Three new genera representing novel lineages of Sordariomycetidae (Sordariomycetes, Ascomycota) from tropical freshwater habitats in Costa Rica

Astrid Ferrer¹

Department of Plant Biology, University of Illinois, Room 265 Morrill Hall, 505 South Goodwin Avenue, Urbana, Illinois 61801

Andrew N. Miller

Illinois Natural History Survey, University of Illinois, 1816 South Oak Street, Champaign, Illinois 61820

Carolina Sarmiento

Universidad de los Andes, Cra. 1 No. 18A-10, Bogotá, Colombia

Carol A. Shearer

Department of Plant Biology, University of Illinois, Room 265 Morrill Hall, 505 South Goodwin Avenue, Urbana, Illinois 61801

Abstract: Three new genera are established in the Sordariomycetidae based on morphological and molecular data (SSU and LSU nrDNA) to accommodate five ascomycete species collected from submerged woody debris in freshwater habitats from Costa Rica. The genus Bullimyces contains three new species, B. communis, B. costaricensis and B. aurisporus. Bullimyces is characterized by globose to subglobose, membranous, black, ostiolate ascomata; deliquescent, hyaline, globose cells that fill the center of the centrum; unitunicate asci that deliquesce early in some species; and septate, thick-walled ascospores with or without gelatinous sheaths or appendages. Bullimyces species form a well supported clade with 100% bootstrap support, but the position of the genus in the Sordariomycetidae remains unclear. The second genus, Riomyces, is represented by a single species, R. rotundus. Riomyces is characterized by globose to subglobose, membranous, black, ostiolate ascomata, unitunicate, cylindrical asci, hyaline, globose cells that fill the hamathecium and septate, thick-walled ascospores with a gelatinous sheath. Although Riomyces is morphologically similar to Bullimyces, the two genera did not group together with support in any analysis. The third genus, Hydromelitis, is represented by a single species, H. pulchella. Hydromelitis is characterized by pyriform, membranous, black, ostiolate ascomata, unitunicate asci lacking an apical structure, simple, thin-walled, septate paraphyses and hyaline to golden yellow,

multiseptate, thick-walled ascospores with a gelatinous sheath. *Bullimyces*, *Riomyces* and *Hydromelitis* were nested within an unsupported clade consisting of members of the Ophiostomatales, Magnaporthales and freshwater Annulatacaceae sensu lato and sensu stricto.

Key words: aquatic, ascomycetes, fungal systematics, LSU, phylogenetics, SSU

INTRODUCTION

Aquatic ascomycetes are microscopic, saprobic fungi that colonize and decompose submerged substrates in freshwater and marine habitats. At present 278 freshwater and 275 marine species have been reported in the Sordariomycetes from aquatic habitats (Jones et al. 2009, http://fungi.life.illinois.edu/) and all the major lineages contain aquatic species (Zhang et al. 2006). Aquatic species share several morphological characters including the presence of elaborate gelatinous ascospore sheaths and appendages, which presumably function in attaching spores to substrates in water (Shearer 1993; Jones 1994, 2006). Phylogenetic studies have shown that these orders have evolved independently from terrestrial ancestors (Spatafora et al. 1998, Vijaykrishna et al. 2006). The position of various genera remains incertae sedis at the ordinal level as new species from the tropics are described. During a comparative survey across four sites in Costa Rica, we found five new species of freshwater ascomycetes representing three new genera. The genus Bullimyces contains three new species, B. communis, B. costaricensis and B. aurisporus, the genus *Riomyces* is based on a single species, R. rotundus, and Hydromelitis is represented by a single species, H. pulchella. We provide a description of these species and use both morphological and molecular sequence data from partial 18S small subunit (SSU) and 28S large subunit (LSU) nuclear ribosomal DNA to determine their placement as novel freshwater Sordariomycetidae lineages.

MATERIALS AND METHODS

Collection, isolation and morphological examination.—Methods for the collection, isolation and morphological examination of specimens are presented in Ferrer and Shearer (2005). Specimens are deposited in the Fungarium of the University of Illinois at Urbana-Champaign (ILL).

Molecular study.—Fungal mycelia were removed from cultures grown on potato dextrose agar (PDA, Difco) and ground in liquid nitrogen. DNA was extracted with the

Submitted 6 Apr 2011; accepted for publication 16 Dec 2011.

¹Corresponding author. E-mail: aferrer@life.uiuc.edu

TABLE I. Strains used in this study, their origin and GenBank accession nun	Table I.	Strains used	in this study,	their origin an	d GenBank accession	numbers
---	----------	--------------	----------------	-----------------	---------------------	---------

Taxa	Isolate number	Origin	SSU	LSU
Bullimyces aurisporus	AF316-1a	Costa Rica: Alajuela	JF758615	
Bullimyces aurisporus	AF316-1b	Costa Rica: Alajuela	JF758614	JF775590
Bullimyces communis	AF281-3	Costa Rica: Heredia	JF758617	JF775585
Bullimyces communis	AF281-4	Costa Rica: Alajuela	JF758618	JF775586
Bullimyces communis	AF281-5	Costa Rica: Alajuela	JF758619	JF775587
Bullimyces costaricensis	AF317-1a	Costa Rica: Limon		JF775591
Bullimyces costaricensis	AF317-1b	Costa Rica: Limon	JF758616	JF775592
Hydromelitis pulchella	AF284-2	Costa Rica: Alajuela	JF758613	JF775588
Riomyces rotundus	AF303-1	Costa Rica: Heredia	JF758612	JF775589

DNeasy Plant Mini Kit (QIAGEN Inc., Valencia, California) according to the kit's instructions. Fragments of SSU and LSU were PCR amplified with PureTaqTM Ready-To-Go PCR beads (Amersham Bioscience Corp., Piscataway, New York) according to Promputtha and Miller (2010). Primers NS1 and NS4 (White et al. 1990) for SSU and LROR and LR6 for LSU (Rehner and Samuels 1994, Vilgalys and Hester 1990) were used for PCR amplification. PCR products were purified with the QIAquick PCR purification kit (QIAGEN Inc., Valencia, California) and subsequently used in 11 µL sequencing reactions with BigDye® Terminators 3.1 (Applied Biosystems, Foster City, California) and primers NS1, NS2, NS3 and NS4 for SSU and LROR, LR3, LR3R and LR6 for LSU. Sequences were generated at the University of Illinois Biotechnology Center using an ABI 3730XL highthroughput automated sequencer. Sequences were assembled and edited manually in Sequencher 4.7 (Gene Codes Corp. 1991).

