New acremonium-like taxa in the Bionectriaceae and Plectosphaerellaceae

Alejandra Giraldo [1, 2, 3], Josepa Gené [1], Deanna A. Sutton [2], Nathan Wiederhold [2], Josep Guarro [1]

[1] Unitat de Micologia, Facultat de Medicina i Ciències de la Salut and IISPV, Universitat Rovira i Virgili, C/ Sant Llorenç 21, 43201 Reus, Tarragona, Spain.
[2] CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands
[3] Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa
[4] Fungus Testing Laboratory, University of Texas Health Science Center, San Antonio, Texas, USA.

Corresponding author: Josepa Gené, e-mail address: josepa.gene@urv.cat

Abstract Several molecular studies have demonstrated that species traditionally assigned to the form genus *Acremonium* are polyphyletic, while *Acremonium sensu stricto* is a central element of the Bionectriaceae (Hypocreales). Based on phenotypic characters and molecular phylogenetic analyses, two new *Acremonium* species, *A. moniliforme* and *A. dimorphosporum,* are described. The former is related to *Emericellopsis* and is characterized by cylindrical conidia, acicular phialides and abundant moniliform hyphae. *Acremonium dimorphosporum* resembles *Acremonium borodinense.* It produces cylindrical, smooth-walled and ellipsoidal, rough-walled conidia. The new genus *Brunneomyces* is proposed based on three species, including *B. brunnescens* (formerly *A. brunnescens*), *B. europaeus* and *B. hominis.* All of them are characterized by brown hyphae, sympodial conidiophores and chains of ovoidal to ellipsoidal conidia. Also, the proposed new species *Chordomyces albus* is characterized by its light-coloured colonies, simple or branched conidiophores, phialides with percurrent proliferations and cylindrical collarettes, and ellipsoidal to cylindrical conidia. The combined analysis of the LSU, ITS,

*RPB*2 and *TEF1-α* loci supports the inclusion of *B. brunnescens, B. europaeus, B. hominis and C. albus* in Plectosphaerellaceae.

Key words *Emericellopsis,* Hypocreales, Plectosphaerellaceae, Phylogeny, Taxonomy

Introduction

Acremonium accommodates saprobic species that can colonize diverse substrates (Gams 1971, 1975; Domsch et al. 2007), important plant pathogens (Alfaro-García et al. 1996; Lin et al. 2004) or agents of opportunistic infections in humans (Summerbell 2003; Guarro 2012; de Hoog et al. 2015). Species-level identifications in *Acremonium* is difficult on the basis of morphological characters because their asexual structures are poorly differentiated. Molecular phylogenetic analyses have demonstrated that the genus is polyphyletic. Recent phylogenetic studies have shown that Acremonium species cluster in different lineages throughout the Ascomycota, mainly in the Sordariomycetes (Glenn et al. 1996; Zare et al. 2007; Schoch et al. 2009; Gräfenhan et al. 2011; Perdomo et al. 2011; Summerbell et al. 2011; Giraldo et al. 2012, 2015). Epitypification of the type species of the genus, *A. alternatum*, linked *Acremonium sensu stricto* to the Bionectriaceae (Hypocreales) (Summerbell et al. 2011), which also accommodates several other, partly teleomophically typified genera with an acremonium-like anamorph, such as *Emericellopsis*, *Hapsidospora*, *Nigrosabulum*, *Bulbithecium* and *Mycoarachis* (Gams 1971; Summerbell et al. 2011). Other species of *Acremonium* are distantly related to the type species of the genus and belong to the Glomerellales or other families of the Hypocreales (Zare et al. 2007; Gräfenhan et al. 2011; Carlucci et al. 2012; Giraldo et al. 2012; Grum-Grzhimaylo 2013a; Maharachchikumbura et al. 2015, 2016; Lombard et al. 2015).

In a previous study on *Acremonium* species from clinical samples in USA (Perdomo et al. 2011), some of the isolates distributed in different groups within the Hypocreales (informally named groups J and N) and Plectosphaerellaceae (groups Q and R), could not be identified. The taxonomy of those isolates and of other *Acremonium* species in Plectosphaerellaceae was resolved in the

present study by using multilocus DNA sequence analyses and phenotypic methods.

Materials and methods

Fungal isolates and sequences

The fungi included in this study are shown in Table 1. Six clinical isolates provided by the Fungus Testing Laboratory at the University of Texas Health Science Center (UTHSC) were tentatively identified as *A. hyalinulum* and previously linked to Hypocreales or Plectosphaerellaceae (Perdomo et al. 2011). In addition, one *Acremonium* isolate (FMR 11785) obtained from soil with the procedure described in Giraldo et al. (2012), and five ex-type or reference strains provided by the CBS-KNAW Fungal Biodiversity Centre (CBS) were also included in our study. Numerous DNA sequences of *Acremonium* species and related genera reported in different studies (Sigler et al. 2004; Zuccaro et al. 2004; Zare et al. 2007; Summerbell et al. 2011; Carlucci et al. 2012; Grum-Grzhimaylo et al. 2013a,b, 2016; Giraldo et al. 2014) were retrieved from public databases (Table 2) and included in the phylogenetic analyses.

Phenotypic studies

Morphological features were examined on potato dextrose agar (PDA; Pronadisa, Madrid, Spain) and oatmeal agar (OA; filtered oat flakes after 1 h of simmering, 30 g; agar, 20 g; distilled water to final volume of 1 000 mL). Cultures were incubated at 25 °C in the dark for 4 wk. Colony diameters were measured after 14 days of incubation and the colony colour rated after Kornerup and Wanscher (1978). Microscopic features were examined and measured from cultures grown on OA under an Olympus CH-2 light microscope (Olympus Corporation, Tokyo, Japan) from direct wet mounts with either 85 % lactic acid or Shear's solution, or from slide cultures. At least 30 randomly selected elements were measured for each structure using an ocular micrometer. Photomicrographs were obtained with a Zeiss Axio-Imager M1 light microscope (Zeiss, Oberkochen, Germany), using phase contrast and Nomarski differential interference. The ability of the fungi to grow at 4, 12, 15, 20, 25, 30, 32, 35, 37 and 40 °C was determined on PDA in duplicate.

DNA extraction, amplification and sequencing

Total genomic DNA was extracted from fresh colonies using PrepMan Ultra Sample Preparation Reagent (Applied Biosystems, Foster City, CA, USA), following the manufacturer's protocol. The DNA was quantified using a NanoDrop 3000 fluorospectrometer (Thermo Scientific, Asheville, NC, USA). The internal transcribed spacer (ITS) regions and the 5' end of the 28S nrDNA gene (LSU) were amplified and sequenced with the primer pairs ITS5/ITS4 (White et al. 1990) and LR0R/LR5 (Vilgalys and Hester 1990; Vilgalys and Sun 1994), respectively. Fragments of the translation elongation factor 1-alpha (*TEF1-α*), RNA polymerase II second largest subunit (*RPB2*) and β-tubulin (*BT2*) genes were amplified with the following primer sets: EF 983F/EF 2218R (Rehner and Buckley 2005) for *TEF1-α*, RPB2-5F/RPB2-7R (Liu et al. 1999) for *RPB2* and Bt1a/Bt1b (Glass and Donaldson 1995) for *BT2* using PCR protocols described elsewhere (Zuccaro et al. 2004; Grum-Grhimaylo et al. 2013a). PCR products were purified and sequenced at Macrogen Europe (Amsterdam, The Netherlands) with the same primers used for amplification. The program SeqMan v. 7.0.0 (DNASTAR, Madison, WI, USA) was used to obtain consensus sequences of each isolate.

