



## South Florida microfungi: a new species of *Taeniolella* (anamorphic Sordariomycetes) isolated from cabbage palm

Gregorio Delgado<sup>1,2\*</sup> and Andrew N. Miller<sup>3</sup>

<sup>1</sup> EMLab P&K Houston, 6310 Rothway St., Houston, TX 77040, U.S.A.

<sup>2</sup> Department of Mycology, Institute of Ecology, Evolution and Diversity, Goethe Universität Frankfurt, Max-von-Laue-Str. 13, 60438 Frankfurt am Main, Germany

<sup>3</sup> Illinois Natural History Survey, University of Illinois, 1816 South Oak St., Champaign, IL 61820, U.S.A.

With 2 figures

**Abstract:** *Taeniolella sabalicola* sp. nov., isolated from a petiole of a dead leaf of *Sabal palmetto* collected in south Florida, U.S.A., is described and illustrated based on morphological, cultural and molecular data. The fungus is characterized by forming slowly growing, black, restricted colonies on culture media and effuse colonies with abundant aerial mycelium on natural substrate after incubation, semi-macronematous or micronematous, long, unbranched conidiophores and clavate, ellipsoidal or cylindrical, smooth or verruculose, brown to blackish brown, multiseptate conidia with transverse, longitudinal and oblique septa, often surrounded by a mucilaginous sheath and usually in simple or branched acropetal chains. Phylogenetic analyses based on partial nuclear ribosomal large subunit (LSU) and internal transcribed spacer (ITS) sequence data also suggest the fungus is distinct from other *Taeniolella* species and possess affinities with members of Sordariomycetidae (Ascomycota) but its ordinal or familial position within the subclass remains uncertain. Molecular data also confirm that *Taeniolella* sensu lato is polyphyletic and show that *T. sabalicola* is unrelated to the generic type, *T. exilis*, recently placed in the family Kirschsteinietheliaceae within the class Dothideomycetes.

**Key words:** lichenicolous, *Peyronelia*, phylogeny, saprobic, taxonomy.

### Introduction

The genus *Taeniolella* S.Hughes, based on *T. exilis* (P.Karst.) S.Hughes as the type species, was first introduced by Hughes (1958) to accommodate fourteen anamorphs previously placed in several different genera and characterized by semi-macronematous, caespitose or scattered, usually short conidiophores, unbranched or sparingly branched

---

\*Corresponding author: gdelgado@emlabpk.com

near the base and bearing monoblastic, integrated, terminal, determinate, cylindrical or doliiform conidiogenous cells producing didymo- or phragmoconidia commonly in long, simple or branched acropetal chains that often secede with difficulty (Ellis 1971, Hawksworth 1979, Seifert et al. 2011). According to the MycoBank Database ([www.mycobank.org](http://www.mycobank.org)) *Taeniolella* currently comprises 51 validly published names of which Seifert et al. (2011) accepted about 37 taxa. They range from saprobic species on wood, bark, litter, other fungi or submerged plant material as well as many lichenicolous taxa, the saprobic ones usually having multiseptate conidia and the lichenicolous ones only (0–)1(–2)-septa (Nash et al. 2004). Also two species, *T. stilbospora* (Corda) S.Hughes and *T. exilis*, have been reported as human pathogens causing cutaneous lesions in the face of a human patient and subcutaneous phaeohyphomycosis, respectively (de Hoog et al. 2000). The majority of them are known only from their asexual state but teleomorph connections have been established for a very few taeniolella-like anamorphs (Minter & Holubová-Jechová 1981, Zelski et al. 2011). *Taeniolella* as currently circumscribed has been recognized as broadly defined (Gulis & Marvanová 1999) and polyphyly has been previously suggested based on indirect molecular and taxonomic evidence (Summerell et al. 2006, Zelski et al. 2011, Réblová et al. 2016). Recently, based on mitochondrial and nuclear ribosomal DNA sequence data, the generic type species was placed in the family Kirschsteinioteliaceae within the class Dothideomycetes (Ertz et al. 2016). Additionally, DNA of five novel or already described lichenicolous taxa was also sequenced and found to be restricted to the order Asterotexiales of the same class in a first comprehensive step toward resolving the highly polyphyletic status of the genus.

During studies of microfungi associated with dead leaves of cabbage palm trees collected in south Florida, a peculiar dematiaceous anamorph forming short acropetal chains of conidia was isolated following substrate incubation. Morphologically, the fungus showed a strong resemblance with *T. phialosperma* Ts. Watan., a species originally isolated from strawberry rhizosphere and paddy field soils in Japan (Watanabe 1992). Phylogenetic analyses of nuclear ribosomal DNA sequence data, however, revealed that they are not conspecific or even closely related and, along with micromorphological and cultural comparisons between this and other saprobic *Taeniolella* species, the Florida fungus is considered distinct and is described here as a new species.

## Materials and methods

**ISOLATION AND MORPHOLOGICAL STUDY:** Samples of dead leaves of *Sabal palmetto*, the cabbage palm, were collected in forested areas of north Broward County, southeastern Florida, U.S.A., during the winter of 2014. They were first washed off under running tap water to remove debris and spores of fast-growing contaminants. Then they were cut in smaller pieces for incubation at room temperature in a plastic container lined with moist paper towels followed by periodical examinations until development of reproductive structures. Conidia were transferred aseptically to 2% Malt Extract Agar (MEA: Healthlink, Jacksonville, Florida) and incubated at 25°C until sporulation was observed. Single-spore isolates were obtained according to Choi et al. (1999) and colonies originated from single conidia were subcultured on three different media: MEA, Potato Dextrose Agar (PDA) and Modified Cellulose Agar (MCA). Colony features were observed and measured on MEA and PDA after 28 days at 25°C for comparison with culture descriptions of the morphologically similar *T. phialosperma* (Watanabe 1992) but also on MCA after 2 months based on the slow growth in all media. Fungal structures from both natural substrate and cultures grown as above were mounted in

lactophenol-cotton blue for microscopic observation. Minimum, maximum, 5th and 95th percentiles were calculated after measurement of each structure (n=100) and outliers are shown in parentheses. The holotype specimen was air-dried and deposited in the Herbarium of the U.S. National Fungus Collections (BPI) along with semi-permanent slides and a dried culture. An isotype culture was also deposited at the Illinois Natural History Survey Fungarium (ILLS) and an ex-type culture is preserved in the Centraalbureau voor Schimmelcultures (CBS). A search for the type specimen of *Peyronelia sirodesmioides* in herbaria housing collections of R.Ciferri and R.Gonzalez-Fragoso (MA, L and W) was also conducted.