Phylogenetic analyses.—DNA sequences for Bullimyces, Hydromelitis and Riomyces are provided (TABLE I). To determine the familial placement of the new genera, taxa sequenced in this study along with sequences obtained from GenBank from various subclasses currently circumscribed within the Sordariomycetes based on Zhang et al. (2006) and Réblová (2006, 2009) were aligned with MUSCLE® (Edgar 2004) as implemented in the program SeaView 4.1 (Galtier et al. 1996, Guoy et al. 2010). The SSU and LSU datasets were initially analyzed separately and then concatenated and analyzed as a single dataset after no conflict among the bootstrap values of well supported clades was observed (Wiens 1998). A second analysis was performed for LSU data with a more extensive taxon sampling and including members in the Annulatascaceae sensu lato and stricto clades (Réblová 2006, 2009). Models of evolutionary change were determined with Modeltest 3.7 (Posada and Crandall 1998). Maximum likelihood analyses (ML) were conducted with an online version of RAxML (http:// phylobench.vital-it.ch/raxml-bb/index.phpwith) (Stamatakis 2008) under the GAMMA model with 100 bootstrap replicates. Bayesian analyses employing Markov chain Monte Carlo (MCMC) were performed with MrBayes 3.1.2 (Huelsenbeck et al. 2001, Huelsenbeck and Ronquist 2001) as an additional means of assessing branch support. Bayesian analyses using a uniform model (GTR + I + G)

were conducted using 10 000 000 generations with trees sampled every 100th generation resulting in 100 000 total trees. Two independent analyses were performed with four chains using default settings to ensure that trees were being sampled from the same tree space. The first 10 000 trees, which extended beyond the burn-in phase in each analysis, were discarded, and the remaining 90 000 trees were used to calculate posterior probabilities. The consensus of 90 000 trees was generated in PAUP 4.0b10 (Swofford 2002). Phylogenetic trees were drawn with Figtree 1.2.2.

RESULTS

Phylogenetic analyses.—The combined SSU and LSU included 2407 characters from 46 taxa. A total of 364 ambiguously aligned characters were excluded, yielding a total of 2043 characters. The ML analysis resulted in a single most likely tree (Fig. 1), which was similar in topology and placement of the major orders of Sordariomycetes to the phylogeny presented by Zhang et al. (2006). Bullimyces, Riomyces and Hydromelitis grouped within an unsupported clade consisting of members of the Ophiostomatales and Magnaporthales along with species of Sordariomycetidae inc. sed. The Bullimyces clade was well supported with 100% maximum likelihood bootstrap (MLB) support and 100% Bayesian posterior probability (BPP); the three sequences of B. communis formed a well supported clade and were sister to B. costaricensis and B. aurisporus. Riomyces was basal to Bullimyces with no support. Ceratostomella pyreneica was basal to Bullimyces but was not supported by MLB. Hydromelitis formed a clade with Lentomitella cirrhosa with no support.

Final alignment of the partial LSU sequences of nrDNA included 1179 characters from 67 taxa. A total of 154 ambiguously aligned characters were excluded, yielding a total of 1025 characters. The LSU data was expanded to include additional related species from GenBank, most of which lacked a corresponding SSU sequence. The tree obtained with the ML analysis showed a topology similar to the SSU and LSU tree

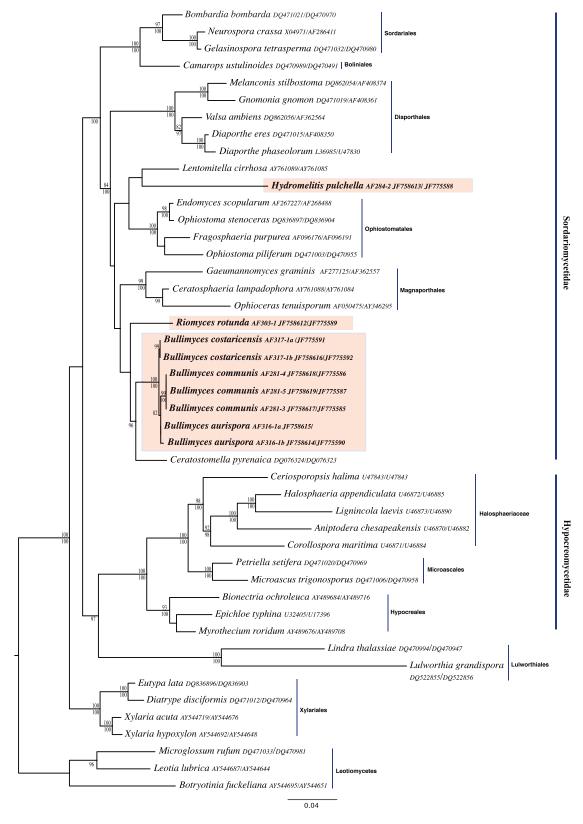


Fig. 1. Most likely tree based on a combined SSU and LSU nrDNA sequence data obtained with RAxML. Numbers above the branches indicate ML bootstrap support $\geq 75\%$ and numbers below indicate Bayesian posterior probabilities $\geq 95\%$. GenBank accession numbers are given after taxon names. Species sequenced for this study are highlighted.

(FIG. 2), with *Bullimyces*, *Riomyces* and *Hydromelitis* within an unsupported clade consisting of members of the Ophiostomatales, Magnaporthales and freshwater Annulatascaceae sensu lato and sensu stricto. The three sequences of *B. communis* formed a monophyletic group with 99% MLB and 100% BPP values and formed a well supported clade to *B. costaricensis* and *B. aurisporus* with 98% MLB and 100% BPP. Because ordinal or familial placement for the three genera was not supported, they should remain in the Sordariomycetidae inc. sed.

TAXONOMY

Bullimyces A. Ferrer, A.N. Mill., C. Sarmiento et Shearer gen. nov.

MycoBank MB561094

Ascomata in ligno submerso, partim immersa vel immersa, globosa vel subglobosa, membranacea, nigra, ostiolati. Collum cylindricum, atrobrunneae. Centris ascocarpiorum cellulis psedoparenchymaticis, globosis, hyalinis, deliquescentibus. Asci unitunicati, cylindrici, tenuitunicati, sine poro apicali, octospori, uniseriati, persistentes vel deliquescentes. Ascosporae ellipsoideae-fusiformes, hyalinae vel lutea, septatae, ad septum non constrictae, pachydermaticae, cum vel sine tunica gelatinosa praeditae et appendages.

Typus generic: Bullimyces communis A. Ferrer, A.N. Mill., C. Sarmiento et Shearer

Etymology: From Latin Bulla = bubble; + Greek Myces = fungus, in reference to the round cells filling the hamathecium.

Ascomata on submerged wood immersed to erumpent in the substrate, globose to subglobose, membranous, black, ostiolate. Neck cylindrical, dark brown. Pseudoparenchyma of thin-walled globose, hyaline cells, filling the centrum, deliquescent. Asci unitunicate, cylindrical, thin-walled, lacking an apical pore and apical structures, eight-spored, uniseriate, deliquescing early in some species. Ascospores broadly ellipsoidal-fusiform to ellipsoidal, hyaline becoming dark yellow with age, septate, not constricted at septa, thick-walled, with or without a gelatinous sheath and appendages.

Bullimyces communis A. Ferrer, A.N. Mill., C. Sarmiento et Shearer sp. nov. FIGS. 3–16 MycoBank MB561095

Ascomata in ligno submerso, 350– 650×340 – $660 \mu m$, immersa, globosa, membranacea, nigra, ostiolati. Collum 100– 170×60 – $80 \mu m$, cylindricum, atrobrunneae. Centris ascocarpiorum cellulis psedoparenchymaticis, 38– $90 \mu m$ diam, globosis, hyalinis, deliquescentibus. Asci 310– 430×18 – $22 \mu m$, unitunicati, cylindrici, tenuitunicati, sine poro apicali, octospori, uniseriati, deliquescentes. Ascosporae 40– 48×19 – $22 \mu m$, ellipsoideae-fusiformes, hyalinae, 3-septatae,

ad septum non constrictae, pachydermaticae, hyaline calyptra bipolare.