Phylogenetic analysis

Phylogenetic analyses based on LSU sequences determined relatedness of taxa to either the "J and N" groups of the Hypocreales or to the "Q and R" groups of the Plectosphaerellaceae. Subsequently, several multilocus sequence analyses for each particular clade were performed to confirm the results obtained with the LSU data. ITS, *BT2, RPB2* and *TEF1-α* loci were used for the isolate of the group N; ITS and LSU for the group J; and ITS, LSU, *RPB2* and *TEF1-α* for the isolates included in groups Q and R. Sequences were aligned and concatenated in MEGA v. 6.06 (Tamura et al. 2013) using the Clustal W and MUSCLE applications (Thompson et al. 1994; Edgar 2004). Manual corrections of the alignments, selection of the best-fit nucleotide substitution models for each locus and for the combined dataset, and Maximum Composite Likelihood (ML) phylogenetic analyses were performed in MEGA 6.06. Gaps or missing data were treated as partial deletion with a site coverage cut-off of 95 %

and Nearest-Neighbor-Interchange (NNI). The internal branch support was assessed by a search of 1000 bootstrapped data sets. A bootstrap support (BS) ≥ 70 was considered as statistically significant. Phylogenetic distance values among isolates were estimated with Kimura 2-parameter as nucleotide substitution model under the same software. A second phylogenetic reconstruction via Bayesian inference (BI) was done using MrBayes v. 3.2.1 (Ronquist and Huelsenbeck 2003; Ronquist et al. 2012). Markov chain Monte Carlo (MCMC) sampling was performed with two simultaneous runs for 3 million generations, with samples taken every 100 generations. Bayesian posterior probabilities (PP) were obtained from the 50 % majority-rule consensus tree after removing the first 25 % of the collected trees. A PP value ≥ 0.95 was considered statistically significant. The best nucleotide substitution model for each gene in the Bayesian analysis (GTR+G+I) was determined using MrModelTest v. 2.3 (Nylander 2004). Congruency of the sequence datasets for the separate loci were determined using tree topologies of 70 % reciprocal Neighbour-Joining (NJ) bootstrap trees with Maximum Likelihood distances for identifying topology conflict visually (Gueidan et al. 2007). Because no incongruence was observed, the different matrices were combined in the final phylogenetic analyses. All novel DNA sequences were deposited in GenBank (Table 1), the alignments and the resulting trees in TreeBASE (http://www.treebase.org), and taxonomic novelties in MycoBank (http://www.MycoBank.org; Crous et al. 2004).

Results

The phylogenetic analysis based on LSU sequences of the isolates UTHSC 08-2284 (group N), UTHSC 08-3639 (group J) and FMR 11785 together with hypocrealean *Acremonium* species and related genera reported by Summerbell et al. (2011) is shown in the Figure 1. The final tree is based on 75 aligned sequences, 847 characters including gaps, of which 580 were conserved, 267 were variable and 195 were phylogenetically informative. Tamura-Nei with gamma distribution (TN+G) and the general time reversible with gamma distribution and a portion of invariable sites (GTR+G+I) were found as the best-

fit nucleotide substitution models for ML and BI, respectively. The phylogenetic tree revealed that the isolates clustered in the "*Emericellopsis"* and "*fusidioides"* clades (Bionectriaceae) as defined by Summerbell et al. (2011). The isolates UTHSC 08-2284 and FMR 11785 fell into the *Emericellopsis* clade (BS = 98 %, PP = 1.00) together with the type species of *Emericellopsis*, *E. terricola* (CBS 120.40), *A. exuviarum* (UAMH 9995), *A. fuci* (CBS 113889) and *A. salmoneum* (CBS 721.71). The two mentioned unidentified isolates showed identical sequences and were grouped in a highly supported subclade (*Acremonium* sp. I). The isolate UTHSC 08-3639 (*Acremonium* sp. II) was represented by a single branch, phylogenetically related (BS = 83 %, PP = 1.0) to *A. fusidioides, A. hennebertii* and the recently described species *A. citrinum, A. parvum* and *A. pilosum* (Giraldo el al. 2014), all belonging to the *fusidioides* clade (Fig. 1).

To better resolve the phylogenetic relationships obtained from the LSU analyses of *Acremonium* sp. I and *Acremonium* sp. II, a multilocus study was performed for each of the unidentified species and their respective closely related species. The first one (Fig. 2) was based on ITS, *BT2, RPB2* and *TEF1-α* sequences and targeted the two isolates of *Acremonium* sp. I, members of the *Emericellopsis* clade, and additional species previously reported to be related to *Emericellopsis* (Sigler et al. 2004; Zuccaro et al. 2004, Grum-Grzhimaylo et al. 2013b) such as *Stanjemonium grisellum*, *S. ochroroseum* and *Acremonium potronii*. The data set included 48 sequences of different strains and 2807 characters (2004 conserved, 803 variables and 604 phylogenetically informative). *Verrucostoma freycinetiae* and *Selinia pulchra* were used as outgroup. Tamura 3-parameter with gamma distribution (T92+G) and GTR+G+I were found to be the best nucleotide substitution models for ML and BI, respectively. The trees generated by using ML and BI had a similar topology. The phylogenetic tree was consistent with previously reported phylogenies (Sigler et al. 2004; Zuccaro et al. 2004; Grum-Grzhimaylo et al. 2013b). The two isolates of *Acremonium* sp. I formed a highly supported basal clade (BS = 84 %, PP = 1.00), distant from the species of *Acremonium*, *Emericellopsis* and *Stanjemonium*. *Acremonium* sp. I is described below as a new species, named *Acremonium moniliforme*.

The other analysis (Fig. 3) included a combination of the ITS and LSU sequences of *Acremonium* sp. II and the ex-type and reference strains of the

Acremonium species from the *fusidioides* clade. The data set consisted of 11 sequences of different strains and 915 characters (731 conserved, 184 variable and 135 phylogenetically informative). The ex-type strains of *Acremonium pinkertoniae* and *A. borodinense* were used as outgroup. ML/BI analyses were done with Kimura-two parameter with gamma distribution (K2+G) as the best-fit nucleotide substitution model. In this analysis, *Acremonium* sp. II clustered distantly from *Acremonium* species forming dimorphic conidia (*A. fusidioides, A. pilosum* and *A. borodinense*) and other species with elongate conidia in chains (*A*. *hennebertii, A. parvum* and *A. citrinum*). *Acremonium* sp. II is proposed as a new species, *A. dimorphosporum*.