**DNA EXTRACTION, PCR AMPLIFICATION AND SEQUENCING:** A fungus isolate grown on MEA for 21 days at 25°C was sent to a sequencing facility, Laragen, Inc. (Culver City, California), where genomic DNA was extracted and the D1/D2 domains of the nuclear ribosomal 28S large subunit DNA (LSU nrDNA) were PCR amplified, purified and sequenced following the company's protocols for Fungal Identification Service (FunID [http://laragen.com/laragen\\_micro\\_fungal.html](http://laragen.com/laragen_micro_fungal.html)) using primers NL1-NL4 (O'Donnell 1993). The returned LSU sequences were checked and assembled using CAP3 Sequence Assembly program (Huang & Madan 1999) on the PRABI-Doua website (<http://doua.prabi.fr/software/cap3>). In the case of the ITS region the genomic DNA was extracted from a culture using a DNeasy® Mini Plant extraction kit (Qiagen Inc., Valencia, California) following the manufacturer's protocols and detailed methods used for PCR amplification and sequencing followed Promputtha & Miller (2010). ITS sequencing was then performed at the W.M.Keck Center at the University of Illinois Urbana-Champaign and the returned ITS sequences were assembled with Sequencher 5.1 (Gene Codes Corp, Ann Arbor, Michigan).

**PHYLOGENETIC ANALYSES:** The newly generated ITS and LSU nrDNA sequences were subjected to megablast searches in GenBank to first assess the phylogenetic position of *T. sabalicola*. The ITS sequence returned no close matches and therefore was not used for analysis. An LSU dataset was prepared including the closest matches and sequences of *Taeniolella* species belonging to the class Sordariomycetes retrieved from GenBank. They were subjected to megablast searches and closest hits or related taxa from previous phylogenies were also included (Crous et al. 2006, Réblová et al. 2012, 2016) along with representatives of Sordariomycetidae based on Réblová et al. (2015) and Untereiner et al. (2013). Two species of *Xylaria* (Xylariomycetidae) were used as outgroup. Sequences were aligned with MAFFT v. 7.245 (Katoh & Standley 2013) on the online server using the automatically selected L-INS-i strategy (Katoh et al. 2005). Alignment was visually checked and ambiguously aligned regions were removed with Gblocks online v. 0.91b (Castresana 2000, Talavera & Castresana 2007) using the less stringent selection parameters. Phylogenetic relationships were inferred by Maximum Likelihood (ML) analysis performed in MEGA v. 6.06 (Tamura et al. 2013) and Bayesian Inference (BI) implemented in MrBayes v. 3.2.2 (Ronquist & Huelsenbeck 2003, Ronquist et al. 2012). The best-fit substitution model as determined by MEGA using the corrected Akaike Information Criterion value was the General Time Reversible model with Gamma distributed rates plus invariant sites (GTR+G+I) and was used for both ML and BI. An initial BioNJ tree was automatically constructed and the Nearest-Neighbor-Interchange (NNI) algorithm was used as the ML heuristic method. Statistical support for internal branches was estimated by nonparametric bootstrapping (Felsenstein 1985) with 1000 replicates and bootstrap support (BS)  $\geq 70\%$  was considered significant (Hillis & Bull 1993). Bayesian analysis consisted of two independent runs of four Markov Chain Monte Carlo chains starting from different random trees and 10 million generations each with trees sampled every 100th generation. Standard deviation of split frequencies  $<0.01$  was set as a convergence diagnostic. The first 25% of trees were discarded as burn-in and a 50% majority rule consensus tree was constructed from the remaining trees to estimate posterior probabilities (BPP) for each node. Clades with BPP  $\geq 95\%$  were considered statistically significant and highly supported (Alfaro et al. 2003). Trees were finally viewed and edited with MEGA or FigTree v1.4.2 (Rambaut 2009) and refined using Inkscape ([inkscape.org](http://inkscape.org)).

## Results

Sequences of the entire ITS and partial LSU nrDNA were obtained and deposited in GenBank. The final LSU alignment consisted of 1082 characters and 50 sequences

representing 46 taxa including the outgroup. The ML analysis resulted in a single most likely tree (Fig. 1). The majority rule consensus tree of the 97,442 sampled trees resulting from the Bayesian analysis was nearly identical in topology (data not shown). *Taeniolella sabalicola* clusters in both trees with the only LSU sequence currently available of *Ellisembia leonensis* (M.B.Ellis) McKenzie on a single branch without significant BS support or BPP. They form an unsupported sister clade with members of Magnaporthales in the Sordariomycetes and group with species of *Barbatosphaeria* Réblová, *Xylomelasma sordida* Réblová and *Xylochrysis lucida* Réblová, V.Stepanek & R.K.Schumach., all non-stromatic perithecial ascomycetes, and the aero-aquatic fungus *Cancellidium applanatum* Tubaki, all incertae sedis within Sordariomycetidae. Molecular analyses also confirmed the polyphyletic status of *Taeniolella* at the subclass and ordinal levels with the genus split across two subclasses within Sordariomycetes: *T. phialosperma* and *T. alta* (Ehrenb.) S.Hughes were both placed in Sordariomycetidae within strongly supported clades belonging to the orders Sordariales (BS 99%, BPP 99%) and Diaporthales (BS 100%, BPP 100%), respectively. *Taeniolella rudis* (Sacc.) S.Hughes is placed on a long branch within the highly-supported Pleurotheciales clade (BS 100%, BPP 100%) in the subclass Hypocreomycetidae. This clade also includes the following accessions: *Pleurothecium recurvatum* (Morgan) Höhn. ( $\equiv$  *Carpoligna pleurothecii* F.A.Fernández & Huhndorf) JQ429235 & AF261070, *Pleurotheciella rivularia* Réblová, Seifert & J.Fourn. JQ429232, *P. centenaria* Réblová, Seifert & G.P.White JQ429234 and *Sterigmatobotrys macrocarpa* (Corda) S.Hughes GU017317 & GU017316.