Holotype: COSTA RICA. ALAJUELA, Caño Negro Reserve, Rio Frio, 10°53′N, 84°45′W, water 27.5 C, pH 5, on submerged wood, 15 Dec 2005, Astrid Ferrer & Marlon Salazar, AF281-1 (ILL).

Etymology: From Latin *Communis* = common, in reference to being the most collected species in Costa Rica.

Ascomata on submerged wood, $350\text{-}650 \times 340\text{-}660 \, \mu\text{m}$, immersed in the substrate, globose, membranous, black, ostiolate, brown. Neck $100\text{-}170 \times 60\text{-}80 \, \mu\text{m}$, cylindrical, dark brown. Pseudoparenchyma of thin-walled cells $38\text{-}90 \, \mu\text{m}$ diam, globose, hyaline, filling the centrum, deliquescent. Asci $310\text{-}430 \times 18\text{-}22 \, \mu\text{m}$, unitunicate, cylindrical, thin-walled, lacking an apical pore and apical structures, floating free within the centrum, eight-spored, uniseriate. Ascospores $40\text{-}48 \times 19\text{-}22 \, \mu\text{m}$ (mean = $43.70 \times 20.20 \, \mu\text{m}$, n = 30), broadly ellipsoidal-fusiform to ellipsoidal, hyaline, three-septate, not constricted at septa, thick-walled $(2\text{-}3 \, \mu\text{m})$, with hyaline, gelatinous caps at both apices, $2\text{-}3 \, \mu\text{m}$ long, staining in aqueous nigrosin, ascospores accumulate as a mass at tip of the neck after discharge.

Known distribution: COSTA RICA: Alajuela, Heredia. *Habitat:* On submerged, dead woody debris.

Additional specimens examined: COSTA RICA. ALA-JUELA: Caño Negro Reserve, Rio Frio, 10°53′N, 84°45′W, water 27.5 C, pH 5, on submerged wood, 15 Dec 2005, Astrid Ferrer & Marlon Salazar, AF281-4, AF281-5, AF281-6, AF281-7. HEREDIA: La Selva Biological Station, La Selva Stream, 10°25′N, 84°01′W, water 25 C, pH 5, on submerged wood, 10 Jan 2006, Marlon Salazar, AF281-3.

Commentary: Bullimyces communis was the most common freshwater ascomycete reported in this study from Costa Rica with six collections. The presence of globose cells in the hamathecium was observed consistently in all collections, although in water the globose, chain-like cells deliquesce promptly (Figs. 11–16). Another interesting aspect of this fungus is that the asci were never observed to be arranged in a hymenial layer but instead floating among the globose cells. Bullimyces communis is characterized by three-septate ascospores with gelatinous caps at both apices. One collection, AF281-6, had hyaline ascospores that became dark yellow with age but was identical to the type specimen in every other feature.

Bullimyces costaricensis A. Ferrer, A.N. Mill., C. Sarmiento et Shearer sp. nov. Figs. 17–24 MycoBank MB561097

Ascomata in ligno submerso, 450– 490×450 – $500 \mu m$, immersa, globosa vel subglobosa, membranacea, nigra, ostiolati. Collum 380– 390×77 – $80 \mu m$, cylindricum, atrobrunneae. Centris ascocarpiorum cellulis psedoparenchymaticis, 35– $55 \mu m$ diam, latae, globosis, hyalinis, deliquescentibus. Collum 280– 390×77 – $80 \mu m$. Asci 430– 600×20 – $23 \mu m$,

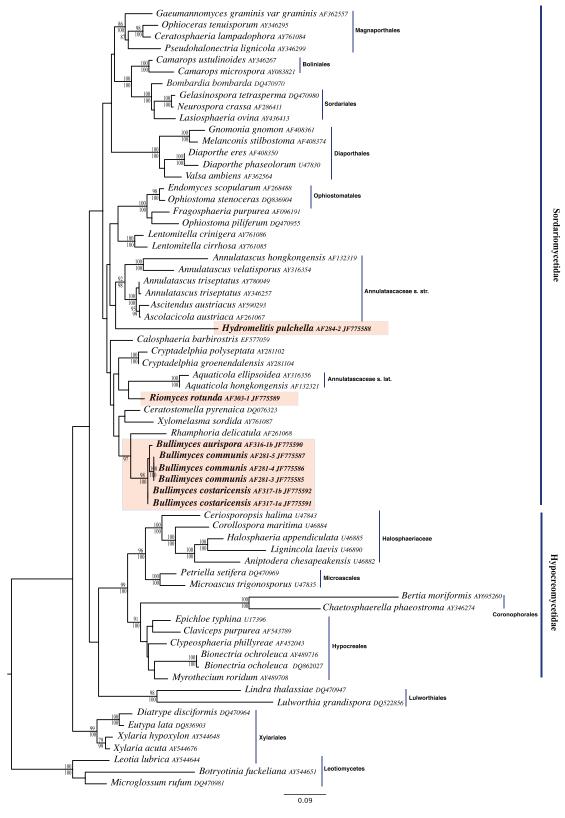
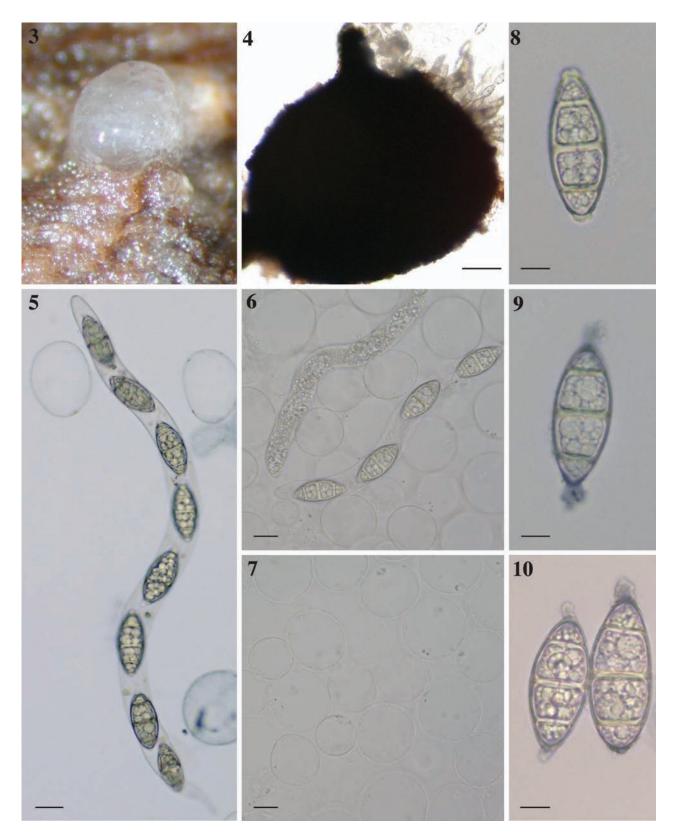
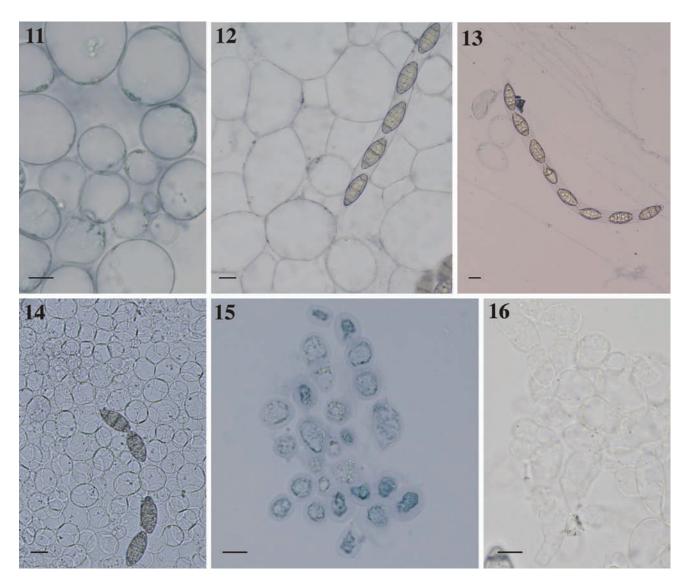


