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Leiothecium cristatum and *Aspergillus posadasensis*, two new species of Eurotiales from rainforest soils in South America

Yasmina Marin-Felix, José Francisco Cano-Lira*, Josep Guarro, Alberto Miguel Stchigel

Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili, C/ Sant Llorenç 21, 43201 Reus, Tarragona, Spain

* Corresponding author: José Francisco Cano-Lira

Tel.: +34 977 759350

Fax.: +34 977 759322

e-mail: jose.cano@urv.cat

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Running title: Two new species of Eurotiales

The GenBank accession numbers for the D1-D2, ITS, *Cct8*, *RPB1* and *RPB2* loci sequences of the ex-type strain of *Leiothecium cristatum* sp. nov. are HG529487, KF732838, HF954979, HF954982, and HF954976, respectively. The GenBank accession numbers for the D1-D2, ITS, *Cct8*, *RPB1*, *RPB2*, *CAL* and *BT2* loci sequences of the ex-type strain of *Aspergillus posadasensis* sp. nov. are HG529485, HG529483, HF954980, HF954983, HF954977, HG529488 and HG529481, and for the strain of the same species, FMR 12322, are HG529486, HG529484, HF954981, HF954984, HF954978, HG529489, and HG529482, respectively. The GenBank accession number for the D1-D2 locus sequence of the ex-type strain of *Leiothecium ellipsoideum* is KF732839.

The MycoBank (http://www.mycobank.org) accession numbers of *Leiothecium cristatum* and *Aspergillus posadasensis* are MB803513 and MB803514, respectively.

Abstract

We describe two new fungi isolated from soil samples collected in Northern Argentina and belonging to the family Aspergillaceae of the order Eurotiales: *Leiothecium cristatum* sp. nov. and *Aspergillus posadasensis* sp. nov. *Leiothecium cristatum*, represented by the ex-type strain FMR 11998^T (= CBS 134260^T = NBRC 109843^T), is distinguishable morphologically from the type species of the genus, *L. ellipsoideum*, by the presence of irregular reticulate ascospores with two prominent equatorial crests, and *A. posadasensis*, represented by the ex-type strain FMR 12168^T (= CBS 134259^T = NBRC 109845^T) is differentiated from *Aspergillus acanthosporus*, the nearest species phylogenetically, by its non-sclerotioid ascomata and a lack of an asexual stage on all culture media tested. The taxonomic proposals are supported by the analysis of the sequences of the internal transcribed spacer region, the D1-D2 domains of the 28S rRNA gene and the fragments of the RNA polymerase II largest subunit, of the putative chaperonin complex related to TCP-1, of β-tubulin and of calmodulin genes.

Keywords. Argentina, Aspergillaceae, *Aspergillus*, Eurotiales, *Leiothecium*, soil.

INTRODUCTION

The members of the order Eurotiales G.W. Martin ex Benny & Kimbr. (1980) are mainly characterized by the production of spherical to ovoid, thin-walled evanescent (prototunicate) asci, which arise free on the mycelium or are, more usually, produced within globose, nonostiolate ascomata, and by one-celled, globose or lenticular, smooth-walled or ornamented ascospores (spinulose, reticulate, tuberculate, etc.),

frequently with equatorial thickenings or crests. Their asexual stages are mostly phialidic, but can also show a retrogressive conidiogenesis. Currently, the order comprises three monophyletic families, Aspergillaceae, Thermoascaceae and Trichocomaceae (Houbraken & Samson, 2011).

The genus *Aspergillus* is the most common and largest of the Aspergillaceae and of the order Eurotiales. Gams et al. (1985) divided the genus into six subgenera and 18 sections. However, Peterson (2008), using a multigene phylogeny based on sequences of partial fragments of β-tubulin (*BT2*), calmodulin (*CAL*) and RNA polymerase II (*RPB2*) genes, and ribosomal (ITS and LSU) genes, only accepted five subgenera (*Aspergillus*, *Circumdati*, *Fumigati*, *Nidulantes* and *Ornati*). Most recently, Houbraken & Samson (2011) also used the sequences of *RPB2* and other structural genes (*RPB1*, the putative ribosome biogenesis protein (*Tsr1*) and the putative chaperonin complex component TCP-1 (*Cct8*)), and they concluded that most of the morphospecies traditionally belonging to the genus *Aspergillus* were included in the *Aspergillus s. str.* clade, which was divided into four subgenera and 17 sections. *Cristaspora* has a single species that lacks an anamorph stage (Fort & Guarro, 1984); *Phialosimplex* has conidiogenous cells consisting of simple phialides, sometimes proliferating to form a second opening (Sigler et al., 2010); and *Polypaecilum* has conidiogenous cells that are polyphialides (Smith, 1961). All three of these genera are morphologically very dissimilar to the typical *Aspergillus* and were surprisingly also placed in the mentioned *Aspergillus s. str.* clade (Houbraken & Samson, 2011).