The phylogenetic reconstruction using the LSU, ITS, *TEF1-α* and *RPB2* loci from the clinical isolates of the groups Q (UTHSC 06-415 and UTHSC R-3853) and R (UTHSC 06-874 and UTHSC 08-3693), and other representative species of the Plectosphaerellaceae (Fig. 4) is based on a combined dataset consisting of 3271 characters, including 805 phylogenetically informative positions (135 LSU, 151 ITS, 158 *TEF1-α* and 361 *RPB2*), and 39 strains or taxa including the outgroup *Colletotrichum orbiculare* and *C. lagerarium.* The best-fit nucleotide substitution model for ML and BI analysis was K2+G. The phylogenetic tree showed that the isolates UTHSC 06-874 and UTHSC 08-3693 clustered in *Chordomyces* (Grum-Grzhimaylo et al. 2016). While UTHSC 08-3693 was grouped with the ex-type strain of *C. antarcticus* (BS = 85 %; PP = 0.98), UTHSC 06-874 clustered with strain CBS 987.87 in a separated subclade (BS = 86 %; PP = 0.98). Because the last two isolates were phylogenetically distant from the clade of *C. antarcticum,* the new species *Chordomyces albus* is proposed. In the same analysis, a monophyletic group (BS = 94 %; PP = 1.00) was formed by all isolates of the group R, two reference strains of *A. hyalinulum* formed a well-supported clade (BS = 98 %; PP = 1.00), two clinical isolates (UTHSC R-3853 and UTHSC 06-415) clustered together with high support (BS = 97 %; PP = 1.00), while the ex-type strain of *A. brunnescens* formed a single branch. This novel lineage of acremonium-like fungi within the Plectosphaerellacae is proposed as a new genus, *Brunneomyces* based on *A. brunnescens*, and the two new species, *B. hominis* and *B. europaeus*.

Taxonomy

Acremonium dimorphosporum Giraldo, Deanna A. Sutton & Gené, **sp. nov.** [**MB 811461**] Fig. 5

Etymology. The name refers to the dimorphic conidia produced by the species.

Colonies at 25 °C after 14 days on OA reaching 10–11 mm diam, white (1A1) to yellowish white (4A2), flat, with scarce aerial mycelium, reverse colourless; at 25 °C after 14 days on PDA reaching 14–15 mm diam, pinkish white (7A2), flat, cottony, reverse orange (6A6). *Mycelium* consisting of hyaline, smooth- and thin-walled, 1.5–2 µm wide hyphae. *Conidiophores* erect, usually reduced to single phialides emerging from vegetative hyphae, occasionally basitonously branched and then bearing 2–4 phialides, straight, up to 60 µm long, hyaline, smooth, with cell walls usually thicker than those of the vegetative hyphae. *Phialides* subulate, 17–30(45) µm long, 1–1.5 µm wide at the base, hyaline, thick- and smooth-walled, often borne on short cylindrical subtending cells; percurrently proliferating phialides are occasionally present. *Conidia* arranged in slimy heads, 1-celled, hyaline, of two types: i) cylindrical with more or less rounded ends, 3–7 × 1–1.5 µm, thin- and smooth-walled; ii) ellipsoidal, 3–4 × 2–3 µm, thick- and rough-walled. *Chlamydospores* and *sexual morph* not observed.

Cardinal temperatures for growth: Optimum 20–25 ºC, maximum 30 ºC, minimum 15 ºC.

Specimen examined. **USA**, Texas, from bronchoalveolar lavage fluid, 2008, D.A. Sutton (holotype CBS H-22021, dried culture on OA; cultures ex-type CBS 139050 = FMR 10548 = UTHSC 08-3639).

Notes: Although *A. dimorphosporum* is phylogenetically distant to *A. borodinense*, it is morphologically similar to that species in producing both ellipsoidal rough-walled and cylindrical smooth-walled conidia (Ito et al. 2000). However, *A. borodinense* differs from *A. dimorphosporum* by its faster growth at 25 ºC (27–29 mm diam. after 10 d) and by its ability to grow at 37 ºC. Furthermore, its cylindrical conidia are slightly curved and smaller (4.5–5.5 µm long), and its ellipsoidal and rough-walled conidia are larger (4.2–5.5 × 3–4 µm) than those of *A. dimorphosporum.*

Acremonium moniliforme Giraldo, Deanna A. Sutton & Guarro, **sp. nov.** [**MB 811462**] Fig. 6

Etymology. The name refers to the presence of monilifom hyphae.

Colonies at 25 ºC after 14 days on OA reaching 45–60 mm diam, yellowish white (4A2), flat, glabrous; reverse colourless; at 25 ºC after 14 days on PDA reaching 36–50 mm diam, pinkish white (7A2), radially folded, zonate towards the periphery, felty, greyish red (7B4); reverse salmon (6A4). *Mycelium* consisting of branched, septate, hyaline, smooth- and thick-walled hyphae, initially 2–2.5 µm wide, often swelling at maturity, becoming barrel-shaped, up to 7 µm wide. *Conidiophores* reduced to conidiogenous cells, emerging laterally from hyphae. *Phialides* acicular with a slightly flexuose apex, 30–50 µm long, 1.5–2 µm wide at the base, with a distinct periclinal thickening, thick- and smooth-walled, hyaline. *Conidia* arranged in slimy heads, 1-celled, cylindrical with rounded ends, 3–5(6) × 1–2 µm, hyaline, thick- and smooth-walled. *Chlamydospores* and *sexual morph* not observed.

Cardinal temperatures for growth: Optimum 25–30 ºC, maximum 37 ºC, minimum below 4 ºC.

Specimens examined: **Spain**, Aragón, Huesca province, Ordesa y Monte Perdido National Park, from forest soil, 2011, coll. A. Giraldo, M. Hernández, & J. Capilla, isol. A. Giraldo (holotype CBS H-22022, dried culture on OA; cultures ex-type CBS 139051 = FMR 11785). **USA**, Utah, from toe nail, 2008, D.A. Sutton (FMR 10363 = UTHSC 08-2284).

Notes: Acremonium monilifome is phylogenetically distant from the species of the *Emericellopsis* clade. It can be morphologically differentiated from other *Acremonium* species by the production of abundant moniliform hyphae. *Acremonium fuci* occasionally produces small rounded hyphal swellings, similar to the moniliform hyphae of *A. moniliforme*. However, both species can be distinguished by the conidial shape, which is obovoid or broadly ellipsoidal in the former, and cylindrical in the latter. Additionally, the maximum temperature for growth in *A. fuci* is 33 ºC (Zuccaro et al. 2004), while in *A. moniliforme* it is 37 ºC.

Brunneomyces Giraldo, Gené & Guarro, **gen. nov**. [**MB 811471**]

Type species. *Brunneomyces brunnescens* (W. Gams) Giraldo, Gené & Guarro

Etymology. The name refers to brownish pigmented hyphae formed by the type species of this genus.

Mycelium consisting of branched, septate, hyaline and thin-walled hyphae, often becoming dark brown, verrucose and thick-walled with age. *Conidiophores* erect, unbranched or poorly branched, often proliferating sympodially, showing conidiogenous cells as short lateral and cylindrical projections. *Conidiogenous cells* enteroblastic, mono- and polyphialidic, hyaline, terminal, lateral or intercalary (adelophialides), subulate, lageniform or cylindrical, usually with short cylindrical collarettes, often subhyaline or pale brown, and with a distinct periclinal thickening at the conidiogenous locus. *Conidia* arranged in chains, 1-celled, pyriform or ellipsoidal, hyaline or brown. *Sexual morph* unknown.