Fig. 2. Most likely tree from LSU nrDNA sequence data obtained with RAxML. Support values and highlighting as illustrated (Fig. 1).



FIGS. 3–10. *Bullimyces communis* (from Holotype). 3. Ascomata on the substrate. 4. Whole mount of ascoma. 5. Asci stained with aqueous nigrosin. 6. Asci and globose cells. 7. Globose cells filling the venter of the ascomata. 8. Ascospore in water. 9, 10.



FIGS. 11–16. *Bullimyces communis* (from Holotype). 11, 12. Globose cells stained with aqueous nigrosin (AF281-1). 13. Globose cells stained with aqueous nigrosin, and remains of stained, deliquescent globose cells (AF281-1). 14. Ascospores and globose cells (AF281-4). 15. Deflated globose cells stained with aqueous nigrosin (AF281-4). 16. Globose cells (AF281-5). Bar = 10 μm.

unitunicati, cylindrici, tenuitunicati, sine poro apicali, octospori, uniseriati, deliquescentes. Ascosporae 40–68 \times 15–21 µm, ellipsoideae-fusiformes, hyalinae demum atrantes, 5-septatae, ad septum non constrictae, pachydermaticae.

Holotype: COSTA RICA. LIMON: Barra del Colorado and Tortuguero National Park, Las Palmas Stream, 10°35′N, 83°31′W, water 25 C, pH 5, on submerged wood, 18 Dec 2005, Astrid Ferrer & Marlon Salazar, AF317-1 (ILL).

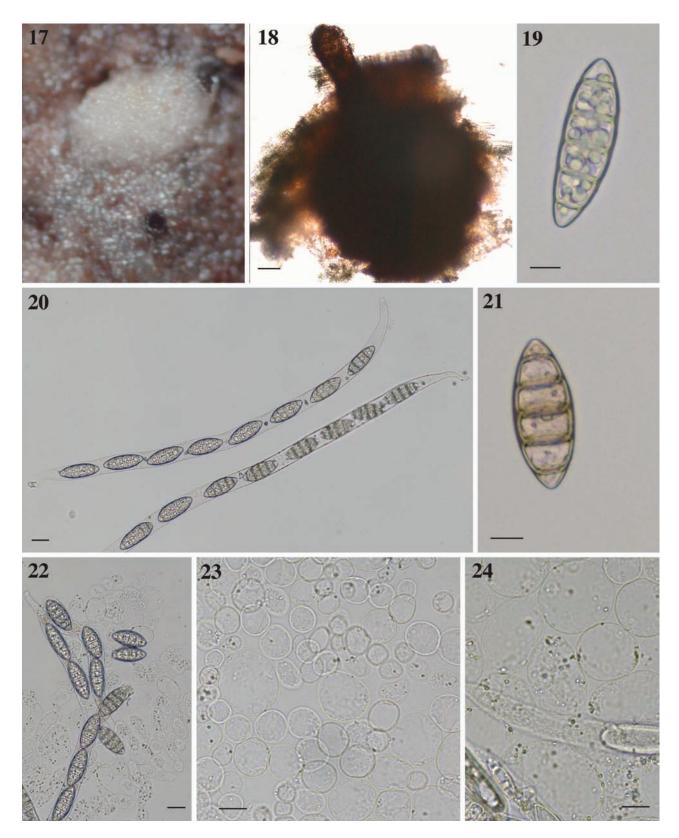
Etymology: Costaricensis, in reference to the country (Costa Rica), where this fungus was collected.

Ascomata on submerged wood, 450– 490×450 – $500 \mu m$, immersed to erumpent in the substrate, globose to subglobose, membranous, black, ostiolate. Neck 280– 390×77 – $80 \mu m$, cylindrical, dark brown. Pseudoparenchyma of thin-walled cells, 35– $55 \mu m$

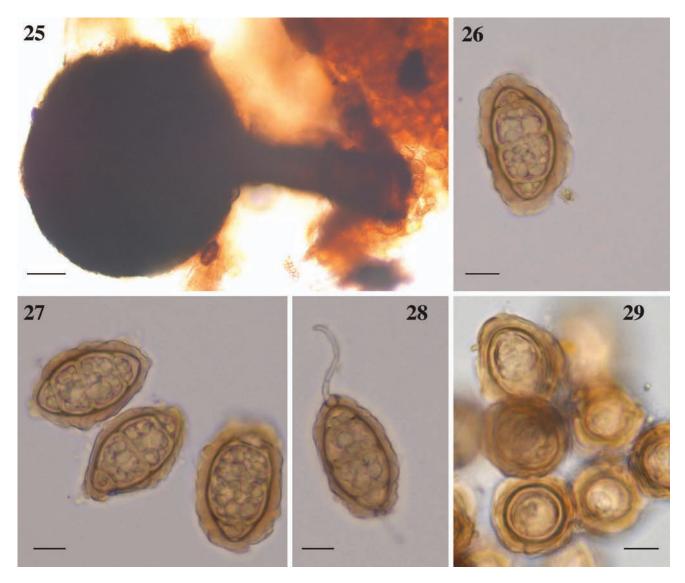
diam, globose, hyaline, filling the centrum, deliquescent. Asci 430–600 \times 20–23 µm, unitunicate, cylindrical, short pedicellate, thin-walled, lacking an apical pore, floating free within the centrum, eight-spored, uniseriate, irregularly arranged, early deliquescent. Ascospores 40–68 \times 15–20 µm (mean = 48 \times 19 µm, n = 30), broadly ellipsoidal-fusiform to ellipsoidal, hyaline, becoming dark yellow with age, five-septate, not constricted at septa, thick-walled (3–5 µm), ascospores accumulate in a mass at the tip of the neck after discharge.

Known distribution: COSTA RICA: Limón (known only from the type specimen).