During a survey on soil-borne ascomycetes from Northern Argentina, two fungi apparently related with some members of the Eurotiales were isolated in pure culture.

These fungi were phenotypically and molecularly characterized and are proposed here as new species.

METHODS

Soil sampling and fungal isolation. Soil samples were collected in Misiones Province, Argentina, at two locations: the Iguazú National Park (-25° 41' 28.5", -54° 26' 54.9594") and the Alberto Roth botanical garden (-27° 24' 28.6092", -55° 53' 48.1158"). Both locations are included in the Paranaense phytogeographical province of the Amazonian domain at the neotropical region. They have a hot, wet climate with an average annual temperature of 21 °C, an average maximum temperature of about 32 °C and an average minimum temperature of about 10 °C. The total annual rainfall is about 1900 mm. The Iguazú National Park is situated in the boundaries of the Iguazú River, and has an area of around 550 square kilometres. The soil is acidic, red and lateritic. The park has more than 300 species of plants, including trees, ferns, shrubs, lianas, epiphytes and herbs. The Alberto Roth botanical garden is on the south side of the city of Posadas, and has an area of 11 ha. The altitude ranges from 75 to 100 m, and the terrain is mostly basaltic. This location also has a broad diversity of trees, shrubs and herbs, of which 109 are native species.

To carry out the isolation of the soil-borne ascomycetes, we followed a previously described protocol (Stchigel et al., 2001). Approximately 1 g of each soil sample was suspended in 5 mL of 5% v/v acetic acid, shaken vigorously for 5 min and left for 5 min. The liquid layer was decanted and the residual soil was resuspended in 9 ml of sterile water and plated onto three Petri dishes of 9 cm diam. Melted potato carrot agar (PCA: grated potatoes, 20 g; grated carrot, 20 g; agar-agar, 20 g; L-

chloramphenicol, 100 mg; 1% w/v dieldrin™ in dimethyl-ketone, 20 drops; tap water, 1 L) at 50-55 °C was placed on top of the soil suspension and mixed by hand. All cultures were incubated at 15, 25 and 35 °C. The ascomata of the taxonomically interesting fungi were transferred using a sterile needle to two 5 cm diam Petri dishes containing oatmeal agar (OA: oatmeal flakes, 30 g; agar-agar, 20 g; tap water, 1 L) and incubated under the same conditions as described above.

Phenotypic study. For cultural characterization, the isolates were grown for up to 30 days on OA, PCA, potato dextrose agar (PDA; Pronadisa, Madrid, Spain), *Czapek yeast extract agar* (CYA: sucrose, 30 g; sodium nitrate, 3 g; yeast extract, 5 g; potassium phosphate, 1 g; potassium chloride, 0.5 g; magnesium sulphate, 0.5 g; iron sulphate, 0.01 g; agar, 15 g; tap water, 1 L) and malt extract agar (MEA: bacteriological peptone, 1 g; glucose, 20 g; malt extract, 20 g; agar, 15 g; tap water, 1 L) at 25 °C. Colour notations in parentheses are from Kornerup & Wanscher (1984). To induce the production of asexual reproductive structures, the isolates were grown on MEA + 40% of sucrose (Samson et al., 2007) at 25 and at 37 °C. In order to determine the minimum and maximum temperatures of growth of the isolates, a 5 °C increment from 5 to 40 °C, and 2 °C increment from 40 to 50 °C, were used. Fertile fungal structures were mounted and measured in water and in lactic acid. Photomicrographs of the structures were taken with a Zeiss Axio Imager M1 light microscope. The scanning electron microscope (SEM) techniques used were described previously by Figueras & Guarro (1988). SEM micrographs were taken with a Jeol JSM 840 at 15 keV.