Brunneomyces brunnescens (W. Gams) Giraldo, Gené & Guarro, **comb. nov.** [**MB 811472**] Fig. 7

Basionym*. Acremonium brunnescens* W. Gams, Trans. Br. Mycol. Soc., 64: 398. 1975.

Specimen examined. **Sri Lanka,** Hakgala Bot. Gardens, from dead stem of *Dendrocalamus giganteus*, Jan. 1973, W. Gams (holotype CBS H-6641, dried plant material; cultures ex-type CBS 559.73 = ATCC 32180 = IMI 185378).

Notes: Although the three species of *Brunneomyces* show a similar conidiogenous apparatus to that of the genus *Acremonium*, they can be distinguished by the presence of sympodial conidiophores and dark brown, verrucose, thick-walled hyphae. The combination of these morphological features are usually absent in the species of *Acremonium* and other genera of plectosphaerellaceous fungi. In addition, *Brunneomyces* is the only genus of the Plectosphaerellaceae with conidial chains.

A detailed description of *B. brunnescens* was given in Gams (1975). Most relevant features of the ex-type strain of this species (CBS 559.73) studied here were: slow growing colonies (6–8 mm and 21–22 mm diam. after 14 d on PDA and OA, respectively) with a mushroom-like odour, pigmented verrucose hyphae and dark brown conidia appearing after 21 days, phialides with short

cylindrical and slightly pigmented collarettes, adelophialides of 6–10 × 1.5–2.5 µm, and conidial chains often collapsing soon in slimy heads. In addition, this fungus was unable to grow above 32 ºC.

Brunneomyces hominis Giraldo, Deanna A. Sutton & Gené*,* **sp. nov***.* [**MB811473**] Fig. 8

Etymology*:* The name refers to the isolation source of the type strain, human clinical samples.

Colonies at 25 °C after 14 days on OA reaching 26–28 mm diam, orange white (6A2), flat, dusty; reverse colourless; at 25 °C after 14 days on PDA reaching 17–18 mm diam, grey (5F1) at the centre, yellowish white (4A2) at the periphery, crateriform and radially folded, felty; reverse grey (5F1). Strong mushroom-like (moist soil) odour. *Mycelium* consisting of septate, hyaline, smooth- and thin-walled hyphae, 1.5–2 µm wide at the beginning, becoming dark brown, verrucose and thick-walled, up to 3 µm wide with age. *Conidiophores* erect, mostly unbranched, occasionally with a few branches and proliferating sympodially, straight or slightly bent, up to 35 µm long, hyaline, smooth-walled. *Phialides* subulate, 12–20(30) µm long, 1.5–2 µm wide at the base, hyaline at first, dark brown in old cultures, thick- and smooth-walled, with conspicuous periclinal thickening and cylindrical collarettes; adelophialides sometimes present, up to 10 µm long; polyphialides with up to two conidiogenous loci commonly present. *Conidia* arranged in long dry chains, 1-celled, pyrifom or ellipsoidal, 4–5(6) × 2–2.5 µm, with truncate base, subhyaline, thin- and smooth-walled. *Chlamydospores* and *sexual morph* not observed.

Cardinal temperatures for growth: Optimum 25–30 ºC, maximum 35 ºC, minimum below 4 ºC.

Specimens examined. **USA**, Minnesota, from human sputum, 2006, D.A. Sutton (holotype CBS H-22023, dried culture on OA; cultures ex-type CBS 139053 = FMR 10429 = UTHSC 06-415). California, from human sputum, D.A. Sutton (CBS 139054 = FMR 10437 = UTHSC R-3853).

Notes: The colourless colony reverse on OA distinguishes *B. hominis* from the dark grey reverse in *B. brunnescens*. *Brunneomyces hominis* produces long, dry conidial chains, while in *B. europaeus* and *B. brunnescens* chains tend

to collapse in slimy heads. It is the only *Brunneomyces* species able to grow at 35 ºC.

Brunneomyces europaeus Giraldo, Gené & Guarro*,* **sp. nov.** [**MB811474**] Fig. 9

Etymology*:* The name refers to the geographic origin of the isolates, Europe.

Colonies at 25 °C after 14 days on OA reaching 31–50 mm diam, yellowish white (4A2), flat, dusty; reverse colourless; at 25 °C after 14 days on PDA reaching 25–36 mm diam, greyish brown (6E2) at the centre, white (1A1) to orange-white (6A2) towards the periphery, radially folded, felty; reverse brown (6E2). Slight mushroom-like (moist soil) odour. *Mycelium* consisting of septate, hyaline, smooth- and thin-walled hyphae, 2–2.5 µm wide, becoming brownish, verrucose and thick-walled with age. *Conidiophores* erect, usually unbranched, some proliferating sympodially, up to 45 µm long, straight or slightly bent, hyaline to subhyaline, smooth-walled. *Phialides* subulate or somewhat cylindrical, 15–35(40) µm long, 2–3 µm wide at the base, hyaline, thick- and smooth-walled, with a distinct periclinal thickening at the conidiogenous locus and short cylindrical collarettes; adelophialides sometimes present, up to 15 µm long; polyphialides with up to three conidiogenous loci commonly present. *Conidia* forming chains that soon collapse in slimy heads, 1-celled, ovoidal to ellipsoidal, 5–6(7) × 2–3 µm, with a distinctly truncate base, subhyaline, thin- and smooth-walled. *Chlamydospores* and *sexual morph* not observed.

Cardinal temperatures for growth: Optimum 20–25 ºC, maximum 32 ºC, minimum below 4 ºC.

Specimens examined. **Spain**, Riumar, from sediments of Ebro River, 1991, coll. K. Ulfig, isol. J. Gené (holotype CBS H-22024, dried culture on OA; cultures ex-type CBS 652.96 = FMR 3962). **France**, Provence, from leaf of *Bambusa* sp., Dec. 1986, O. Petrini (CBS 560.86 = FMR 3406).

Notes: The two isolates of *B. europaeus* were previously identified wrongly as *A. hyalinulum* because they form brownish pigmented and verrucose hyphae, sympodially proliferating conidiophores and intercalary phialides that all are not mentioned in the protologue of *A. hyalinulum* (Gams 1971). The latter was described with hyaline smooth-walled hyphae, and lacking adelophialides. However, there is no ex-type strain of *A. hyalinulum* for a reliable comparison

and, according to different studies, it seems to be a polyphyletic species (Perdomo et al. 2011; Summerbell et al. 2011).