Habitat: On submerged, dead woody debris.



FIGS. 17–24. Bullimyces costaricensis. (AF317-1). 17. Ascomata on the substrate (note mass of hyaline ascospores. 18. Whole mount of ascoma. 19. Ascospore in water. 20. Elongated asci with eight ascospores. 21. Ascospore becoming pale brown with age. 22, 23, 24. Globose cells. Bar = $10 \mu m$.



Figs. 25–29. Bullimyces aurisporus (AF316-1). 25. Whole mount of ascoma. 26 & 27. Ascospores in water showing gelatinous sheath. 28. Germinating ascospores. 29. Top view of ascospores. Bar = $10 \mu m$.

Commentary: Bullimyces costaricensis is morphologically similar to the type species B. communis, with dark ascomata, globose hamathecial cells, thin-walled ascilacking an apical pore, and thick-walled, hyaline, multiseptate ascospores. However B. costaricensis differs from B. communis in ascus and ascospore morphology. The asci of B. costaricensis are particularly long (430–600 μ m compared to 310–430 μ m in B. communis), and the ascospores of B. costaricensis are larger (40–68 μ m long in B. costaricensis compared to 40–48 μ m in B. communis), have more septa and lack appendages.

Bullimyces aurisporus A. Ferrer, A.N. Mill., C. Sarmiento et Shearer sp. nov. Figs. 25–29 MycoBank MB561098

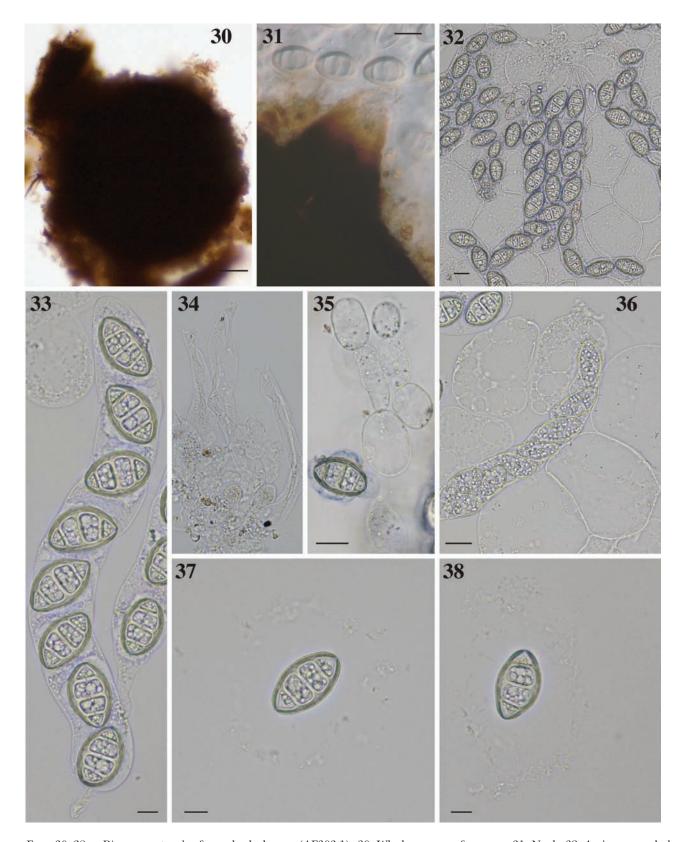
Ascomata in ligno submerso, 260–310 \times 290 μ m, partim immersa vel immersa, subglobosa vel obpyriforma, mem-

branacea, nigra, ostiolati. Collum $224\times62~\mu m$, cylindricum, atrobrunneae. Asci deliquescentes. Ascosporae $34–38\times17–20~\mu m$, ellipsoideae, lutea, three-septatae, ad septum non constrictae, pachydermaticae, tunica gelatinosa praeditae.

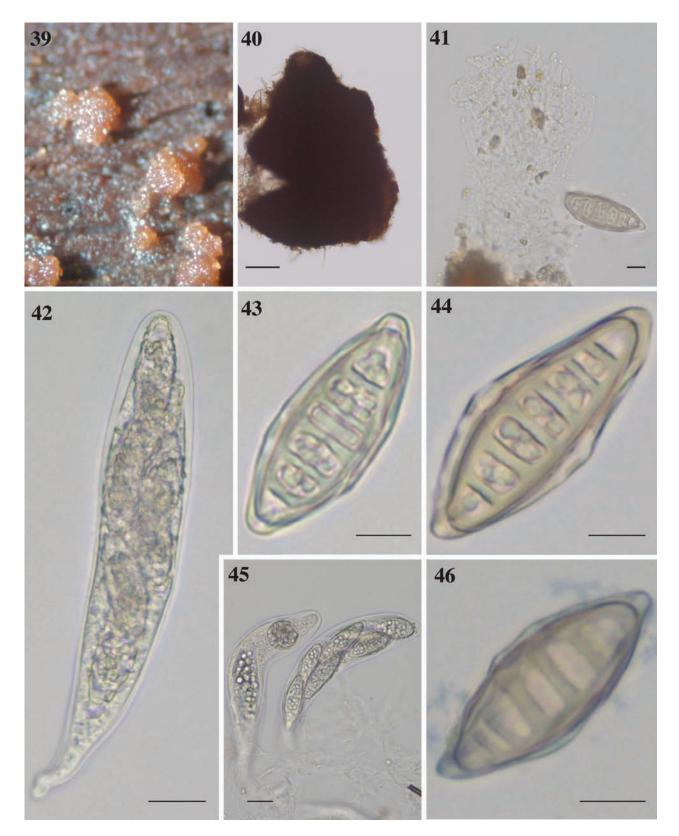
Holotype: COSTA RICA. ALAJUELA: Caño Negro Reserve, Caño Blanco stream 10°50′N, 84°7′W, water 26 C, pH 5, on submerged wood, 16 Dec 2005, Astrid Ferrer & Marlon Salazar, AF316-1 (ILL).

Etymology: From Latin Aurum = gold; Spora = spore, in reference to the color of the ascospores.

Ascomata on submerged wood, $260\text{--}310 \times 290~\mu\text{m}$, immersed to erumpent in the substrate, subglobose to obpyriform, membranous, black, ostiolate. Neck cylindrical, dark brown, $224 \times 62~\mu\text{m}$. Asci not observed, early deliquescent. Ascospores $34\text{--}38 \times 17\text{--}20~\mu\text{m}$, ellipsoidal, dark yellow, three-septate, not constricted at septa, thick-walled $(2.0~\mu\text{m})$, surround-



Figs. 30–38. Riomyces rotundus from the holotype (AF303-1). 30. Whole mount of ascoma. 31. Neck. 32. Asci surrounded by globose cells. 33. Unitunicate ascus. 34. Empty Asci. 35, 36. Globose cells. 37, 38. Ascospores showing gelatinous sheath expanding in water. Bar = $10~\mu m$.



FIGS. 39–46. Hydromelitis pulchella from the holotype (AF284-1). 39. Ascomata on the substrate. 40. Whole mount of ascoma. 41. Paraphyses. 42, 45. Young ascus. 43. Ascospores in water. 44. Ascospore becoming pale yellow with age. 46. Ascospore stained with aqueous nigrosin. Bar = $10 \mu m$.

ed by an irregular gelatinous sheath about 3–5 μ m wide, ascospores accumulate in a mass at the tip of the neck after discharge.