BLAST search and phylogenetic study. The DNA of the isolates of interest (see Supplementary Table S1 in IJSEM online) was extracted and purified directly from fungal colonies according to the Fast DNA Kit protocol (MP Biomedicals, Solon, Ohio). D1-D2, ITS, *RPB1*, *RPB2* and *Cct8* genes were amplified for all isolates, and *BT2* and *CAL* genes also for the isolates FMR 12168^{T} and FMR 12322, according to Cano et al. (2004) (D1-D2 and ITS), Houbraken & Samson (2011) (*RPB1*, *RPB2* and *Cct8*), Glass & Donaldson (1995) (*BT2*) and Hong et al. (2005) (*CAL*). The sequences of these amplicons were obtained using the protocol of the Taq Dye-Deoxy Terminator Cycle Sequencing Kit. PCR products were purified and sequenced at Macrogen Europe (Amsterdam, The Netherlands) with a 3730XL DNA analyser (Applied Biosystems). Consensus sequences were obtained using SeqMan (version 7.0.0; DNASTAR, Madison, WI, USA) and they were aligned using Clustal X (version 1.83) (Thompson et al., 1997) followed by manual adjustments with a text editor. Sequences retrieved from GenBank and included in this analysis are also given in Table S1. ITS, D1-D2 and *CAL* BLAST searches were carried out in order to corroborate the previous taxonomical placement of our isolates. The phylogenetic analyses of the combined data set (*RPB1*, *RPB2* and *Cct8*) of our isolates and selected members of the families Aspergillaceae and Thermoascaceae were carried out using MEGA v. 5.05 (Tamura et al., 2011). The combined data set was tested for incongruence with the partition homogeneity test (PHT) as implemented in PAUP* (Swofford, 2002). Maximum Likelihood (ML) method using Tamura-Nei model with gamma distribution, was carried out for the phylogenetic analyses of RPB1, RPB2 and Cct8, and Kimura 2-parameter model with invariable sites for the ML phylogenetic analysis of BT2 sequences, both with the pair-wise deletion of gaps option. The robustness of branches was assessed by bootstrap analysis with 1000

replicates. The sequences generated in this study are deposited in GenBank (see Supplementary Table S1 in IJSEM online) and the alignments used in the phylogenetic analyses are deposited in TreeBASE: (*www.treebase.org*, accession URL:*http://purl.org/phylo/treebase/phylows/study/TB2:S14135*).

RESULTS

Phenotypic study

The isolate FMR 11998^T, from a soil sample of the Iguazú National Park (see Supplementary Table S1 in IJSEM online), was identified as belonging to the genus *Leiothecium* based on the presence of typical morphological features, such as spherical, glabrous, dark brown, non-ostiolate ascomata with a peridium of *textura angularis*; one-celled, hyaline, ellipsoidal, reticulate ascospores; and absence of an asexual stage. Two other isolates, FMR 12168^T and FMR 12322, from two soil samples of the Alberto Roth botanical garden were classified as belonging to the genus *Cristaspora*. They were characterized by the production of orange, spherical, non-ostiolate ascomata covered by a dense mass of aerial hyphae; hyaline to subhyaline ascospores with two equatorial crests and a convex surface verruculose to echinulate and the absence of an asexual stage on all culture media tested.

BLAST search

The BLAST search with the D1-D2 sequence of the isolate FMR 11998^T (HG529487) showed 97% of similarity with the sequence of the type strain of *L. ellipsoideum* (FJ358285) whereas the isolates FMR 12168^T (HG529485) and FMR 12322 (HG529486) showed 99% similarity with *Aspergillus clavatus* (JN938924) and the type strain of *A.*

acanthosporus (EF669992). The most related member of the Eurotiales in the ITS BLAST search of FMR 11998^{T} (KF732838) showed a similarity of less than 90% (*Aspergillus fischerianus*), but the similarity between the sequence of the former with that of the type strain of *L. ellipsoideum*, sequenced by us (KF732839), was 92.76%. The BLAST search of ITS sequences of FMR 12168^{T} (HG529483) and FMR 12322 (HG529484) showed 98.19% and 98.43% similarity with the type strain *A. clavatus*, respectively, and the same percentage for the two isolates (98.42%) with the ITS sequence of the type strain of *A. acanthosporus* (EF669992). The BLAST search with the *CAL* sequences of FMR 12168^{T} (HG529488) and FMR 12322 (HG529489) showed 93% and 93.2% similarity with the type strain of *A. clavatus* (EU078665), respectively, and 90.87% with the type strain of *A. acanthosporus* (EU078676) for both strains.

Phylogenetic study

The lengths of the fragments of the three genes used in the combined data set were: 646 bp (*Cct8*), 708 bp (*RPB1*) and 957 bp (*RPB2*), from which 271, 302 and 396 bp were parsimony informative, respectively. The length of the final alignment was 2311 bp. The result of the partition homogeneity test showed that the datasets for the three loci were congruent (P = 0.29) and could be combined.