## Taxonomy

*Taeniolella sabalicola* G.Delgado & A.N.Mill., **sp. nov.**

Fig. 2 A–H

MycoBank MB 818075

COLONIES on natural substrate effuse, black, forming a cottony, dense, gray aerial mycelium after incubation in moist chamber. MYCELIUM partly immersed and partly superficial, composed of smooth or finely roughened, septate, cylindrical or inflated, subhyaline to light brown or brown, branched hyphae, 2–4(–7)  $\mu$ m wide. CONIDIOPHORES semi-macronematous or micronematous, mononematous, arising terminally or laterally from the hyphae, solitary or caespitose, erect or ascending, straight or flexuous, cylindrical, unbranched, septate, smooth or finely roughened, light brown to brown, up to 530  $\mu$ m long, 2–3(–5)  $\mu$ m wide. CONIDIOGENOUS CELLS monoblastic, integrated, terminal, determinate, cylindrical or subcylindrical, sometimes inflated or doliiform, 5–11(–15)  $\times$  2.5–6  $\mu$ m, often arising directly on the hyphae. CONIDIA holoblastic, acrogenous, narrowly clavate to clavate or long clavate, ellipsoidal, narrowly cylindrical, cylindrical to subcylindrical or long cylindrical, straight or flexuous, euseptate, with 4–23(–29) transverse septa, 0–4 longitudinal septa and 0–3 oblique septa, sometimes slightly constricted at 1–2 transverse septa, smooth or verruculose, brown to blackish brown, sometimes reddish brown, often partially surrounded by a subhyaline mucilaginous sheath, solitary or catenate and forming simple, acropetal chains of 2–3(–5) conidia or branching laterally, each branch producing also short conidial

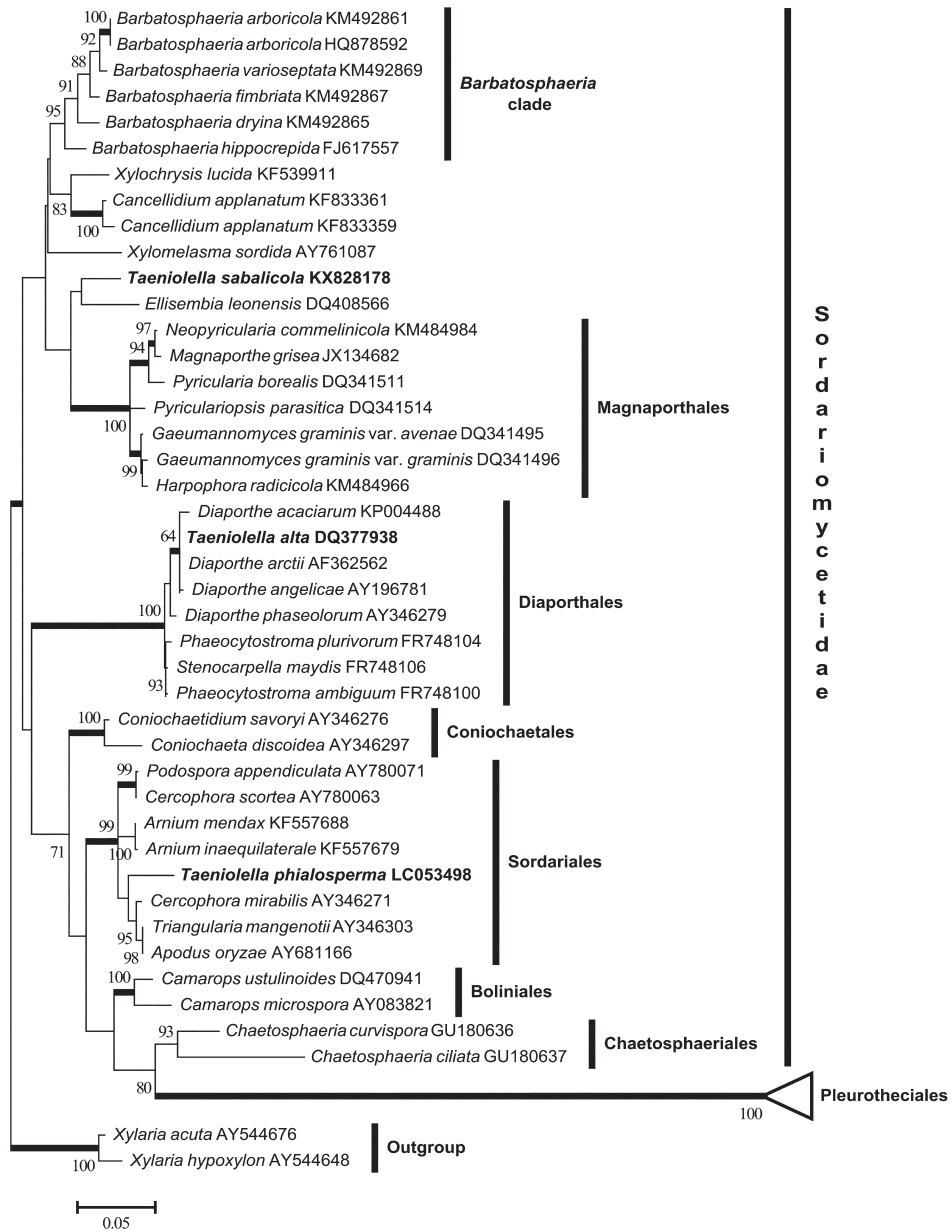
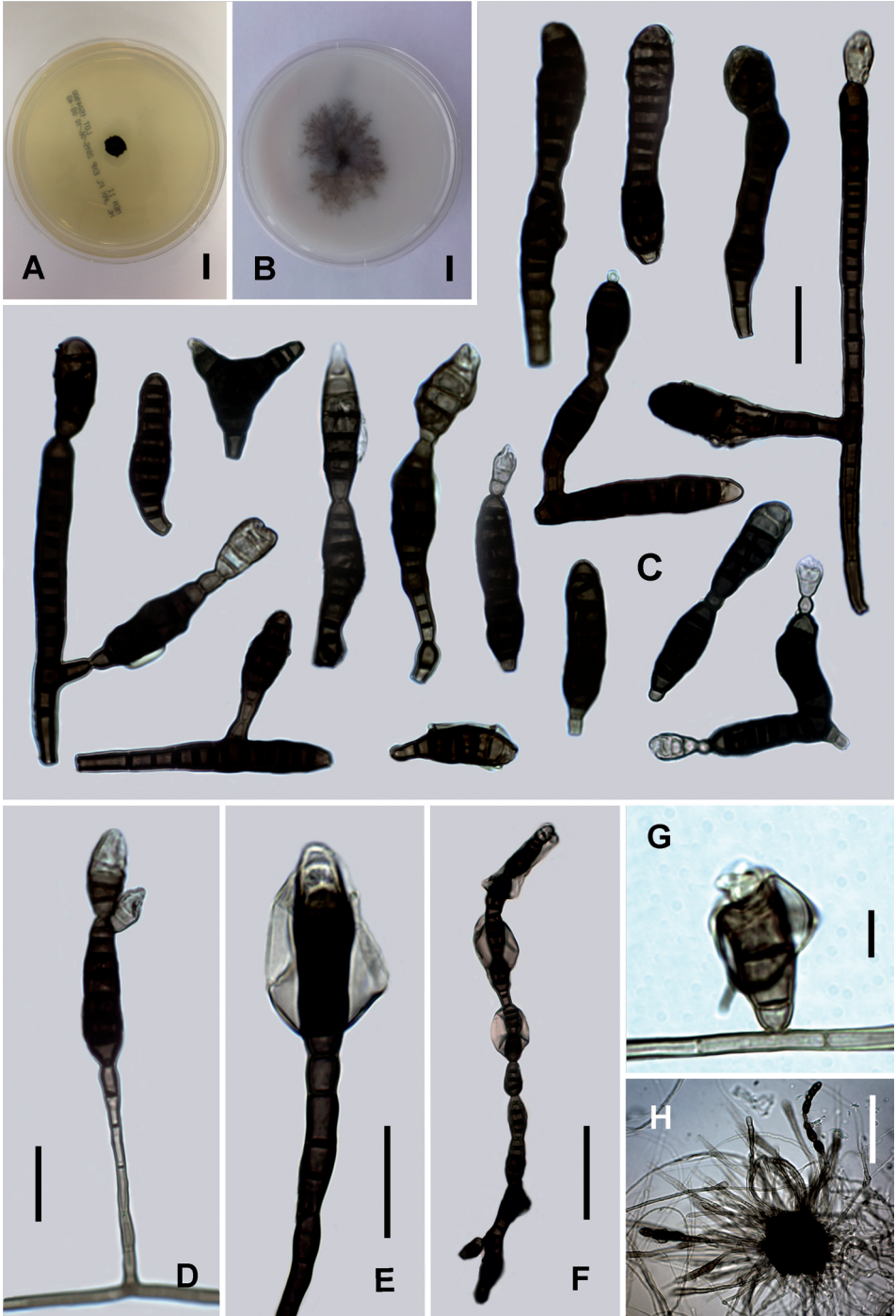


