilum* Samson & Mouch, Antonie van Leeuwenhoek 41: 348. 1975.

Typus: CBS 938.73, holotype. Culture ex-type: CBS 938.73 = NRRL 6131 = IBT 5429 = IBT 5489 = IBT 34503 = DTO 083-A2.

ITS barcode: EF652085. (Alternative markers: *BenA* = EF651923; *CaM* = EF651983; *RPB2* = EF651970).

Colony diam, 7 d (mm): CYA No growth; MEA No growth; CY20S No growth; CY20S 30 °C No growth; CY20S 37 °C No growth; M40Y 60–62; M60Y >75; M60Y 30 °C 65–>75; M60Y 37 °C No growth; CYAS No growth; DG18 39–55; MEA10S 67–>75.

Colony characters: M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and olivaceous buff (89) at centre; texture floccose; sporulation sparse; soluble pigments absent; exudates absent; reverse luteous (12). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and olivaceous buff (89) at centre; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse luteous (12). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium straw (46) and white; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse luteous (12). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium straw (46) and white; margins entire; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse ochreous (44).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 165–330 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose, 4.5–6.5 × 3.5–5 μm, in side view lenticular, furrow present, crests irregular, < 0.5 μm. Conidiophores with smooth stipes, hyaline or light brown, 50–200 × 6.5–9.5–(12) μm. Vesicles globose to subglobose, 40–66 μm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 6–9 × 3.5–6 μm. Conidia globose to subglobose, microtuberculate, 3.5–5.5 × 3–4.5 μm.

Distinguishing characters: Phylogenetically *A. xerophilus* is closely related to *A. osmophilus*, but *A. osmophilus* produces larger ascospores (7–9 × 6–7.5 μm) and grows on M60Y at 37 °C. Morphologically *A. xerophilus* resembles *A. endophyticus* in ascospore ornamentation, but the ascospores of *A. endophyticus* have longer crests (0.5–1 μm).

Additional materials examined: **Egypt**, Western desert, desert soil, isolated by J. Mouchacca, NRRL 6132 = CBS 755.74.

Aspergillus zutongqii A.J. Chen, Frisvad & Samson, **sp. nov.** MycoBank MB818739. Fig. 49.

Etymology: Named in honour of Chinese mycologist Zutong Qi, who wrote first *Aspergillus* monograph in China, and contributed his whole career to *Aspergillus* taxonomy in China.

Diagnosis: Large, verruculose, non-crested ascospores measuring 6–7.5 × 4.5–6 μm.

Typus: **China**, Beijing, peanut shell, 2008, isolated by L. Wang (holotype CBS H-22824, culture ex-type: CBS 141773 = CGMCC 3.13917 = DTO 349-E1 = IBT 34450).

ITS barcode: LT670986. (Alternative markers: *BenA* = LT671206; *CaM* = LT671207; *RPB2* = LT671208).

Colony diam, 7 d (mm): CYA 14–15; MEA 7–17; CY20S 33–38; CY20S 30 °C 13–20; CY20S 37 °C No growth; M40Y >75; M60Y >75; M60Y 30 °C >75; M60Y 37 °C 10–30; CYAS 32–50; DG18 42–50; MEA10S 56–60.

Colony characters: CY20S 25 °C, 7 d: Colonies low to moderately deep, plane; margins entire; mycelium sulphur yellow (15) or ochreous (44); texture floccose; sporulation absent or sparse, conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44). M40Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) to orange (7). M60Y 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) to orange (7). CYAS 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) to umber (9). DG18 25 °C, 7 d: Colonies moderately deep, plane; margins entire; mycelium sulphur yellow (15) and orange (7); texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) to orange (7). MEA10S 25 °C, 7 d: Colonies moderately deep, plane; mycelium sulphur yellow (15); margins entire; texture floccose; sporulation sparse to moderately dense; conidia *en masse* greyish green (50); soluble pigments absent; exudates absent; reverse ochreous (44) to orange (7).

Micromorphology: Ascomata eurotium-like, cleistothecial, superficial, yellow, globose to subglobose, 110–220 μm. Asci 8 spored, globose to subglobose. Ascospores hyaline, in surface view globose to subglobose, spore bodies verruculose, 6–7.5 × 4.5–6 μm, in side view lenticular, furrow pronounced, crests absent. Conidiophores with smooth stipes, hyaline or light brown, 150–500 × 7.5–13 μm. Vesicles globose to subglobose, 25–40 μm wide, fertile over two thirds to entire surface. Phialides flask-shaped, 8–12 × 4–6.5 μm. Conidia subglobose to ellipsoidal, tuberculate, 5.5–10 × 4–7 μm.

Distinguishing characters: Phylogenetically and morphologically, *Aspergillus zutongqii* is close to *A. ruber*, but *A. ruber* produces smaller ascospores (4–6 × 3.5–5 μm).

Additional materials examined: **China**, Ningxia, 2001, CGMCC 3.06103 = DTO 348-F7. **China**, 1969, isolated by Z.T. Qi, CGMCC 3.03980 = DTO 348-D7. **China**, ocular lens, 1969, isolated by Z.T. Qi, CGMCC 3.03961 = DTO 348-D5.