Chordomyces Bilanenko, M.L. Georgieva & Grum-Grzhimaylo [Emmend]

Type species. Chordomyces antarcticus Bilanenko ML, Georgieva & Grum-Grzhimaylo

Modified from original description (Grum-Grzhimaylo et al. 2016): *Colonies* white, tufted, restricted to moderate fast growing. *Mycelium* superficial or immersed, consisting of septate, hyaline, thin- and smooth-walled hyphae. *Conidiophores* phalacrogenous, plectonematogenous or synnematogenous, unbranched or branched, or consisting of single phialides. *Synnemata* when present, hyaline, without a differential sterile base, sometimes branched, appearing fimbriate due to radiating phialides. *Conidiogenous cells* mono- or polyphialidic, tapering to the apex, hyaline, often proliferating sympodially. *Conidia* arranged in slimy heads, 1(-2)-celled, subglobose, limoniform, ellipsoidal to cylindrical, rounded at the apex, sometimes with protuberant hilum, hyaline and smooth-walled. *Sexual morph* unknown.

Chordomyces albus Giraldo, Deanna A. Sutton & Guarro, **sp. nov.** [**MB 811476**] Fig. 10

Etymology*:* The name refers to light coloured colonies formed by the species.

Colonies at 25 °C after 14 days on OA reaching 40–41 mm diam, yellowish white (4A2), flat, dusty; reverse colourless; at 25 °C after 14 days on PDA reaching 10–11 mm diam, pale yellow (4A3), raised, cerebriform; reverse colourless. *Mycelium* consisting of septate, hyaline, smooth- and thin-walled hyphae, 1.5–2 µm wide. *Conidiophores* erect, unbranched, consisting of one or two cells, or with branches from near the middle bearing 3–4 phialides, up to 30 µm long, straight or slightly curved, hyaline to subhyaline, smooth-walled. *Synnemata* absent. *Phialides* cylindrical or subulate, 12–22 µm long, 2–2.5 µm wide at the base, with a distinct periclinal thickening at the conidiogenous locus and cylindrical collarettes, occasionally with a percurrent proliferation, hyaline, thick- and smooth-walled, sometimes with a second conidiogenous locus emerging laterally as an up to 5 µm long cylindrical projection near the basal septum. *Conidia* in slimy heads, 1-celled, ellipsoidal to near cylindrical, 3–4 × 2–

2.5 µm, subhyaline, thick- and smooth-walled. *Chlamydospores* and *sexual morph* not observed.

Cardinal temperature for growth: Optimum 20–25 ºC, maximum 32 ºC, minimum below 4 ºC.

Specimens examined. **Luxembourg,** Hautecharage, on *Hypogymnia physodes,* Dec. 1987, coll. G. Marson, isol. W. Gams (holotype CBS H-8083, dried plant material; cultures ex-type CBS 987.87 = FMR 10886). **USA**, Hawaii, from human sputum, 2006, D.A. Sutton (FMR 10433 = UTHSC 06-874).

Notes: The genus *Chordomyces* was recently proposed by Grum-Grzhimaylo et al. (2016) to accommodate *C. antarcticus*. Most isolates of *C. antarcticus* but CBS 987.87 derived from soda soil and were alkalitolerant. Strain CBS 987.87 was previously wrongly identified as *A. antarcticum;* however, it differs from the protologue of that species in the presence of schizophialides with conspicuous cylindrical collarettes and percurrent conidiophores (Spegazzini 1910; Hawksworth 1979). Furthermore, its DNA sequences differ significantly from *C. antarcticus* strains in Grum-Grzhimaylo et al. (2016). In the present study, CBS 987.87 and the clinical isolate UTHSC 06-874 have been found to be morphologically and genetically similar and, since they formed a novel lineage into the *Chordomyces* clade, they are proposed as a second species in the genus. *Chordomyces albus* morphologically differs from *C. antarcticus* in the absence of synnemata in culture, in having a faster growth on OA at 25 ºC (40–41 mm *vs*. 22–28 mm in 14 days), shorter phialides (12–22 µm long *vs*. 28–30 µm long) and conidia without a protuberant hilum (Grum-Grzhimaylo et al. 2016).

Discussion

Two bionectriaceus species are newly described. *Acremonium dimorphosporum* is phylogenetically related to species of the *fusidioides* clade (Summerbell et al. 2011; Giraldo et al. 2014). Conidial dimorphism seen also in other species of the *fusidioides* clade supports this phylogenetic inference, although no conidial chains but slimy masses were observed in *A. dimorphosporum* (Gams 1971; Ito et al. 2000; Giraldo et al. 2012, 2014). *Acremonium moniliforme* is phylogenetically closely related to species of the *Emericellopsis* clade, a well-

defined monophyletic group within the Bionectriaceae accomodating also the type species of the synnematous genus *Stilbella, S. fimetaria* (Seifert 1985), the type species of *Stanjemonium, S. grisellum* (Gams et al. 1998), and *Acremonium* species, such as *A. tubakii, A. fuci, A. exuviarum* and *A. salmoneum* (Sigler et al. 2004; Zuccaro et al. 2004; Summerbell et al. 2011; Grum-Grzhimaylo et al. 2013b). Members of this clade are commonly isolated from soil, dung, marine water, and occasionally from animal lesions (Sigler et al. 2004; de Hoog et al. 2015; Grum-Grzhimaylo et al. 2013b). The origin of the two strains of *A. moniliforme,* i.e. human nail from USA and soil from Spain, suggests that it is a widespread species as other species of this group.

Phylogenetic analyses of concatenated sequences from four loci support the monophyly of *Brunneomyces* and places the genus in the Plectosphaerellaceae. This family was introduced by Gams, Summerbell and Zare (Zare et al. 2007) and recently assigned to the Glomerellales (Maharachchikumbura et al. 2016). Currently, it comprises nine genera, i.e. *Acrostalagmus, Gibellulopsis, Lectera, Musicillium, Plectosphaerella*, *Stachylidium, Verticillium sensu stricto* and the recently described *Chordomyces* and *Sodiomyces* (Zare et al. 2007; Inderbitzin et al. 2011; Réblová et al. 2011; Cannon et al. 2012; Grum-Grzhimaylo et al. 2013a, 2016). In addition, *Gliocladium cibotii* and some *Acremonium* species, including *A. collariferum*, *A. furcatum, A. nepalense*, *A. restrictum* and *A. stromaticum,* belong to this family (Zare et al. 2007; Weisenborn et al. 2010; Carlucci et al. 2012). Morphologically, species of *Acrostalagmus, Gibellulopsis, Musicillium, Stachylidium* and *Verticillium* are mainly characterized by hyaline or light brown verticillate conidiophores (Hughes 1951; Zare et al. 2007; Inderbitzin et al. 2011; Réblová et al. 2011); *Lectera* produces brightly coloured sporodochia and brown setae (Cannon et al. 2012*);* the asexual morphs of *Sodiomyces* and *Plectosphaerella* have verticillate or penicillate conidiophores and septate conidia (Carlucci et al. 2012; Grum-Grzhimaylo et al. 2013a, 2016); *Chordomyces*, *G. cibotii* and above-mentioned *Acremonium* species form mostly cylindrical or ellipsoidal conidia arranged in slimy heads (Gams 1971, 1975; Zare et al. 2007; Weisenborn et al. 2010; Grum-Grzhimaylo et al. 2016). By contrast, the species of *Brunneomyces* are characterized by the production of sympodially proliferating conidiophores, ovoidal or ellipsoidal conidia arranged in chains and

dark verruculose hyphae. Subglobose to oval conidia, conspicuous funnel-shaped collarette and olive-brown chlamydospores distinguishes *A. collariferum* from *Brunneomyces* although it also forms verruculose hyphae (Weisenborn et al. 2010). In addition, *A. collariferum* did not produce conidial chains in any of the culture media tested here.