Fig. 1. Phylogenetic tree inferred from ML analysis (ln L = -6487.27) of selected LSU sequences belonging to Sordariomycetes showing the phylogenetic position of *T. sabalicola* within the class. Other *Taeniolella* species are marked in bold. The Pleurotheciales clade including *T. rudis* occurred on a long branch and was collapsed for space reasons. Bootstrap support values  $\geq 70\%$  are shown at the nodes and Bayesian posterior probabilities  $\geq 95\%$  are indicated by thickened branches.



chains, occasionally also bifurcating 1–2 times, 31–164(–185) × 6–11(–14) µm; apex often rounded, truncate or spatulate and paler, base truncate. TELEOMORPH unknown.

COLONIES on MEA slowly growing, reaching 6–11 mm diam. after 28 d at 25°C, black, compact, raised at center 1–3 mm, sometimes slightly sulcate, often with a small amount of gray aerial mycelium in the center, margin entire, submerged and cracking the medium or more or less irregular and diffuse, reverse black. COLONIES on PDA similar to MEA, slow growing, reaching 9–11 mm diam. after 28 d at 25°C, black, circular, flat or slightly raising in the center, also with a small amount of gray or black aerial mycelium, margin diffuse, reverse black. COLONIES on MCA reaching 25–48 mm diam. after 2 mo at 25°C, irregular, loosely cottony, gray, reverse not visible. CONIDIOPHORES similar to those on natural substrate, subhyaline to light brown or brown, up to 190 µm long on MEA and PDA, up to 780 µm long on MCA, 1–3(–4) µm wide. CONIDIA also similar to those on natural substrate, brown to dark brown on MEA and PDA, brown to blackish brown on MCA, 21–128(–140) × 5–11(–14) µm, (3–)6–21(–25) transverse septa, 0–2 longitudinal septa, 0–1(–3) oblique septa, forming longer chains of up to 10 conidia, also surrounded by a subhyaline to brown mucilaginous sheath more often as an spherical blob up to 45 µm diam. SCLEROTIAL BODIES produced on MEA and MCA cultures 2 mo or older, consisting of compact masses of hyphae, spherical, light brown to blackish brown, 36–103 µm diam.

ETYMOLOGY: Latin, *sabalicola*, referring to the host genus *Sabal* where the fungus was isolated.

SPECIMEN EXAMINED: United States, Florida, Broward Co., Fort Lauderdale, 26°12'20.5"N 80°09'50.6"W, 2.9 m asl., on petiole of dead leaf of *Sabal palmetto* (Walter) Lodd. ex Schult. & Schult., 25 January 2014, leg. J.M.Perez, holotype (BPI 892972A), isotype (ILLS 80642), ex-holotype strain (CBS 140346), ex-holotype sequences (ITS KX828179, LSU KX828178).