Fig. 1 shows the tree inferred from an ML analysis of the combined dataset. A main clade with a bootstrap support (bs) of 100% grouped the members of the family Aspergillaceae, including our isolates. The isolate FMR 11998^{T} grouped in a terminal clade with the type strain of *L. ellipsoideum* (89% bs) whereas the isolates FMR 12168^{T} and FMR 12322 grouped with the type strain of *A. acanthosporus* and *A. clavatus*

(100% bs), despite these two isolates first being morphologically identified as belonging to the genus *Cristaspora*.

A phylogenetic analysis of the ITS region (415 bp), of the *CAL* (367 bp), and of the *BT2* (381 bp) was carried out in order to assess the genetic relatedness of the isolates FMR 12168^T and FMR 12322 with other members of the sect. *Clavati* of the genus *Aspergillus*. The ITS and *CAL* ML trees showed the same topology that we observed in the *BT2* ML tree. We only included results of the last locus (see Supplementary Fig. S1 in IJSEM online) because *BT2* was the most phylogenetically informative and sequences of all the species of this section were available in the GenBank. The tree revealed two main clades (with bs of 89% and 93%, respectively). The first one encompassed three sister clades, all of them with 100% bs, corresponding to four isolates of *A. clavatus* the first, our two isolates (FMR 12168^T and 12322) the second, and four strains of *A. acanthosporus* the third, respectively. In the second clade (93% bs) other species of this section were located, i.e. *A. rhizopodus*, *A. clavatonicus*, *A. longivesica* and *A. giganteus*.

TAXONOMY

The previous data demonstrated that our isolate FMR 11998^T belongs to the genus *Leiothecium* but is distinguishable molecularly from the only species of this genus *L. ellipsoideum* and also morphologically mainly by the presence of irregular reticulate ascospores with two prominent equatorial crests in our isolate; our studies also provide evidence that the isolates FMR 12168^T and FMR 12322 are molecularly and morphologically different from *A. acanthosporus* and *A. clavatus*, the nearest phylogenetic species, by the production of non-sclerotioid ascomata and the absence

of an anamorphic stage in our isolates. Therefore, we propose the following new species:

Description of *Leiothecium cristatum* Y. Marín, Stchigel & Cano, sp. nov. (Fig. 2)

Leiothecium cristatum (cris.ta'tum. L. neut. adj. *cristatum*, referring to the equatorial crests of the ascospores).

Colonies on PDA attaining a diam of 71–73 mm after 7 days at 25 °C, cottony, white, margins fringed; reverse yellowish-white to pale yellow (M. 3A2 to 3A3). Hyphae thick- and smooth-walled, hyaline to pale brown, septate, 3–9 µm wide. Ascomata initials arising on aerial and submerged hyphae as lateral branches, consisting of single coils. Ascomata superficial and immersed on the medium, spherical, glabrous, dark brown, non-ostiolate, 100–220 µm diam; peridium brown, 3-layered, 15–20 µm thick, *textura angularis*, composed of polyhedric flattened cells of 10–20 µm diam. Asci 8-spored, broadly clavate to spherical, non-catenulate, 12–16 x 10–14 µm, evanescent. Ascospores one-celled, hyaline, ellipsoidal, 6–8.5 x 4.5–5.5 µm, irregularly reticulated due to the anastomosing low ridges, with two prominent crests of 0.5–1 µm. Chlamydospores mostly terminal, sometimes intercalary, hyaline, subspherical to ellipsoidal, smooth- and thick-walled, 12–19 x 13–18.5 µm. Anamorph not observed. Colonies on MEA similar to those on PDA. After 7 days at 25 °C, colonies on OA and PCA of 34–36 and 61–64 mm diam, respectively. Minimum and maximum temperature of growth 15 and 35 °C, respectively.

Holotype is CBS-H 21130, a dried culture; isotype FMR 11998^{T}.

Mycobank accession no. MB803513.

The ex-type culture is FMR 11998^{T} (= CBS 134260^{T} = NBRC 109843^{T}), isolated from rainforest soil sample, in Iguazú National Park, Misiones province, Argentina, -25° 41' 28.5", -54° 26' 54.9594", 2 Aug 1997, M. Calduch, J. Guarro and A. M. Stchigel.

Description of *Aspergillus posadasensis* Y. Marín, Stchigel & Cano, sp. nov. (Fig. 3)

Aspergillus posadasensis (po.sa.das.en'sis. N.L. masc. adj. posadasensis, belonging to Posadas, capital city of the Misiones province, Argentina).