The genus *Phaeoacremonium* (Togniniaceae, Diaporthales) resembles *Brunneomyces* in having verruculose, pale brown hyphae and polyphialides. However, it is phylogenetically distant and its species produce conidia in slimy heads (Crous et al. 1996; Mostert et al. 2006).

Our phylogenetic analysis supports the monophyly of *Chordomyces* and the existence of a new species, *C. albus*. Based on morphological features of *C. antarcticus* the monotypic genus was restricted to fungi with cylindrical to ellipsoidal conidia (Grum-Grzhimaylo et al. 2016). However, UTHSC 08-3693 produced subglobose to limoniform conidia in all media tested. Therefore, the concept of *Chordomyces* is emended here accordingly.

The habitats of the members of Plectosphaerellaceae are quite diverse. *Verticillium*, *Musicillium*, *Plectosphaerella* and *Lectera* are well-known pathogens of different kinds of plants, including legumes, banana, cucurbits, potatoes, and others (Cannon et al. 2012; Carlucci et al. 2012; Masudi and Bonjar 2012; Hyde et al. 2014). *Acrostalagmus luteoalbus* has been reported also as a fungicolous species (Gams et al. 2004); *Gibellulopsis nigrescens* and most of the plectosphaerellaceous *Acremonium* species are soil-borne saprobes (Gams 1975; Domsch et al. 2007; Zare et al. 2007). *Gibellulopsis piscis* and *Plectosphaerella oratosquillae* have occasionally been reported as pathogens of fish and shrimp, respectively (Batista and da Silva 1959; Duc et al. 2009), and some species such as *Stachylidium bicolo*r, *Acremonium alcalophilum, Chordomyces* and *Sodiomyces* species possess alkaliphilic or alkalitolerant abilities (Grum-Grzhimaylo et al. 2013a,b; 2016). The species of *Brunneomyces* and *Chordomyces* studied here seem to be saprotrophic; they are typically recovered from plant debris. Although, the isolates included in *B. hominis,* and some of *C. albus* and *C. antarcticus* are from human specimens (human nails and sputum), their human-related pathogenic role is unknown.

Acknowledgements The authors would like to thank Prof. Dr, G.S. de Hoog and the curator of the culture collection CBS-KNAW Fungal Biodiversity Centre for providing valuable strains from their collection. This study was supported by the Spanish Ministerio de Economía y Competitividad, grant CGL2013-43789-P.

References

Alfaro-García A, Armengol J, Bruton BD, Gams W et al (1996) The taxonomic position of the causal agent of *Acremonium* collapse of muskmelon. Mycologia 88:804–808

Batista A, Silva da H (1959) Uma nova doença fungica de peixe ornamental. Anais Soc Biol Pernambuco 16:153–159

Cannon P, Buddie AG, Neergaard de E, Lübeck M, Askar MM (2012) *Lectera*, a new genus of the Plectosphaerellaceae for the legume pathogen *Volutella colletotrichoides.* MycoKeys 3:23–36

Carlucci A, Raimondo ML, Santos J, Phillips AJL (2012) *Plectosphaerella* species associated with root and collar rots of horticultural crops in southern Italy. Persoonia 28:34–48

Castlebury LA, Rossman AY, Sung GH, Hyten AS, Spatafora JW (2004) Multigene phylogeny reveals new lineage for *Stachybotrys chartarum*, the indoor air fungus. Mycol Res 108:864–872

Chaverri P, Salgado C, Hirooka Y, Rossman AY, Samuels GJ (2011) Delimitation of *Neonectria* and *Cylindrocarpon* (Nectriaceae, Hypocreales, Ascomycota) and related genera with *Cylindrocarpon*-like anamorphs. Stud Mycol 68:57–78

Crous PW, Gams W, Stalpers JA, Robert V, Stegehuis G (2004) MycoBank: an online initiative to launch mycology into the 21st century. Stud Mycol 50:19–22

Crous PW, Gams W, Wingfield MJ, van Wyk, PS (1996) *Phaeoacremonium* gen. nov. associated with wilt and decline diseases of woody hosts and human infections. Mycologia 88:786–796

578 Crous PW, Wingfield MJ, Le Roux JJ, Richardson DM et al (2015) Fungal
579 Planet description sheets. Persoonia 35:264–327
580
581 De Hoog GS, Guarro J, Gené J, Figueras MJ (2015) Atlas of clinical fungi. USB
582 version 4.1. CBS-KNAW Fungal Biodiversity Centre, Utrecht
583
584 Domsch KH, Gams W, Anderson TH (2007) Compendium of soil fungi, 2nd edn.
585 IHW Verlag, Eching
586
587 Duc PM, Hatai K, Kurata O, Tensha K et al (2009) Fungal infection of mantis
588 shrimp (*Oratosquilla oratoria*) caused by two anamorphic fungi found in Japan.
589 Mycopathologia 167:229–247
590
591 Edgar RC (2004) MUSCLE: multiple sequence alignment with high accuracy
592 and high throughput. Nucleic Acids Res 32:1792–1797
593
594 Gams W (1971) *Cephalosporium*-artige Schimmelpilze (Hyphomycetes).
595 Gustav Fischer Verlag, Stuttgart
596
597 Gams W (1975) *Cephalosporium*-like hyphomycetes: some tropical species.
598 Trans Br Mycol Soc 64:389–404
599
600 Gams W, Diederich P, Põldmaa K (2004) Fungicolous fungi. Chapter 17. In:
601 Müller G, Bills GF, Foster MS (eds) Measuring and monitoring biological
602 diversity: standard methods for fungi. Academic Press, New York
603
604 Gams W, O'Donnell K, Schroers H-J, Christensen M (1998) Generic
605 classification of some more hyphomycetes with solitary conidia borne on
606 phialides. Can J Bot 76:1570–1583
607
608 Giraldo A, Gené J, Cano J, Hoog S de et al (2014) *Acremonium* with catenate
609 elongate conidia: phylogeny of *Acremonium fusidioides* and related species.
610 Mycologia 106:328–338
611