## Discussion

*Taeniolella sabalicola* fits well within the current broad generic concept of *Taeniolella* in having semi-macronematous or micronematous, unbranched conidiophores, monoblastic, determinate conidiogenous cells and phragmoconidia forming short, branched acropetal chains. Morphological and molecular data clearly support it as a new and distinct taxon within the genus. On the natural substrate the immersed mycelium is composed of thick-walled, brown hyphae with inflated cells up to 7 µm wide but the aerial hyphae are cylindrical, thinner and light brown to brown. Conidiophores on the substrate surface are short and frequently caespitose but after incubation and the subsequent formation of aerial mycelium over the fungus colonies they are very long,

Fig. 2. *Taeniolella sabalicola* (holotype). A. Colony on MEA after 28 days incubation at 25°C. B. Colony on MCA after 2 months incubation at 25°C. C. Conidia on natural substrate. D. Conidiophore, conidiogenous cell and conidia in chain on natural substrate. E. Detail of a conidium surrounded by a mucilaginous sheath on MCA. F. Conidia in long chain on MEA. G. Young conidium born on the hyphae. H. Sclerotial body and conidia on MCA. Scale bars A, B = 1 cm, C, D, E = 20 µm, F, H = 50 µm, G = 5 µm.

erect, developing solitarily and arising laterally or terminally from the aerial hyphae. Similarly, conidiophores developed in culture on the colony surface or from immersed hyphae were comparatively shorter than those developed from the aerial mycelium, especially in MCA where the colony was cottony, with abundant aerial mycelium and very long conidiophores. On MEA and PDA colonies were restricted and compact. Terminal conidiophores are often formed gradually at the tip of the hyphae, becoming darker and thicker-walled until a long, narrowly cylindrical conidium is formed, the basal part of it is usually hard to distinguish from the remaining conidiophore.

Conidia on natural substrate are usually in short chains of two or three, rarely five, but in artificial media chains were longer and composed of up to 10 conidia, usually shorter in length when in long chains. Nevertheless, constrictions along the conidia are not distinct enough to distinguish whether they separate different conidia or are merely constrictions within a conidium. Slender, subhyaline to light brown cells sometimes appeared between conidia, or some cells are wider and darker along the conidial length that could be interpreted as a different conidium in the chain, especially on MEA. Conidia can branch even in early developmental stages on one side and sometimes bifurcate later once or twice, each branch being able to produce a new conidium or a small conidiogenous cell that also produces a new conidium. The apex or the conidial body or both are often surrounded by a mucilaginous sheath that in culture media often turns into a distinctive mucoid sphere, brown and stiff in appearance when conidia arise from the aerial mycelium or the colony surface, probably due to desiccation. A chain consisting of a few conidia can have up to three of these blobs (Fig. 2 F) or even a single conidium can have two of them. Conidiogenous cells can arise directly on the aerial hyphae and produce short, sessile conidia or the conidia can often arise directly on the hyphae as well. In general the fungus behaves more or less similarly under natural and artificial conditions but sometimes subhyaline, two to five or conglomerates of several, more or less spherical cells were formed at the apex of conidia immersed or developed right on top of the medium surface as an apparent artifact of culture growth not seen on natural substrate. Brown to dark brown sclerotial bodies comprising densely packed hyphal masses were also found immersed in old cultures and surrounded by short, few-celled, mostly clavate, subhyaline to light-brown or brown conidia (Fig. 2 H).

Among saprobic species of *Taeniolella* with multiseptate conidia, *T. sabalicola* morphologically resembles *T. phialosperma* (Watanabe 1992, Matsushima & Matsushima 1995) in having semi-macronematous, long conidiophores and brown to dark brown, clavate, ellipsoidal or cylindrical, relatively large conidia in chains of similar number that can be simple or branched and are often completely or partially surrounded by a mucilaginous sheath. This is a thermotolerant fungus known so far from soils across eastern Asia and with affinities to the Sordariales (Liang et al. 2011, Réblová et al. 2016). Ertz et al. (2016) proposed its exclusion from *Taeniolella* based on unusual morphological features and its phylogenetic position unrelated to the generic type species. An LSU sequence (LC053498) derived from an ex-type culture of *T. phialosperma* (FFPRI TW 73-466) grouped distantly from *T. sabalicola* despite their morphological similarities. *Taeniolella phialosperma* also differs in having larger conidia ( $35\text{--}315 \times 9\text{--}26 \mu\text{m}$ ) with up to 32-transverse septa, very rarely a longitudinal



septum and the presence of a phialophora-like synanamorph with simple or branched, often verticillate conidiophores, phialides with a conspicuous collarette and hyaline or subhyaline, globose, smooth, 1-celled conidia. Its colonies on PDA are also different, dark yellowish green at first, later becoming dark gray in color, often covered with a golden yellow aerial mycelium and reaching 48–55 mm after 28 days at 25 °C (Watanabe 1992).

In our phylogeny the closest relative of *T. sabalicola* was *Ellisembia leonensis* (Ellis 1958, McKenzie 1995, Wu & Zhuang 2005), a morphologically different sporidesmium-like anamorph of uncertain placement within the class (Shenoy et al. 2006) with macronematous conidiophores that proliferate percurrently up to three times and solitary, fusiform, 9–17-distoseptate conidia. The poorly supported relationship between these two taxa and with members of Magnaporthaceae as well as other Sordariomycetidae incertae sedis may require a more extensive taxon sampling and the use of additional molecular markers to further resolve their phylogenetic relationships. The remaining two *Taeniolella* species used for analysis, *T. alta* and *T. rudis*, did not show a close relationship with *T. sabalicola* but grouped within two other strongly supported clades in Sordariomycetidae and Hypocreomycetidae, respectively. *Taeniolella alta* showed affinities with members of Diaporthales as previously seen in a peripheral study aiming to resolve phylogenetic lineages within the family Botryosphaeriaceae (Crous et al. 2006). Ertz et al. (2016) recently questioned the reliability of that sequence because the source culture failed to sporulate and the morphological features of *T. alta* strongly differ from those of diaporthaceous fungi. Consequently, further specimens will be necessary to clarify the phylogenetic placement of this species. *Taeniolella rudis*, on the other hand, nested in a fully supported clade with *Sterigmatobotrys macrocarpa* as previously seen in phylogenetic studies including both taxa (Réblová et al. 2012, 2016). This is a dematiaceous hyphomycete with macronematous conidiophores terminating in penicillate heads and hyaline, 2–3-septate conidia which has repeatedly been reported as the synanamorph of *T. rudis* (Hughes 1980b, Gareth-Jones et al. 2002). They grouped together with members of *Pleurothecium* Höhn. and *Pleurotheciella* Réblová, Seifert & J.Fourn. within the recently established order Pleurotheciales belonging to Hypocreomycetidae (Réblová et al. 2016). Both of these genera include holomorphic ascomycete taxa whose perithecial, chaetosphaeria-like teleomorphs are morphologically similar to the recently discovered teleomorph of *S. macrocarpa* (Réblová & Seifert 2011). Ertz et al. (2016) transferred *T. rudis* to *Sterigmatobotrys* based on similar results and its distant phylogenetic position from *T. exilis*, the type species of *Taeniolella*, but retained it as distinct from *S. macrocarpa* due to morphological differences. Although a MycoBank number is available for the name *S. rudis*, the combination was not publicly released at the moment of submitting this paper and, therefore, was not used here.