Colonies on PDA attaining 52–58 mm in diam in 14 days at 25 °C , velvety, white, irregularly folded and with margins fringed; reverse yellowish-white to pale yellow (M. 3A2 to 3A3). Ascomata superficial, spherical, tomentose, orange to brown at maturity, non-ostiolate, 330–720 µm diam; peridium 20–30 µm thick, composed of an outer layer of orange-brown moniliform hyphae, and 3–5 inner layers of flattened, prismatic, brown cells 6–12 µm in diam. Asci 8-spored, globose to subglobose, 9–12.5 x 8.5–10 µm, evanescent at maturity. Ascospores one-celled, hyaline to subhyaline, globose to subglobose, 3.5–4.5 x 3–4 µm, with two equatorial crests, 0.5–1 µm wide; convex surface of ascospores ornamented with triangular projections, long ridge lines and microtubercles. Anamorph not observed in any of the culture media tested, including MEA + 40% sucrose. Colonies on PCA attaining a diameter of 52–58 mm in 14 days at 25 °C, velvety to cottony, with margins fringed, white; reverse white to yellowish-white (M. 2A2). Colonies on MEA attaining 18–20 mm in diam after 14 days at 25 °C , velvety, white, with orange grey to brownish-grey (M. 5B2 to 5C2) margins, fimbriate; reverse brownish-orange to yellowish-brown (M. 5C4 to 5E4), white to yellowish-white (M. 4A1 to 4A2) at the margins; ascomata produced. Colonies on CYA attaining 16–20 mm in diam after 14 days at 25 °C, flattened, mycelium mostly submerged, yellowish-

white (M. 2A2); reverse yellowish-white (M. 2A2); ascomata not formed. Minimum and maximum temperature of growth 15 and 42 °C, respectively.

Holotype is CBS-H 21131, a dried culture; isotype FMR 12168^{T}.

Mycobank accession no. MB803514.

The ex-type culture is FMR 12168^{T} (=CBS 134259^{T} =NBRC 109845^{T}), isolated from a soil sample, in Alberto Roth botanical garden, Misiones province, Argentina, -27° 24' 28.6092", -55° 53' 48.1158", 2 Aug 1997, M. Calduch, J. Guarro and A.M. Stchigel.

Other specimen examined: FMR 12322 (from the same origin and source).

DISCUSSION

The genus *Leiothecium* was erected by Samson & Mouchacca (1975) to include an ascomycete isolated from soil in Greece. Later, this fungus was also reported from soil in South America, Asia and Europe, and from seeds of the capsicum and nest material of a ground-nesting solitary bee in North America, in areas of temperate climate. This fungus shows some similarities with *Ascorhiza* and *Hapsidospora* (Samson & Mouchacca, 1975) because of the presence of cleistothecial ascomata and reticulate ascospores. They also mentioned the possible relationship of *Leiothecium* with *Monascus*, but they remarked on the differences among them (ascomata with a very thin, plectenchymatous peridial wall in *Monascus* vs. prosenchymatous and thickness in *Leiothecium*; smooth-walled ascospores in *Monascus* vs. reticulate in *Leiothecium*; and the presence of an anamorph with retrogressive ontogeny in *Monascus*, which is absent in *Leiothecium*). Despite *Hapsidospora* and *Leiothecium* producing dark coloured, closed ascomata, *Leiothecium* can be differentiated morphologically from *Hapsidospora* because the latter produces dark, globose ascospores of 5–7.5 µm diam

(Guarro et al., 2012), which are hyaline and ellipsoidal, of 7–8.5 x 4.5–5.5 µm in *Leiothecium*. *Ascorhiza* lacks of original type material, and has a poor description (Lechtova-Trnka, 1931) lacking of any illustrations, therefore it cannot be compared with *Leiothecium,* and its validity as a taxon is doubtful.

A recent phylogenetic study carried out by Houbraken & Samson (2011), based on the nucleotidic sequences of *Cct8*, *RPB1*, *RPB2* and *Tsr1* genes demonstrated that *Leiothecium* belongs to the family Aspergillaceae, while in a previous molecular study, based on the analysis of SSU and LSU rRNA gene sequences (Suh & Blackwell, 1999), *Hapsidospora* had been placed in the Hypocreales. Our molecular analysis, using three of those genes, demonstrates that the isolate FMR 11998^{T} represents a new species of *Leiothecium*. This fungus is morphologically distinguishable from *L. ellipsoideum* by the presence of two prominent equatorial crests (absent in *L. ellipsoideum*) and an irregular pattern in its ascospore wall ornamentation (which is more regularly reticulate in *L. ellipsoideum*).