612 Giraldo A, Gené J, Cano J, Hoog S de, Guarro J (2012) Two new species of
613 *Acremonium* from Spanish soils. Mycologia 104:1456–1465
614
615 Giraldo A, Gené J, Sutton DA, Madrid H et al (2015) Phylogeny of *Sarocladium*
616 (Hypocreales). Persoonia 34:10–24.
617
618 Glass NL, Donaldson GC (1995) Development of primer sets designed for use
619 with the PCR to amplify conserved genes from filamentous Ascomycetes. Appl
620 Environ Microb 61:1323–1330
621
622 Glenn A, Bacon CW, Price R, Hanlin RT (1996) Molecular phylogeny of
623 *Acremonium* and its taxonomic implications. Mycologia 88:369–383
624
625 Gräfenhan T, Schroers HJ, Nirenberg HI, Seifert KA (2011) An overview of the
626 taxonomy, phylogeny, and typification of nectriaceous fungi in *Cosmospora*,
627 *Acremonium, Fusarium, Stilbella*, and *Volutella*. Stud Mycol 68:79–113
628
629 Grum-Grzhimaylo AA, Debets AJM, Diepeningen AD van, Georgieva ML,
630 Bilanenko EN (2013a) *Sodiomyces alkalinus*, a new holomorphic alkaliphilic
631 ascomycete within the Plectosphaerellaceae. Persoonia 31:147–158
632
633 Grum-Grzhimaylo AA, Georgieva ML, Bondarenko SA, Debets AJM, Bilanenko
634 EN (2016) On the diversity of fungi from soda soils. Fungal Divers 76:27–74
635
636 Grum-Grzhimaylo AA, Georgieva ML, Debets AJM, Bilanenko EN (2013b) Are
637 alkalitolerant fungi of the *Emericellopsis* lineage (Bionectriaceae) of marine
638 origin? IMA Fungus 4:381–443
639
640 Guarro J (2012) Taxonomía y biología de los hongos causantes de infección en
641 humanos. Enferm Infec Micr Cl 30:33–39.
642
643 Gueidan C, Roux C, Lutzoni F (2007) Using multigene phylogeny analysis to
644 assess generic delineation and character evolution in Verrucariaceae
645 (Verrucariales, Ascomycota). Mycol Res 111:1145–1168

Hawksworth, DL (1979) The lichenicolous Hyphomycetes. Bull Br Mus nat Hist Bot 6:183–300.

Hughes SJ (1951) *Stachylidium, Gonytrichum, Mesobotrys, Chaetopsis and Chaetopsella*. Trans Br Mycol Soc 34:551–559.

Hujslová M, Kubátová A, Chudíčková M, Kolarik M (2009) Diversity of fungal communities in saline and acidic soils in the Soos National Natural Reserve, Czech Republic. Mycol Prog 9:1–15

Hyde KD, Nilsson RH, Alias SA, Ariyawansa HA et al (2014) One stop shop: backbones trees for important phytopathogenic genera: I. Fungal Divers 64:21–125

Inderbitzin P, Bostock RM, Davis RM, Usami T et al (2011) Phylogenetics and taxonomy of the fungal vascular wilt pathogen *Verticillium*, with the descriptions of five new species. PLoS ONE 6:e28341

Irinyi L, Serena C, Garcia-Hermoso D, Arabatzis M et al (2015) International Society of Human and Animal Mycology (ISHAM)-ITS reference DNA barcoding database-the quality controlled standard tool for routine identification of human and animal pathogenic fungi. Med Mycol:313–337

Ito T, Okane I, Nakagiri A, Gams W (2000) Two species of *Acremonium* section *Acremonium*: *A. borodinense* sp. nov. and *A. cavaraeanum* rediscovered. Mycol Res 104:77–80.

Kornerup A, Wanscher JH (1978) Methuen handbook of colour. 3rd ed. Eyre Methuen, London

Lehr NA, Meffert A, Antelo L, Sterner O et al (2006) Antiamoebins, myrocin B and the basis of antifungal antibiosis in the coprophilous fungus *Stilbella erythrocephala* (syn. *S. fimetaria*). FEMS Microbiol Ecol 55:105–112

Lin H-J, Chien C-Y, Huang J-W (2004) Pathogenicity and host range of *Acremonium lactucae* sp. nov., the causal agent of leaf brown spot of lettuce. Plant Pathology Bulletin 13:91–96

Liu Y, Whelen S, Hall B (1999) Phylogenetic relationships among Ascomycetes: evidence from an RNA polymerase II subunit. Mol Biol Evol 16:1799–1808

Lombard L, van der Merwe NA, Groenewald JZ, Crous PW (2015) Generic concepts in Nectriaceae. Stud Mycol 80:189–245

Maharachchikumbura SSN, Hyde KD, Gareth Jones EB, McKenzie EHC, Huang SK (2015) Towards a natural classification and backbone tree for Sordariomycetes. Fungal Divers 72:199–301

Maharachchikumbura SSN, Hyde KD, Gareth Jones EB, McKenzie EHC, Bhat JD (2016) Families of Sordariomycetes. Fungal Divers 79:1–317

Masudi S, Bonjar GHS (2012) Fulfillment of Koch's postulates for *in vitro* pathogenicity of *Musicillium theobromae* (turconi) Zare & Z. Gams as the cause of banana cigar end rot disease. J Plant Prot Res 52:410–414

Mazzaferro L, Piñuel L, Minig M, Breccia JD (2010) Extracellular monoenzyme deglycosylation system of 7-O-linked flavonoid beta-rutinosides and its disaccharide transglycosylation activity from *Stilbella fimetaria*. Arch Microbiol 192:383–393

Mostert L, Groenwald JZ, Summerbell RC, Gams W, Crous PW (2006) Taxonomy and pathology of *Togninia* (Diaporthales) and its *Phaeoacremonium* anamorphs. Stud Mycol 54:1–115

Nylander JAA (2004) MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Sweden

714 Perdomo H, Sutton DA, García D, Fothergill AW et al (2011) Spectrum of
715 clinically relevant *Acremonium* species in the United States. J Clin Microbiol
716 49:243–256
717
718 Réblová M, Gams W, Seifert KA (2011) *Monilochaetes* and allied genera of the
719 Glomerellales, and a reconsideration of families in the Microascales. Stud Mycol
720 68:163–191
721
722 Rehner SA, Buckley E (2005) A *Beauveria* phylogeny inferred from nuclear ITS
723 and EF-1alpha sequences: evidence for cryptic diversification and links to
724 *Cordyceps* teleomorphs. Mycologia 97:84–98
725
726 Rehner SA, Samuels GJ (1995) Molecular systematics of the Hypocreales: a
727 teleomorph gene phylogeny and the status of their anamorphs. Can J Bot
728 73:S816–S823
729
730 Ronquist F, Huelsenbeck JP (2003) MrBayes 3: Bayesian phylogenetic
731 inference under mixed models. Bioinformatics 19:1572–1574
732
733 Ronquist F, Teslenko M, van der Mark P, Ayres DL (2012) MrBayes 3.2:
734 efficient bayesian phylogenetic inference and model choice across a large
735 model space. Syst Biol 61:539–542
736
737 Schoch CL, Sung GH, López-Giráldez F, Townsend JP et al (2009) The
738 Ascomycota tree of life: a phylum wide phylogeny clarifies the origin and
739 evolution of fundamental reproductive and ecological traits. Syst Biol 58:224–
740 239
741
742 Seifert KA (1985) A monograph of *Stilbella* and some allied Hyphomycetes.
743 Stud Mycol 27:1–235
744
745 Shenoy BD, Jeewon R, Wu WP, Bhat DJ, Hyde KD (2006) Ribosomal and
746 *RPB2* DNA sequence analyses suggest that *Sporidesmium* and morphologically
747 similar genera are polyphyletic. Mycol Res 110:916–928

Sigler L, Zuccaro A, Summerbell RC, Mitchell JI, Paré JA (2004) *Acremonium exuviarum* sp. nov., a lizard-associated fungus with affinity to *Emericellopsis*. Stud Mycol 50:409–413