Notes

Aspergillus taklimakanensis Abliz & Y. Horie, Mycoscience 42: 289. 2001. MycoBank MB474683

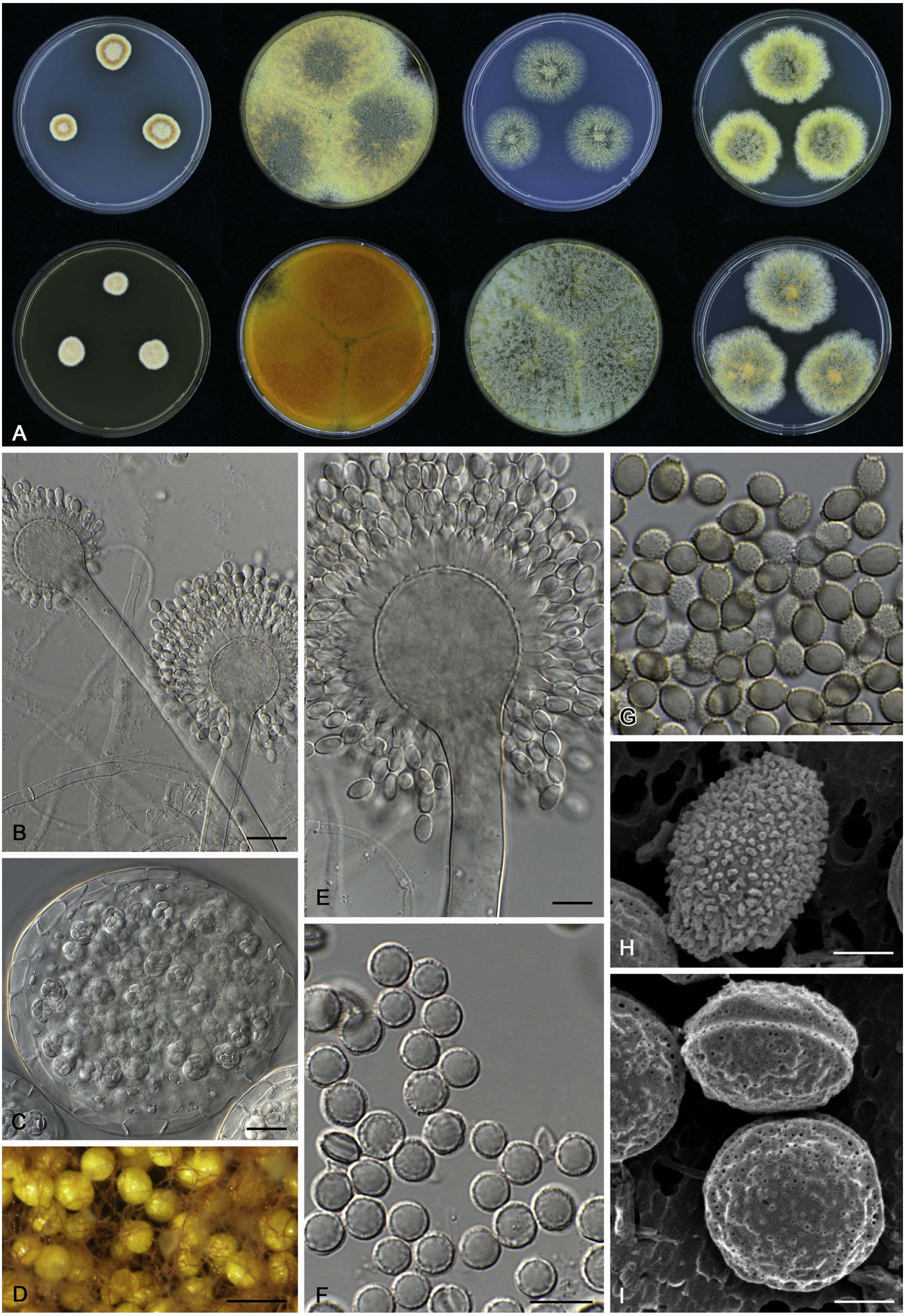


Fig. 49. *Aspergillus zutongqii* CBS 141773^T. **A.** Colonies after 7 d at 25 °C: top row left to right, CYA, M40Y, CY20S and CYAS; bottom row left to right, MEA, reverse M40Y, M60Y and DG18. **B, E.** Conidiophores. **C, D.** Ascomata. **F, I.** Ascospores. **G, H.** Conidia. Scale bars: B, C = 20 µm; D = 250 µm; E–G = 10 µm; H, I = 2 µm.

Synonyms: *Eurotium taklimakanense* Abliz & Y. Horie, Mycoscience 42: 289. 2001.

This species was accepted by Guarro *et al.* (2012), but was treated as invalid by Hubka *et al.* (2013a), because the holotype CBM-FA-876 includes different species (probably *A. cristatus*), and is in conflict with the protologue. No living culture or herbarium material corresponding with the protologue is extant.

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