The molecular study of the isolates FMR 12168^{T} and FMR 12322 shows that they are related to *A. acanthosporus* and *A. clavatus.* The type strain of *A. acanthosporus* was isolated from a soil sample in Solomon Islands, Papua-New Guinea (Udagawa & Takada, 1971), along with another three isolates from the same source of the same country. Houbraken & Samson (2011) placed *A. acanthosporus* into the section *Clavati* of *Aspergillus* subg. *Fumigati*. *Aspergillus posadasensis* is easily distinguishable from *A. acanthosporus* by the non-sclerotioid nature of its ascomata and the absence of an anamorph. Other taxa are morphologically similar to the new species and belong to *Aspergillus* subgenus *Fumigati* are *A. aureola* and *A. spinosus*. They also produce ascospores with two equatorial crests and a similar ornamentation to that of *A.*

posadasensis; however, their ascomata are white or very pale yellow, and both produce an anamorph. There are other *Aspergillus* of which no conidiophores structures have been described. Conidiophore structures in *Aspergillus monodii*, which is accommodated in *Aspergillus* section *Usti*, are also not known. However, *A. monodii* has different ascospores and produces Hülle cells and ascomata in stromata.

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Fig. 1. Maximum Likelihood (ML) rooted tree obtained from the combined DNA sequence data from three loci (*Cct8*, *RPB1* and *RPB2*) of our isolates and 11 selected species belonging to the family Aspergillaceae, chosen because of their molecular or morphological similarity to our isolates. *Rasamsonia byssochlamydoides* (CBS 413.71^{T}) and *Talaromyces flavus* (CBS 310.38^{T}) (family Trichocomaceae) were used as outgroup. Bootstrap support values above 70% are indicated at the nodes. Branch lengths are proportional to distance. Type and Neotype strains of the different species are indicated with ^{T} and ^{NT} respectively. New species proposed in this study are indicated in bold font.

Fig. 2. *Leiothecium cristatum* (FMR 11998^{T}). (a), (b) Ascoma; (c) detail of the peridium; (d) asci and terminal chlamydospores; (e), (f) ascus; (g) ascospores (SEM). Bars: (a), 50 µm; (b), 25 µm; (c), 20 µm; (d), (e), 10 µm; (f), 5 µm; (g), 5 µm.

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387 **Fig. 3.** *Aspergillus posadasensis* (FMR 12168^{T}). (a) Ascoma; (b) detail of the peridium;

388 (c), (d) asci; (e), (f) ascospores. Bars: (a), 100 µm; (b), 20µm; (c), 10 µm; (d), 10 µm; (e),

389 5 µm; (f), 2.5 µm.