Spatafora JW, Sung GH, Johnson D, Hesse C et al (2006) A five-gene phylogeny of Pezizomycotina. Mycologia 98:1018–1028

Spatafora JW, Sung GH, Sung JM, Hywel-Jones NL, White JF Jr (2007) Phylogenetic evidence for an animal pathogen origin of ergot and the grass endophytes. Mol Ecol 16:1701–1711

Spegazzini C (1910) Mycetes Argentinenses (Series V). An. Mus. nac. Hist. nat. B. Aires. 20:329–467

Summerbell RC (2003) Ascomycetes: *Aspergillus, Fusarium, Sporothrix, Piedraia* and their relatives. In: Howard DH (ed.) Pathogenic fungi in humans and animals, 2nd edn. Marcel Dekker, New York, pp 237–498

Summerbell RC, Gueidan C, Schroers HJ, Hoog GS de et al (2011) *Acremonium* phylogenetic overview and revision of *Gliomastix*, *Trichothecium* and *Sarocladium*. Stud Mycol 68:139–162

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S (2013) MEGA 6: Molecular Evolutionary Genetics Analysis version 6.0. Mol Biol Evol 30:2725–2729

Thompson JD, Higgins DG, Gibson TJ (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res 22:4673–4680

780 Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of
781 enzymatically amplified ribosomal DNA from several *Cryptococcus* species. J
782 Bacteriol 172: 4238–4246
783
784 Vilgalys R, Sun BL (1994) Ancient and recent patterns of geographic speciation
785 in the oyster mushroom *Pleurotus* revealed by phylogenetic analysis of
786 ribosomal DNA sequences. Proc Natl Acad Sci 91(10):4599–4603
787
788 Weisenborn JLF, Kirschner R, Piepenbring M (2010) A new darkly pigmented
789 and keratinolytic species of *Acremonium* (Hyphomycetes) with relationship to
790 the Plectosphaerellaceae from human skin and nail lesions in Panama. Nova
791 Hedwigia 90:457–468
792
793 White TJ, Bruns T, Lee J, Taylor SB (1990) Amplification and direct sequencing
794 of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH,
795 Sninsky JJ, White TJ (eds) PCR Protocols: a guide to methods and
796 applications. Academic Press, San Diego, pp 315–322
797
798 Zare R, Gams W, Starink-Willemse M, Summerbell RC (2007) *Gibellulopsis*, a
799 suitable genus for *Verticillium nigrescens*, and *Musicillium*, a new genus for *V.*
800 *theobromae*. Nova Hedwigia 85:463–489
801
802 Zuccaro A, Summerbell RC, Gams W, Schoers HJ, Mitchell JI (2004) A new
803 *Acremonium* species associated with *Fucus* spp., and its affinity with a
804 phylogenetically distinct marine *Emericellopsis* clade. Stud Mycol 50:283–297
805

Figure legends

Fig. 1 Maximum composite likelihood tree based on analyses of partial LSU sequences of selected genera of the Hypocreales including *Acremonium* (abbreviated as *A.*), *Emericellopsis* (*E.*), *Gliomastix* (*G.*), *Leucosphaerina* (*L.*), *Linkosia* (*Li.*), *Niesslia* (*N.*), *Phialemonium* (*P.*), *Sarocladium* (*S.*) and *Stilbella* (*St.*). Clade names are based on Summerbell et al. (2011). Bootstrap support values above 70%/ Bayesian posterior probability values above 0.95 are shown at the nodes. ^{T}, Type strain. *Acremonium* sp. I represents newly described *A. moniliforme* and *Acremonium* sp. II, *A. dimorphosporum*

Fig. 2 Maximum composite likelihood tree based on sequences of ITS and partial protein encoding genes (*BT2, RPB2* and *TEF1-α*) of selected acremonium-like taxa of the Bionectriaceae. Bootstrap support values above 70 % / Bayesian posterior probability values above 0.95, are shown at the nodes. ^{T}, Type strain

Fig. 3 Maximum composite likelihood tree based on sequences of ITS and partial LSU genes from *A. dimorphosporum* and species of the *fusidioides* clade. Bootstrap support values above 70 % / Bayesian posterior probability values above 0.95, are shown at the nodes. ^{T}, Type strain

Fig. 4 Maximum composite likelihood tree based on analysis of ITS and partial LSU, *RPB2* and *TEF1-α* sequences of genera of the Plectosphaerellaceae and related genera. Bootstrap support values above 70 % / Bayesian posterior probability values above 0.95, are shown at the nodes. ^{T}, Type strain

Fig. 5 *Acremonium dimorphosporum* UTHSC 08-3639. **a** Colonies on OA, after 21 days at 25 ºC. **b**, **c** Simple conidiophores and conidia forming heads. **d**, **e** Phialides with percurrent proliferation (arrow). **f–h** Smooth-walled, ellipsoidal (f) and thick-walled, verrucose, ovoidal conidia (h). *Scale bars:* b–f = 10 µm, g, h = 5 µm

Fig. 6 *Acremonium moniliforme* FMR 11785. **a** Colonies on PDA after 14 days at 25 ºC. **b, c** Simple conidiophores arising laterally from ropes of hyphae. **d** Monilifom hyphae. **e** Phialide with periclinal thickening at the apex. **f, g** Conidia. *Scale bars* = 10 µm

Fig. 7 *Brunneomyces brunnescens* CBS 559.73. **a** Colonies on OA after 14 days at 25 ºC. **b** Brown pigmented hyphae. **c** Discrete phialides. **d** Phialides with slightly pigmented collarettes and conidial chains collapsing in slimy heads. **e** Sympodial conidiophore. **f** Conidia. *Scale bars* = 10 µm

Fig. 8 *Brunneomyces hominis* a–c, f, g UTHSC 06-415; d, e UTHSC R-3853. **a** Colonies on OA after 14 days at 25 ºC. **b**, **c** Colonies on PDA after 21 days at 25 ºC obverse and reverse, respectively. **d** Unbranched conidiophores. **e** Unbranched conidiophores with terminal polyphialides and a sympodial conidiophore (arrow). **f** Pigmented verrucose hyphae and intercalary phialide (arrow). **g** Conidia. *Scale bars* = 10 µm

Fig. 9 *Brunneomyces europaeus* a–c, f–h, k, l CBS 560.86; d, e, i, j CBS 652.96. **a** Colonies on OA after 14 days at 25 ºC. **b**, **c** Colonies on PDA after 14 days at 25 ºC obverse and reverse, respectively. **d**. Phialide producing a long conidial chain. **e** Pigmented verrucose hyphae. **f** Polyphialide. **g** Adelophialide. **h** Sympodial conidiophore. **i**, **j** Phialides with short cylindrical collarettes. **k**, **l** Conidia. *Scale bars* = 10 µm

Fig. 10 *Chordomyces albus* CBS 987.87. **a**, **b** Colonies on PDA and OA, respectively, after 14 days at 25 ºC. **c** Unbranched conidiophores. **d**, **e** Phialides with percurrent proliferations. **f**, **g, h** Phialides with cylindrical collarettes and conidia. *Scale bars* =10 µm