Known distribution: COSTA RICA: Alajuela (known only from the type specimen).

Habitat: On submerged, dead woody debris.

Commentary: Bullimyces aurisporus is morphologically similar to the type species of the genus, B. communis, with dark ascomata and thick-walled, three-septate ascospores. However the ascospores of B. aurisporus are shorter (34–38 μm in B. aurisporus compared to 40–48 μm in B. communis) and have a thick, irregular mucilaginous sheath surrounding the ascospore. Although we do not have information about ascus and hamathecium morphogy, molecular data support its placement in this genus. We were not able to induce sexual reproduction in culture for B. aurisporus.

Riomyces A. Ferrer, A.N. Mill., C. Sarmiento et Shearer gen. nov.

MycoBank MB561099

Ascomata in ligno submerso, partim immersa vel immersa, globosa ad subglobosa, membranacea, nigra, ostiolati. Collum breve, atrobrunneae. Hamathecium ascocarpiorum cellulis psedoparenchymaticis, globosis, hyalinis, deliquescentibus. Asci unitunicati, cylindrici, tenuitunicati, breve deicellati, sine poro apicali, octospori, uniseriati. Ascosporae, ellipsoideo-fusiformes, hyalinae, septatae, ad septum non constrictae, pachydermaticae, tunica gelatinosa praeditae.

Typus generic: Riomyces rotundus A. Ferrer, A.N. Mill., C. Sarmiento et Shearer

Etymology: From the Spanish word Rio = river + Greek Myces = fungus, in reference to the freshwater habitat of the fungus.

Ascomata on submerged wood, immersed to erumpent in the substrate, globose to subglobose, membranous, black, ostiolate. Neck short, dark brown. Hamathecium composed of globose, hyaline, deliquescent cells. Asci unitunicate, broadly cylindrical, thin-walled, short-pedicellate, lacking an apical pore and other apical structures, eight-spored, uniseriate. Ascospores ellipsoidal-fusiform, hyaline, septate, not constricted at septa, thick-walled, surrounded by a gelatinous sheath.

Riomyces rotundus A. Ferrer, A.N. Mill., C. Sarmiento et Shearer sp. nov. FIGS. 30–38 MycoBank MB561100

Ascomata in ligno submerso, $440\text{--}720 \times 440\text{--}600 \, \mu\text{m}$, partim immersa vel immersa, globosa vel subglobosa, membranacea, nigra, ostiolati. Collum $76 \times 84 \, \mu\text{m}$, breve, atrobrunneae. Hamathecium ascocarpiorum cellulis psedoparenchymaticis, $35\text{--}100 \, \mu\text{m}$ diam, globosis, hyalinis, deli-

quescentibus. Asci $250-340\times25-29~\mu m$, unitunicati, cylindrici, tenuitunicati, breve deicellati, sine poro apicali, octospori, uniseriati, deliquescentes. Ascosporae $30-40\times20-25~\mu m$, ellipsoideo-fusiformes, hyalinae, 3-septatae, ad septum non constrictae, pachydermaticae, tunica gelatinosa praeditae.

Holotype: COSTA RICA. HEREDIA: La Selva Biological Station, Arboleda Stream 10°25′N, 84°00′W, water 25 C, pH 7, on submerged wood, 9 Jan 2006, *Marlon Salazar*, *AF303-1* (ILL).

Etymology: From Latin *rotunda* = round, globular, in reference to the cells of the hamathecium.

Ascomata on submerged wood, $440-720 \times 440-$ 600 µm, immersed to erumpent in the substrate, globose to subglobose, membranous, black, ostiolate. Neck short, dark brown, $76 \times 84 \mu m$. Hamathecium composed of globose, wide, hyaline, deliquescent cells, 35–100 μ m diam. Asci 250–340 \times 25–30 μ m, unitunicate, broadly cylindrical, thin-walled, with a short pedicel, lacking an apical pore and other apical structures, eight-spored, uniseriate. Ascospores 30-40 \times 20–25 µm (mean = 35 \times 22 µm, n = 30), broadly ellipsoidal-fusiform, hyaline, three-septate, not constricted at septa, thick-walled (4-5 µm), surrounded by an irregular gelatinous sheath extending about ca. 10–20 μm from the ascospore wall; sheath margins stain in aqueous nigrosin, ascospores accumulate in a mass at the tip of the neck after discharge.

Known distribution: COSTA RICA: Alajuela and Heredia.

Habitat: On submerged, dead woody debris.

Additional specimens examined: COSTA RICA. HEREDIA: La Selva Biological Station, Esquina Stream, 10° 24′ N, 84° 00′ W, water 25° C, pH 5, on submerged wood, 9 Jan 2006, Marlon Salazar, AF303-2. ALAJUELA: Caño Negro Reserve, Río Frío, 10° 53′ N, 84° 45′ W, water 27° C, pH 5, on submerged wood, 15 Dec 2005, Astrid Ferrer & Marlon Salazar, AF303-3.

Commentary: Riomyces rotundus is morphologically similar to species in the genus Bullimyces in having dark ascomata, the unique hyaline, globose cells filling the centrum, thin-walled asci lacking an apical pore, and thick-walled, hyaline, multiseptate ascospores. It was observed in this fungus that the asci were attached to a hymenial layer but with time the asci become unattached and surrounded by the globose cells filling the centrum, some empty asci were observed still attached to the hymenium (Fig. 34).

Hydromelitis A. Ferrer, A.N. Mill., C. Sarmiento et Shearer gen. nov.

MycoBank MB561101

Ascomata in ligno submerso, partim immersa vel immersa, pyriformia, membranacea, nigra, ostiolati. Paraphysibus simplicis, sepatatis. Asci unitunicati, clavati, tenuitunicati, breve deicellati, sine poro apicali, octospori, biseriati vel

interdum triseriati. Ascosporae, ellipsoideae, hyalinae vel flavus, septatae, ad septum non constrictae, pachydermaticae, tunica gelatinosa praeditae.

Ascomata on submerged wood, immersed to erumpent, pyriform, membranous, black, ostiolate. Paraphyses simple, thin-walled, septate. Asci unitunicate, clavate, thin-walled, short-pedicellate, lacking an apical pore and other apical structures, eight-spored, biseriate. Ascospores ellipsoidal, hyaline to golden yellow, multiseptate, septa with or without a central channel, not constricted at septa, thick-walled, surrounded by a gelatinous sheath.

Typus generic: Hydromelitis pulchella A. Ferrer, A.N. Mill., C. Sarmiento et Shearer.

Etymology: From Latin *Hydromelitis* = honey-water, in reference to the color of the ascospores and the spore mass on the wood.