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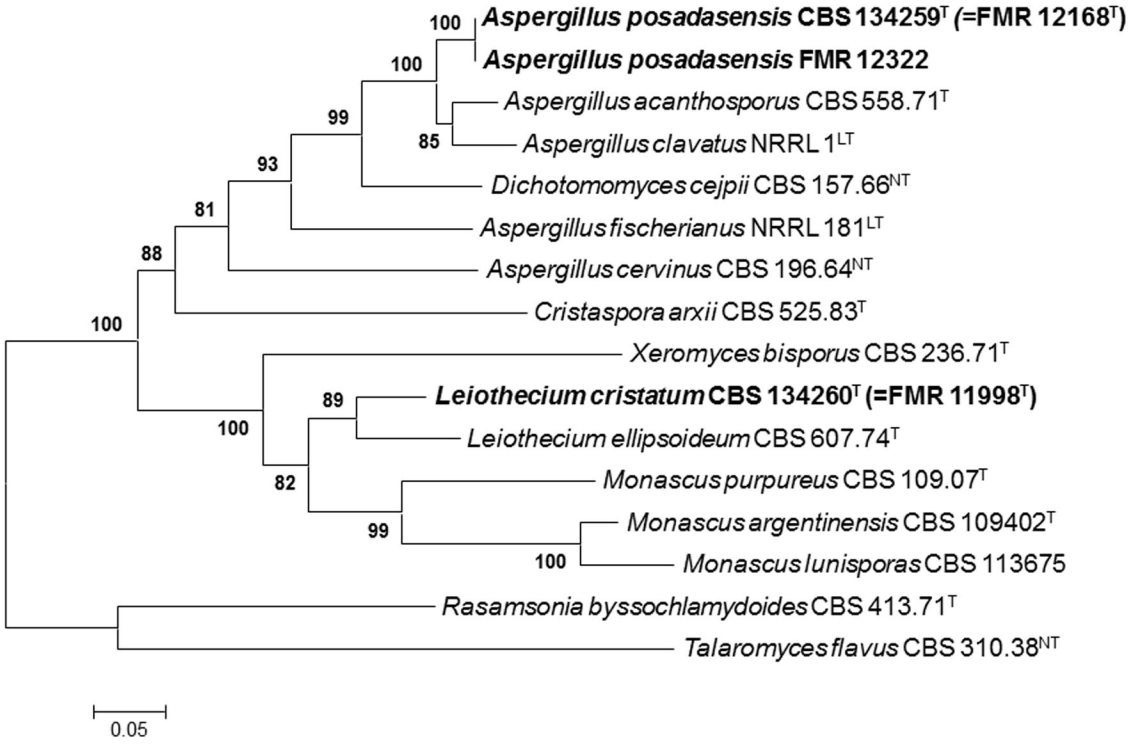
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Aspergillus posadasensis CBS 134259T (=FMR 12168T)
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Aspergillus posadasensis FMR 12322
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Aspergillus acanthosporus CBS 558.71T
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Aspergillus clavatus NRRL 1LT
93
Dichotomomyces cejpii CBS 157.66NT
81
Aspergillus fischerianus NRRL 181LT
88
Aspergillus cervinus CBS 196.64NT