Additionally, *Taeniolella stilbospora* (Corda) S.Hughes (Ellis 1971, Melnik 2000) is also morphologically comparable to *T. sabalicola* in having caespitose conidiophores on natural substrate and long, cylindrical, straight or flexuous, brown, smooth, up to 24-septate conidia similar in size and rounded at the apex, some conidial cells producing one or two lateral branches in culture (de Hoog et al. 2000). No LSU sequence of *T. stilbospora* is currently available in GenBank but megablast searches of ITS and SSU

sequences annotated under that name, AY843127 and AY843258, respectively, reveal that *T. stilbospora* has phylogenetic affinities with members of Dothideomycetes. Summerell et al. (2006) placed it within Botryosphaeriaceae based on the ITS sequence mentioned above and therefore, despite their morphological similarities, this species is phylogenetically distant from *T. sabalicola*. Similarly, *T. typhoides* Gulis & Marvanová, known from submerged decaying leaves of *Nuphar lutea* (L.) Smith in Belarus (Gulis & Marvanová 1999), also has lateral or terminal, simple, sometimes extremely long conidiophores, cylindrical, rounded at the apex, multiseptate conidia in short acropetal chains that can arise directly from the hyphae and produce sclerotial bodies similar in size on MEA after several months of incubation under water. Shearer et al. (2009) revealed that *T. typhoides* is related with members of Lindgomycetaceae, a family of freshwater ascomycetes in the Pleosporales (Dothideomycetes), and therefore is unrelated to *T. sabalicola* in the Sordariomycetes. Additionally, conidia are longer and more septate in culture and natural substrate, having a length up to 470 µm and up to 60 septa in the latter, and rarely possess oblique septa.

Moreover, a tentative placement of *T. sabalicola* in *Peyronelia* Cif. & Gonz.Frag. was also considered based on the strong similarity with the anamorph of *Glyphium leptothecium* (Earle) B.Sutton [= *G. corrugatum* (Ellis) Goree] and to a lesser extent with anamorphic *G. schizosporum* (Maire) H.Zogg (Sutton 1970) and *G. grisonense* Math. (Mathiassen 1993). The three species of *Glyphium* with a peyronelia-like anamorph possess ascospores that disarticulate into part-spores before maturity while still within the ascus. They were traditionally included in Mytiliniaceae (Mytiliniales, Dothideomycetes) but were recently placed in Patellariales based on multigene sequence data analyses (Boehm et al. 2015). Sutton (1970) tentatively assigned their anamorphs to the genus *Peyronelia* based on a comparable morphology with the type species, *P. sirodesmioides* Cif. & Gonz.Frag. (Ciferri & Gonzalez-Fragoso 1927, Hughes 1958), and the acropetal development of conidia at a moment when different morphs of a pleomorphic fungus were allowed formal separate names, a practice not allowed today under the provisions of the current code (McNeill et al. 2012). They form long, multiseptate, irregularly verruculose conidia in acropetal chains similar in size, shape and color to *T. sabalicola*, even the distinction between individual conidia in the chains is difficult. The conidia of *G. leptothecium* usually have one or two longitudinal or oblique septa and occur in branched chains, while those of *G. schizosporum* and *G. grisonense* are in unbranched chains with none or occasionally a longitudinal septum (Sutton 1970, Mathiassen 1993, Boehm et al. 2015). However, the disparate phylogenetic affinities between them and *T. sabalicola* and the obscure status of the members of *Peyronelia* precluded placement in this genus despite their close morphological resemblance. Attempts to locate the type specimen of *P. sirodesmioides* in different herbaria were unsuccessful and it is probably lost.

The polyphyletic status of *Taeniolella* was previously realized (Summerell et al. 2006, Zelski et al. 2011, Réblová et al. 2016) based on accumulated evidence from molecular studies of different taxonomic groups including the few saprobic species with available DNA sequence data (Crous et al. 2006, Shearer et al. 2009, Liang et al. 2011, Réblová et al. 2012), or inferred from distantly related ascomycetous fungi with taeniolella-like anamorphs (Minter & Holubová-Jechová 1981, Wijayawardene

et al. 2012, Zelski et al. 2011). Some species were previously transferred to or synonymized with members of other genera e.g. *Anavirga* B.Sutton (Kirk 1983), *Cladophialophora* Borelli (de Hoog et al. 1995), *Corynespora* Güssow (Heuchert & Braun 2006), *Polydesmus* Mont. (Shoemaker & Hambleton 2001) and *Taeniolina* M.B.Ellis (Kirk 1981) but the genus still remained heterogeneous. Recently Ertz et al. (2016), in a phylogenetic reassessment of the genus with emphasis on lichenicolous taxa, confirmed that *Taeniolella* is strongly polyphyletic with its members scattered throughout different classes (i.e. Sordariomycetes and Dothideomycetes). *Taeniolella exilis*, the type species, was recovered as a member of the family Kirschsteinietheliaceae within Dothideomycetes, and five other lichenicolous taxa were found to be confined to the order Asterotexiales in the Dothideomycetes. Based on the rather preliminary knowledge about the phylogenetic relationships among members of the genus and the lack of molecular data for the majority of taxa, they refrained to propose new generic changes and preferred to provisionally retain *Taeniolella* in a broad sense until more data becomes available, a criterion followed here as well to accommodate *T. sabalicola*.