Hydromelitis pulchella A. Ferrer, A.N. Mill., C. Sarmiento et Shearer sp. nov. Figs. 39–46 MycoBank MB561102

Ascomata in ligno submerso, 220–280 \times 190–250 μm , partim immersa vel immersa, pyriformia, membranacea, nigra, ostiolati. Paraphysibus 3–5 μm diam, simplicis, sepatatis, hyalinis. Asci 150–170 \times 30–33 μm , unitunicati, clavati, tenuitunicati, breve deicellati, sine poro apicali, octospori, biseriati vel interdum triseriati. Ascosporae 35–51 \times 13–18 μm , ellipsoideae, hyalinae vel flavus, 6-septatae, ad septum non constrictae, pachydermaticae, tunica gelatinosa praeditae.

Holotype: COSTA RICA. ALAJUELA: Caño Negro Reserve, Río Frío 10°53′N, 84°45′W, water 27.5 C, pH 5, on submerged wood, 15 Dec 2005, Astrid Ferrer & Marlon Salazar, AF284-2 (ILL).

Etymology: From Latin Pulchella = beautiful, in reference to the ascospores.

Ascomata on submerged wood, 220-280 × 190-250 µm, immersed to erumpent in the substrate, pyriform, membranous, black, ostiolate. Paraphyses cylindrical, 3–5 µm diam, simple, thin-walled, septate, hyaline. Asci 150–210 \times 30–33 μ m, unitunicate, clavate, thin-walled, with a short pedicel, lacking an apical pore and other apical structures, eight-spored, biseriate, occasionally triseriate. Ascospores $35-51 \times$ 13–18 μm, ellipsoidal, hyaline to golden yellow, mostly six-septate (3–7), with or without a central channel in the septal walls, not constricted at septa, thick-walled (up to 5 μm); ascospores surrounded by a gelatinous sheath that stains in aqueous nigrosin, 3-7 µm wide at lateral walls of ascospores, tapering toward the apices, ascospores accumulate in a yellow mass at the tip of the neck after discharge.

Known distribution: COSTA RICA: Alajuela and Heredia.

Habitat: On submerged, dead woody debris.

Additional specimens examined: HEREDIA: La Selva Biological Station, El Surá Stream 10°25′N, 84°00′W, water 25 C, pH 7, on submerged wood, 10 Jan 2006, Marlon Salazar, AF284-1; La Selva Biological Station, Panteno, 10°25′8″N, 84°0′22″W, water 25 C, pH 5.5, on submerged decorticated wood, 19 May 2000, Jennifer L. Anderson, Rebecca Wulffen, A468-1; La Selva Biological Station, Rio Puerto Viejo, 10°25′48″N, 84°0′17″W, water 23 C, pH 5.5, on submerged, soft, decorticated wood, 20 May 2000, Jennifer L. Anderson, Rebecca Wulffen, A468-2; La Selva Biological Station, Piper, 10°25′57″N, 84°1′44″W, on submerged decorticated wood, 6 Feb 2001, Cathy Pringle, A468-3; La Selva Biological Station, Arboleda 30, 10°25′47″N, 84°0′39″W, submerged, soft, decorticated wood, 17 May 2000, Jennifer L. Anderson, Rebecca Wulffen, A468-4.

Commentary: Hydromelitis pulchella is morphologically similar to the type species of Bullimyces, B. communis, with dark ascomata, thin-walled asci lacking an apical pore, and thick-walled, multiseptate ascospores with a sheath. However H. pulchella differs from B. communis in ascomal and hamathecial morphology. The ascomata of H. pulchella are pyriform compared to globose in B. communis, and the hamathecium of H. pulchella is formed by simple, thin-walled, septate, hyaline paraphyses, while B. communis has hyaline, globose cells filling the centrum.

DISCUSSION

Bullimyces.—This genus with three new species represents a distinct taxonomic entity based on morphological and molecular data. The three new species placed within Bullimyces share several morphological characteristics including globose to subglobose, membranous, black, ostiolate ascomata, hyaline, globose cells filling the centrum, unitunicate asci; and multiseptate, thick-walled ascospores, which darken with age into a golden color, with or without a gelatinous sheath or appendages. Nonetheless Bullimyces species can be identified based on ascospore morphology and septation. B. communis is characterized by three-septate ascospores with gelatinous caps at both apices; ascospores of B. costaricensis are fiveseptate and lack appendages, and B. aurisporus has three-septate ascospores and a mucilaginous sheath surrounding the ascospore.

Bullimyces is very similar to Riomyces described herein in ascomata and ascus morphology, but the cells filling the centrum in Riomyces are irregular and have thicker walls. Bullimyces and Riomyces both group with members of the Sordariomycetidae but were not sister taxa. Bullimyces shows affinities to Ceratostomella pyrenaica based on SSU and LSU data and to Ceratostomella pyrenaica, Rhamphoria deliculata and Xylomelasma sordida based on LSU data. These genera have similar ascomatal morphology to Bulli-

myces with dark, nonstromatic ascomata with a cylindrical neck, but otherwise they differ greatly in that these genera have asci with prominent apical rings, septate paraphyses that are wide at the base and tapering at the apex and mostly thin-walled ascospores (Réblová 2006). Furthermore Bullimyces and Riomyces differ in habitat from these other genera because Bullimyces and Riomyces occur only in freshwater while Ceratostomella pyrenaica, Rhamphoria deliculata and Xylomelasma sordida have been collected from decayed wood in terrestrial habitats.

The species of *Bullimyces* have a unique combination of morphological characters, which makes it difficult to place them taxonomically within the Sordariomycetes without supporting molecular data. For instance Bullimyces shares some striking morphological similarities to the freshwater genus Luttrellia Shearer, a member of the Halosphaeriaceae (Hypocreomycetideae) (Shearer 1978). The genus Luttrellia currently accommodates four aquatic species (Shearer 1978, Ferrer and Shearer 2007), with similar ascomatal and ascospore morphology, however the hamathecium of Luttrellia is composed of septate, hyaline catenophyses, with the exception of Luttrellia halonata, where catenophyses are hyaline, wide and globose (Ferrer and Shearer 2007). Unfortunately no molecular data are available at present for Luttrellia. Future molecular phylogenetic analysis may clarify whether Luttrellia halonata shares affinities with the genus Bullimyces.

Globose cells that fill the centrum of *Bullimyces* and *Riomyces* have been reported by Nakagiri and Tokura (1987) in the marine genus *Corollospora* (Halosphaeriaceae). *Corollospora* has pseudoparenchyma of hyaline, thin-walled, rounded cells filling the center of young ascocarps. Nonetheless they are distinct from those of *Bullimyces* and *Riomyces* because the pseudoparenchyma cells of *Corollospora* are joined one cell to another by pit connections (Nakagiri and Tokura 1987), a feature not seen in *Bullimyces*.

Riomyces.—The position of Riomyces remains incertae sedis because Riomyces was basal to Bullimyces and grouped with other members of the Ophiostomatales and Magnaporthaceae without support (Figs. 1, 2). Riomyces and Bullimyces may be closely related based on their morphological similarities. However additional taxon sampling in the LSU analyses revealed that Riomyces and Hydromelitis also could be related to freshwater ascomycetes in the Annulatascaceae sensu lato and stricto. Unfortunately no SSU data are available for the Annulatascaceae, perhaps due to the difficulty in sequencing this group (Ferrer pers comm).