Cristaspora arxii CBS 525.83T
100
Xeromyces bisporus CBS 236.71T
89
Leiothecium cristatum CBS 134260T (=FMR 11998T)
100
Leiothecium ellipsoideum CBS 607.74T
82
Monascus purpureus CBS 109.07T
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Rasamsonia byssochlamydoides CBS 413.71T
Talaromyces flavus CBS 310.38NT
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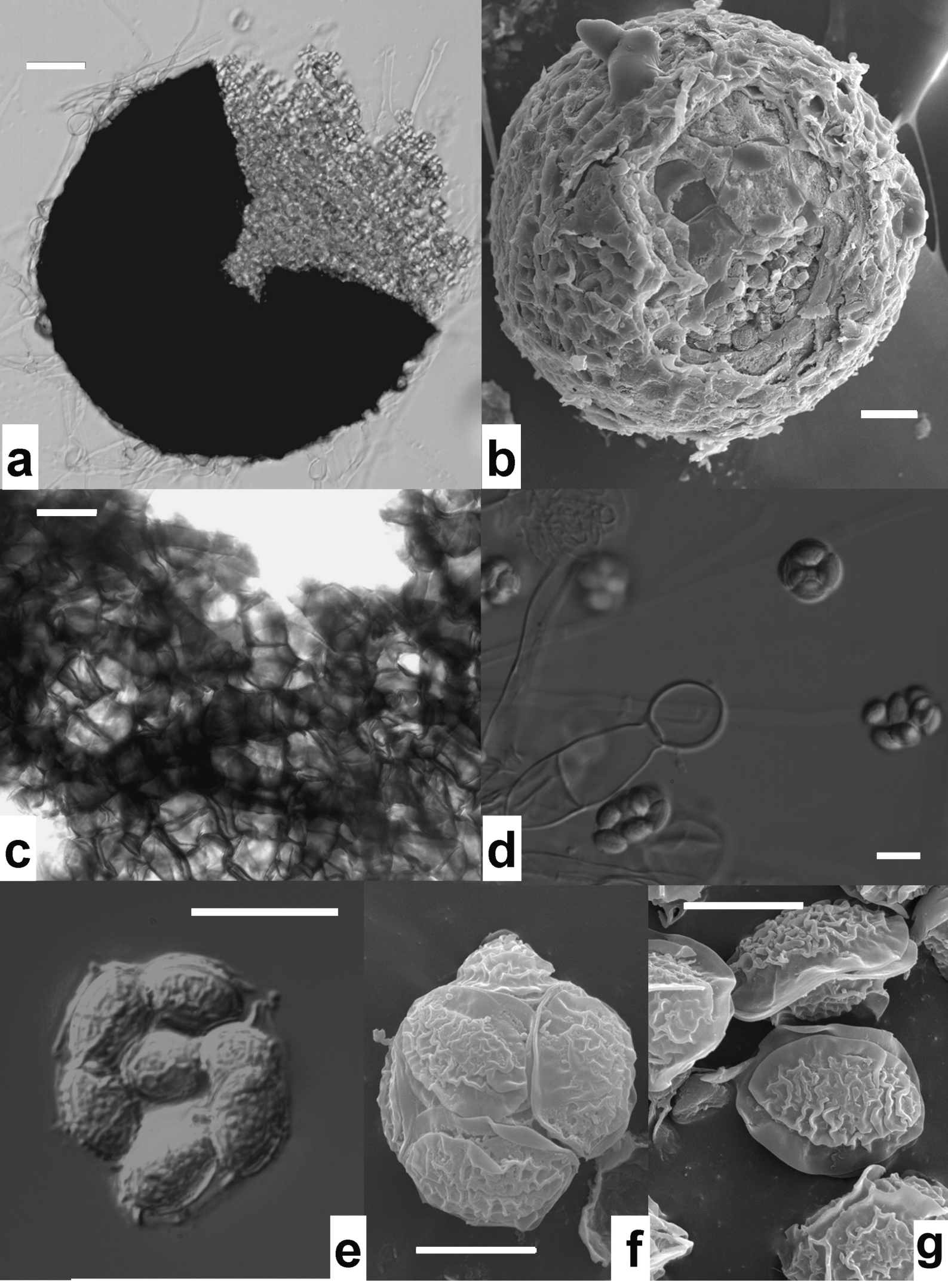
a
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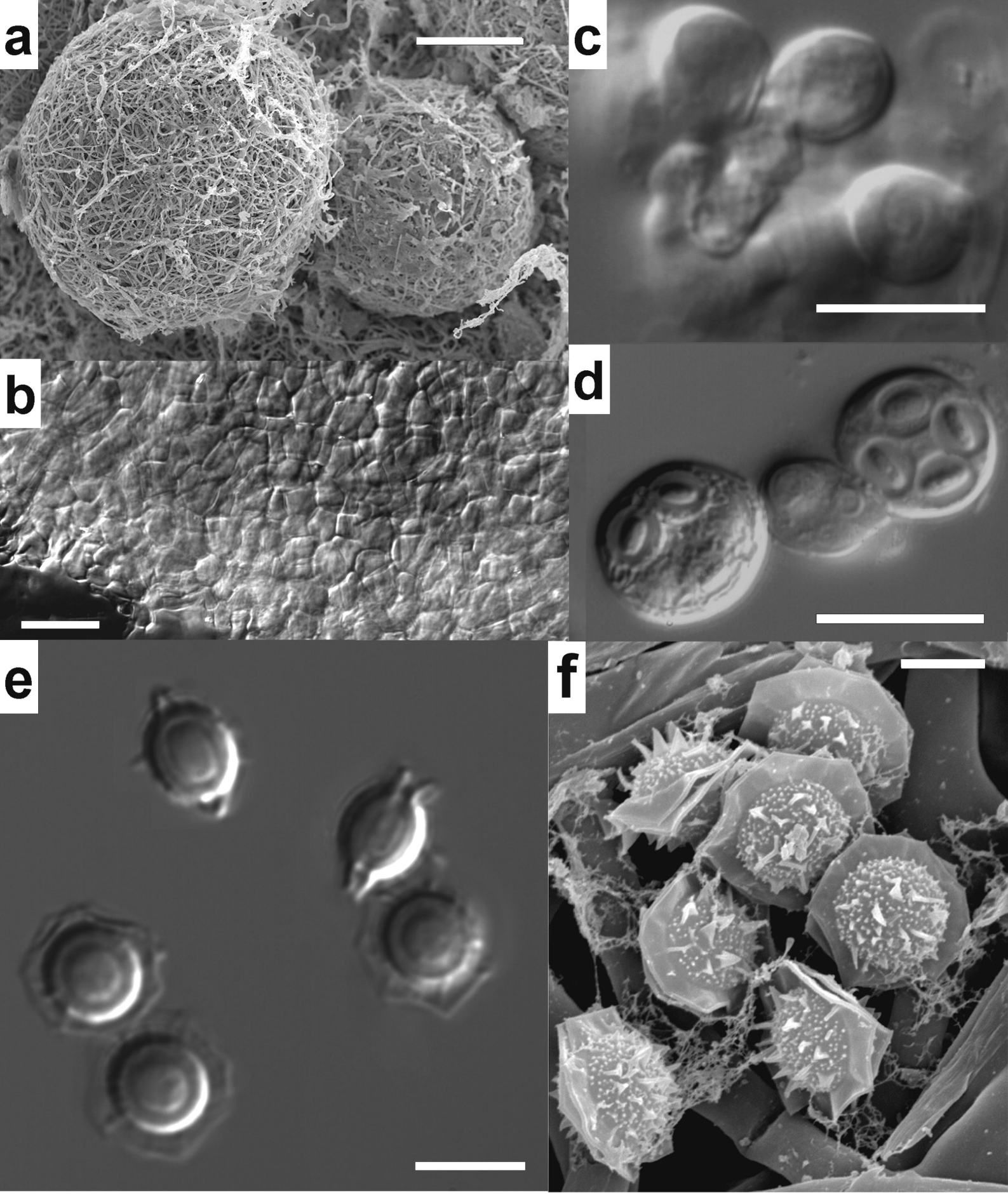
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