### Acknowledgments

We would like to thank Bettina Heuchert (Martin-Luther-Universität Halle-Wittenberg) for serving as a pre-submission reviewer, José M. Pérez (University of Florida, U.S.A.) for collecting the source material for this work, Sayaka Ban (NBRC, Japan) for kindly depositing the ITS-LSU sequences from the ex-type strain of *T. phialosperma* in GenBank and G. Mathiassen (TROM, Norway) for providing relevant literature. We are grateful to the curators of MA, W and L for searching the type specimen of *P. sirodesmioides* in their collections. Kamash Ramanathan and Malcolm Moody (EMLab P&K) are acknowledged for the provision of laboratory facilities and financial support.

### References

- ALFARO, M.E., S. ZOLLER & F. LUTZONI 2003: Bayes or Bootstrap? A simulation study comparing the performance of Bayesian Markov Chain Monte Carlo sampling and bootstrapping in assessing phylogenetic confidence. – *Mol. Biol. Evol.* **20**: 255–266.
- BOEHM, E.W., G. MARSON, G.H. MATHIASSEN, A. GARDIENNET & C.L. SCHOCH 2015: An overview of the genus *Glyphium* and its phylogenetic placement in Patellariales. – *Mycologia* **107**: 607–618.
- CASTRESANA, J. 2000: Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. – *Mol. Biol. Evol.* **17**: 540–552.
- CHOI, Y.W., K.D. HYDE & W.H. HO 1999: Single spore isolation of fungi. – *Fungal Divers.* **3**: 29–38.
- CIFERRI, R. & R. GONZALEZ-FRAGOSO 1927: Hongos parasitos y saprofitos de la Republica Dominicana (12.a Serie). – *Bol. R. Soc. Esp. Hist. Nat.* **27**: 323–334.
- CROUS, P.W., B. SLIPPERS, M.J. WINGFIELD, J. RHEEDER, W.F.O. MARASAS et al. 2006: Phylogenetic lineages in the Botryosphaeriaceae. – *Stud. Mycol.* **55**: 235–253.
- DE HOOG, G.S., J. GUARRO, J. GENE & M.J. FIGUERAS 2000: Atlas of Clinical Fungi. 2<sup>nd</sup> ed. – Centraalbureau voor Schimmelcultures, Utrecht/Universitat Rovira i Virgili, Reus.
- DE HOOG, G.S., E. GUÉHO, F. MASCLAUX, A.H.G. GERRITS VAN DEN ENDE, K.J. KWON-CHUNG et al. 1995: Nutritional physiology and taxonomy of human-pathogenic *Cladosporium-Xylohypha* species. – *J. Med. Vet. Mycol.* **33**: 339–347.

- ELLIS, M.B. 1958: *Clasterosporium* and some allied Dematiaceae-Phragmosporae I. – Mycol. Pap. **70**: 1–89.
- ELLIS, M.B. 1971: Dematiaceous Hyphomycetes. – Commonwealth Mycological Institute, Kew.
- ERTZ, D., B. HEUCHERT, U. BRAUN, C.E. FREEBURY, R.S. COMMON et al. 2016: Contribution to the phylogeny and taxonomy of the genus *Taeniolella*, with a focus on lichenicolous taxa. – Fungal Biology, doi: 10.1016/j.funbio.2016.05.008. In press, corrected proof.
- FELSENSTEIN, J. 1985: Confidence limits on phylogenies: an approach using the bootstrap. – Evolution **39**: 783–791.
- GARETH-JONES, E.B., R.A. EATON & S. SOMRITHIPOL 2002: *Taeniolella rudis* and *Taeniolella longissima* sp. nov. with secondary sympodioconidia from freshwater habitats. – Mycoscience **43**: 201–206.
- GULIS, V. & L. MARVANOVÁ 1999: Three new scolecosporous hyphomycetes from waters in Belarus. – Mycotaxon **72**: 237–250.
- HAWKSWORTH, D.L. 1979: The lichenicolous hyphomycetes. – Bull. Brit. Mus. Nat. Hist. Bot. **6**: 183–300.
- HEUCHERT, B. & U. BRAUN 2006: On some dematiaceous lichenicolous hyphomycetes. –Herzogia **19**: 11–21.
- HILLIS, D.M. & J.J. BULL 1993: An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. – Syst. Biol. **42**: 182–192.
- HUANG, X. & A. MADAN 1999: CAP3: A DNA sequence assembly program. – Genome Res. **9**: 868–877.
- HUGHES, S.J. 1958: Revisiones hyphomycetum aliquot cum appendice de nominibus rejiciendis. – Can. J. Bot. **36**: 727–836.
- HUGHES, S.J. 1980b: *Taeniolella rudis*. – Fungi Canadenses **185**: 1–2.
- KATOH, K. & D.M. STANDLEY 2013: MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. – Mol. Biol. Evol. **30**: 772–780.
- KATOH, K., K. KUMA, H. TOH & T. MIYATA 2005: MAFFT version 5: improvement in accuracy of multiple sequence alignment. – Nucleic Acids Res. **33**: 511–518.
- KIRK, P.M. 1981: New or interesting microfungi I. Dematiaceous hyphomycetes from Devon. – Trans. Br. mycol. Soc. **76**: 71–87.
- KIRK, P.M. 1983: New or interesting microfungi X. Hyphomycetes on *Laurus nobilis* leaf litter. – Mycotaxon **18**: 259–298.
- LIANG, Y., F. WANG, A.N. LI & D.C. LI 2011: Thermotolerant fungi and their phylogenetic analyses based on rDNA-ITS sequences. – Mycosystema **30**: 542–550.
- MATSUSHIMA, K. & T. MATSUSHIMA 1995: Fragmenta Mycologica-I. – Mat. Mycol. Mem. **8**: 45–54.
- MATHIASSEN, G. 1993: Corticolous and lignicolous Pyrenomycetes s. lat. (Ascomycetes) on *Salix* along a mid-Scandinavian transect. – Sommerfeltia **20**: 1–180.
- MCNEILL, J., F.R. BARRIE, W.R. BUCK, V. DEMOULIN, W. GREUTER et al. (eds.) 2012: International Code of Nomenclature for algae, fungi, and plants (Melbourne Code) adopted by the Eighteenth International Botanical Congress Melbourne, Australia, July 2011. <http://www.iapt-taxon.org/nomen/main.php> Last accessed September 2015.
- MCKENZIE, E.H.C. 1995: Dematiaceous hyphomycetes on Pandanaceae. 5. *Sporidesmium* sensu lato. – Mycotaxon **56**: 9–29.