Hydromelitis.—Among the Sordariomycetidae Hydromelitis shows some similarities to the genus Bullimyces in

having multiseptate, thick-walled ascospores surrounded by a gelatinous sheath that darkens into a golden color with age. However the ascomata of *Hydromelitis* are distinctly pyriform rather than globose as in most *Bullimyces* species. In addition the hamathecium of *Hydromelitis* are formed by simple, thin-walled, septate, hyaline paraphyses while *Bullimyces* species have hyaline, globose cells filling the centrum.

The placement of the new genera at the family level is uncertain. The combination of morphological characteristics found in *Hydromelitis* including the membranous, pyriform ascomata and phragmoseptate, thickwalled ascospores with a sheath are not present in any family currently included in the Sordariomycetidae.

Freshwater ascomycetes possess unique morphological characteristics that might be adaptive to freshwater habitats, such as ascospores with elaborate appendages and sheaths (Shearer 1993, Jones 2006). Also in the aquatic Dothideomycetes order Jahnulales the vegetative hyphae are almost 10 times wider than other hyphae reported in the Ascomycota (Inderbitzin et al. 2001, Raja and Shearer 2006). We are of the opinion that these wide hyphae aid the attachment of the ascomata to the soft, decorticated, woody substrates while in water, analogous to an anchor. Bullimyces and Riomyces possess wide, globose cells in the hamathecium that might be adaptive in providing buoyancy to the asci and the ascospores when they are discharged into water. The functional significance of these traits remains unclear, but we hypothesize that these globose cells may be important for dispersion and establishment of fungi on wood in flowing water.

ACKNOWLEDGMENTS

We thank Marlon Salazar, Jennifer Anderson, Rebecca Wulffen and Catherine Pringle for great help with collecting. We appreciate the Organization for Tropical Studies (OTS) for logistic support to collect in Costa Rica. We thank Huzefa Raja for reviewing the manuscript before submission. Financial support by the National Science Foundation (NSF grants Nos. DEB 0316496, DEB 0515558) is gratefully acknowledged. Any opinions, findings and conclusions or recommendations expressed in this publication are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

LITERATURE CITED

Edgar R. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res 32:1792–1797, doi:10.1093/nar/gkh340

Ferrer A, Shearer CA. 2005. New records and a new species of *Canalisporium* from aquatic habitats in Panama. Mycotaxon 93:179–188.

- ——. 2007. Three new species of *Luttrellia* from temperate and tropical freshwater habitats. Mycologia 99:144–151, doi:10.3852/mycologia.99.1.144
- Galtier N, Gouy M, Gautier C. 1996. SeaView and Phylo_win: two graphic tools for sequence alignment and molecular phylogeny. Comput Appl Biosci 12:543–548.
- Gouy M, Guindon S, Gascuel O. 2010. SeaView 4: a multiplatform graphical user interface for sequence alignment and phylogenetic tree building. Mol Biol Evol 27:221–224, doi:10.1093/molbev/msp259
- Huelsenbeck JP, Mark PVD, Ronquist F. 2001. MrBayes: Bayesian inference of phylogenetic trees.3.1.2. http: mrbayes.csit.fsu.edu/download.php [Accessed Jan 2009].
- ———, Ronquist FR. 2001. MrBayes: Bayesian inference of phylogenetic trees. Biometrics 17:754–755.
- Inderbitzin P, Landvik S, Abdel-Wahab A, Berbee ML. 2001. Aliquandostipitaceae, a new family for two new tropical ascomycetes with unusually wide hyphae and dimorphic ascomata. Am J Bot 88:52–61, doi:10.2307/ 2657126
- Jones EBG. 1994. Ultrastructure and taxonomy of the aquatic ascomycetous order Halosphaeriales. Can J Bot 73(Suppl. 1):S790–S801.
- ———. 2006. Form and function of fungal spore appendages. Mycoscience 47:167–183, doi:10.1007/s10267-006-0295-7
- ———, Sakayaroj J, Suetrong S, Somrithipol S, Pang KL. 2009. Classification of marine Ascomycota, anamorphic and Basidiomycota. Fungal Divers 35:1–187.
- Nakagiri A, Tokura R. 1987. Taxonomic studies of the genus *Corollospora* (Halosphaeriales, Ascomycotina) with descriptions of seven new species. Trans Mycol Soc Japan 28:413–436.
- Posada D, Crandall KA. 1998. Modeltest: testing the model of DNA substitution. Bioinformatics 49:817–818, doi:10.1093/bioinformatics/14.9.817
- Promputtha I, Miller AN. 2010. Three new species of *Acanthostigma* (Tubeufiaceae, Pleosporales) from the Great Smoky Mountains National Park. Mycologia 102: 574–587, doi:10.3852/09-051
- Raja HA, Shearer CA. 2006. *Jahnula* species from North and Central America, including three new species. Mycologia 98:312–332, doi:10.3852/mycologia.98.2.319
- Rehner SA, Samuels GJ. 1994. Taxonomy and phylogeny of Gliocladium analysed from nuclear large subunit

- ribosomal DNA sequences. Mycol Res 98:625–634, doi:10.1016/S0953-7562(09)80409-7
- Réblová M. 2006. Molecular systematics of *Ceratostomella* sensu lato and morphologically similar fungi. Mycologia 98:68–93, doi:10.3852/mycologia.98.1.68
- ——. 2009. Teleomorph of *Rhodoveronae* (Sordariomycetidae) discovered and re-evaluation of *Pleurophrag-mium*. Fungal Divers 36:129–139.
- Shearer CA. 1978. Fungi of the Chesapeake bay and its tributaries VII. *Luttrellia estuarina* gen. et sp. nov. (Ascomycetes) Mycologia 70:692–697.
- . 1993. The freshwater ascomycetes. Nova Hedwig 56: 1–33.
- Spatafora JW, Volkmann-Kohlmeyer B, Kohlmeyer J. 1998. Independent terrestrial origins of the Halosphaeriales (Marine Ascomycota). Am J Bot 85:1569–1580, doi:10.2307/2446483
- Stamatakis A. 2006. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics 22:2688–260, doi:10. 1093/bioinformatics/btl446
- Swofford DL. 2002. PAUP*4: phylogenetic analysis using parsimony (*and other methods). Sunderland, Massachusetts: Sinauer Associates.
- Vijaykrishna D, Jeewon R, Hyde KD. 2006. Molecular taxonomy, origins and evolution of freshwater ascomycetes. Fungal Divers 23:367–406.
- Vilgalys R, Hester M. 1990. Rapid identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. J Bacteriol 172:4238– 4246
- White TJ, Bruns T, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JS, White TJ, eds. PCR protocol: a guide to methods and applications. San Diego: Academic Press. p 315–322.
- Wiens JJ. 1998. Combining datasets with different phylogenetic histories. Syst Biol 57:568–581, doi:10.1080/106351598260581
- Zhang N, Castlebury LA, Miller AN, Huhndorf S, Schoch CL, Seifert KA, Rossman AY, Rogers JD, Kohlmeyer J, Volkmann-Kohlmeyer B, Sung G–H. 2006. An overview of the systematics of the Sordariomycetes based on a four-gene phylogeny. Mycologia 98:1076–1087, doi:10.3852/mycologia.98.6.1076