- MELNIK, V.A. 2000: Definitorium fungorum Rossiae. Classis Hyphomycetes. Fasc. 1. Fam. Dematiaceae. – Nauka, St. Petersburg.
- MINTER, D.W. & V. HOLUBOVÁ-JECHOVÁ 1981: New or interesting hyphomycetes on decaying pine litter from Czechoslovakia. – *Folia Geobot. Phytotaxon.* **16**: 195–217.
- NASH, T.H., B.D. RYAN, P. DIEDERICH, C. GRIES & F. BUNGARTZ (eds.) 2004: Lichen Flora of the Greater Sonoran Desert Region. Volume II. – Lichens Unlimited, Tempe.
- O'DONNELL, K. 1993. *Fusarium* and its near relatives. – In: REYNOLDS D.R. & J.W. TAYLOR (eds.): The fungal holomorph: mitotic, meiotic and pleomorphic speciation in fungal systematic, pp. 225–233. – CAB International, Wallingford.
- PROMPUTTHA, I. & A.N. MILLER 2010: Three new species of *Acanthostigma* (Tubeufiaceae, Dothideomycetes) from Great Smoky Mountains National Park. – *Mycologia* **102**: 574–587.
- RAMBAUT, A. 2009: FigTree v1.4: Tree Figure Drawing Tool. <http://tree.bio.ed.ac.uk/software/figtree/>
- RÉBLOVÁ, M., K. RÉBLOVÁ & V. ŠTĚPÁNEK 2015: Molecular systematics of *Barbatosphaeria* (Sordariomycetes): multigene phylogeny and secondary ITS structure. – *Persoonia* **35**: 21–38.
- RÉBLOVÁ, M. & K.A. SEIFERT 2011: Discovery of the teleomorph of the hyphomycete, *Sterigmatobotrys macrocarpa*, and epitypification of the genus to holomorphic status. – *Stud. Mycol.* **68**: 193–202.
- RÉBLOVÁ, M., K.A. SEIFERT, J. FOURNIER & V. STEPÁNEK 2012: Phylogenetic classification of *Pleurothecium* and *Pleurotheciella* gen. nov. and its dactylaria-like anamorph (Sordariomycetes) based on nuclear ribosomal and protein-coding genes. – *Mycologia* **104**: 1299–1314.
- RÉBLOVÁ M., K.A. SEIFERT, J. FOURNIER & V. STEPÁNEK 2016: Newly recognised lineages of perithecial ascomycetes: the new orders Conioscyphales and Pleurotheciales. – *Persoonia* **37**: 57–81.
- RONQUIST, F. & J.P. HUELSENBECK 2003: MrBayes 3: Bayesian phylogenetic inference under mixed models. – *Bioinformatics* **19**: 1572–1574.
- RONQUIST, F., M. TESLENKO, P. VAN DER MARK, D.L. AYRES, A. DARLING et al. 2012: MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. – *Syst. Biol.* **61**: 539–542.
- SEIFERT, K., G. MORGAN-JONES, W. GAMS & B. KENDRICK 2011: The genera of hyphomycetes. – CBS-KNAW Fungal Biodiversity Centre, Utrecht.
- SHEARER, C.A., H.A. RAJA, A.N. MILLER, P. NELSON, K. TANAKA et al. 2009: The molecular phylogeny of freshwater Dothidiomycetes – *Stud. Mycol.* **64**: 145–153.
- SHENOY, B.D., R. JEEWON, W.P. WU, D.J. BHAT & K.D. HYDE 2006: Ribosomal and RPB2 DNA sequence analyses suggest that *Sporidesmium* and morphologically similar genera are polyphyletic. – *Mycol. Res.* **110**: 916–928.
- SHOEMAKER, R.A. & S. HAMBLETON 2001: "*Helminthosporium*" *asterinum*, *Polydesmus elegans*, *Imimyces*, and allies. – *Can. J. Bot.* **79**: 592–599.
- SUMMERELL, B.A., J.Z. GROENEWALD, A. CARNEGIE, R.C. SUMMERBELL & P.W. CROUS 2006: *Eucalyptus* microfungi known from culture. 2. *Alysiidiella*, *Fusculina* and *Phlogicylindrium* genera nova, with notes on some other poorly known taxa. – *Fungal Divers.* **23**: 323–350.
- SUTTON, B.C. 1970: *Glyphium leptotheций* (Earle) comb. nov., *G. schizosporum* (Maire) Zogg, and their imperfect states. – *Trans. Br. mycol. Soc.* **54**: 255–264.
- TALAVERA, G. & J. CASTRESANA 2007: Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. – *Syst. Biol.* **56**: 564–577.

- TAMURA, K., G. STECHER, D. PETERSON, A. FILIPSKI & S. KUMAR 2013: MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. – Mol. Biol. Evol. **30**: 2725–2729.
- UNTEREINER, W.A., M. BOGALE, A. CARTER, H.W. BUD PLATT, S.Å. HANSON et al. 2013: Molecular phylogeny of Boliniales (Sordariomycetes) with an assessment of the systematics of *Apiorhynchostoma*, *Endoxyla* and *Pseudovalsaria*. – Mycologia **105**: 564–588.
- WATANABE, T. 1992: *Taeniolella phialosperma* sp. nov. from Japan. – Mycologia **84**: 478–483.
- WIJAYAWARDENE, D.N.N., E.H.C. MCKENZIE & K.D. HYDE 2012: Towards incorporating anamorphic fungi in a natural classification – checklist and notes for 2011. – Mycosphere **3**: 157–228.
- WU, W.P. & W. ZHUANG 2005: *Sporidesmium*, *Endophragmiella* and related genera from China. – Fungal Diversity Press, Hong Kong.
- ZELSKI, S.E., H.A. RAJA, A.N. MILLER & C.A. SHEARER 2011: *Chaetorostrum quincemilensis*, gen. et sp. nov., a new freshwater ascomycete and its *Taeniolella*-like anamorph from Peru. – Mycosphere **2**: 593–600.

Manuscript submitted October 16, 2015; accepted October 6, 2016.