



UNIVERSIDADE FEDERAL DE SANTA CATARINA
CENTRO DE CIÊNCIAS BIOLÓGICAS
PROGRAMA DE PÓS-GRADUAÇÃO EM BIOLOGIA DE FUNGOS,
ALGAS E PLANTAS

Denyse Kalyne Sousa Guimarães

**Revisão taxonômica e relações filogenéticas em Panaceae (Polyporales,
Basidiomycota) com ênfase nas espécies que ocorrem no Brasil**

Florianópolis
2024

Denyse Kalyne Sousa Guimarães

**Revisão taxonômica e relações filogenéticas em Panaceae (Polyporales,
Basidiomycota) com ênfase nas espécies que ocorrem no Brasil**

Tese submetida ao Programa de Pós-Graduação
em Biologia de Fungos, Algas e Plantas da
Universidade Federal de Santa Catarina para a
obtenção do título de doutora em Biologia de
Fungos, Algas e Plantas.

Orientador: Prof. Elisandro Ricardo Drechsler dos
Santos, Dr.

Coorientador: Prof. Nelson Menolli Júnior, Dr.

Florianópolis

2024

Ficha catalográfica para trabalhos acadêmicos

Sousa Guimarães, Denyse Kalyne
Revisão taxonômica e relações filogenéticas em Panaceae
(Polyporales, Basidiomycota) com ênfase nas espécies que
ocorrem no Brasil / Denyse Kalyne Sousa Guimarães ;
orientador, Elisandro Ricardo Drechsler dos Santos,
coorientador, Nelson Menolli Júnior, 2024.
140 p.

Tese (doutorado) - Universidade Federal de Santa
Catarina, Centro de Ciências Biológicas, Programa de Pós-
Graduação em Biologia de Fungos, Algas e Plantas,
Florianópolis, 2024.

Inclui referências.

1. Biologia de Fungos, Algas e Plantas. 2. Biologia
Estrutural. 3. Taxonomia de Polyporales. 4. Sistemática
filogenética. 5. Biologia Molecular. I. Drechsler dos
Santos, Elisandro Ricardo . II. Menolli Júnior, Nelson.
III. Universidade Federal de Santa Catarina. Programa de
Pós-Graduação em Biologia de Fungos, Algas e Plantas. IV.
Título.

Denyse Kalyne Sousa Guimarães

**Revisão taxonômica e relações filogenéticas em Panaceae (Polyporales,
Basidiomycota) com ênfase nas espécies que ocorrem no Brasil**

O presente trabalho em nível de doutorado foi avaliado e aprovado, em 25 de Abril de 2024, pela banca examinadora composta pelos seguintes membros:

Prof., Genivaldo Alves Silva, Dr.
Universidade Federal de Santa Catarina

Profa., Viviana Motato Vázquez, Dra.
Universidad del Valle

Profa., Mayara Krasinski Caddah, Dra.
Universidade Federal de Santa Catarina

Profa., Fernanda Maria Cordeiro de Oliveira, Dra.
Universidade Federal de Santa Catarina

Certificamos que esta é a versão original e final do trabalho de conclusão que foi julgado adequado para obtenção do título de doutora em Biologia de Fungos, Algas e Plantas



Coordenação do Programa de Pós-Graduação



Prof. Elisandro Ricardo Drechsler dos Santos, Dr.
Orientador(a)

Florianópolis, 2024.

*Esta tese é dedicada à pergunta incessante de amigos e familiares: E aí, já
terminou?*

AGRADECIMENTOS

A Deus, unicamente por ser Ele. Deus é o centro da minha vida, é o meu amor maior, meu Pai e o meu melhor amigo. Todo auxílio que recebi foi por intermédio Dele, isso quando não foi Ele mesmo a lutar no meu lugar. Todas as pessoas que estiveram comigo durante esta fase foram enviadas por Ele.

Eu nunca mais quero ficar longe desse Ser de puro amor que me carregou no colo quando me faltou o chão. Que deu Sua vida em favor da minha. Então é para Ele TODO meu agradecimento!

Obrigada por zelar pela minha vida, Papai! Conseguimos!

AGRADECIMENTOS FORMAIS

Ao meu orientador Ricardo, crescemos e aprendemos bastante um com o outro. Prevalece o respeito e a admiração pela forma como lidou com questões delicadas da minha vida nesse processo, ainda que fosse necessário repreender algumas coisas. Obrigada por ter “pegado junto”, de verdade, fez grande diferença.

Agradeço grandemente ao Genis, pela paciência, entendimento e disposição. Ele foi essencial para a finalização de toda minha pesquisa.

Ao meu corientador Nelson Menolli sempre solícito, os questionamentos dele delinearam muito bem nosso trabalho com *Panus*.

Aos meus colegas do MIND.Funga, que timaço vocês são, admiro a trajetória de cada um de vocês.

Ao PPGFAP-UFSC, MICOLAB-UFSC, LAMEB-BOT e Herbário FLOR.

E a CAPES pela bolsa concedida durante o período vigente.

Neste mundo vocês terão aflições; contudo, tenham ânimo! Eu venci o mundo!

João 16:33

O SENHOR é a minha força e o meu escudo; como todo o coração eu confio Nele. O SENHOR me ajuda; O meu coração está feliz, e com meu cântico lhe darei graças.

Salmos 28:7

Todas as coisas vêm Dele, existem por meio Dele e são para Ele. A Ele seja toda glória para sempre! Amém.

Romanos 11:36

RESUMO

A revisão taxonômica de Panaceae, apesar de sua proposição relativamente recente, é essencial devido à criação da família com base em uma representação limitada, derivada de apenas dois táxons. A aceitação dos gêneros *Cymatoderma* e *Panus* dentro de Panaceae é principalmente respaldada por análises filogenéticas moleculares. Tanto *Cymatoderma* quanto *Panus*, embora sejam gêneros proeminentes e amplamente distribuídos, têm uma história taxonômica complexa, e a sistemática desses gêneros permaneceu instável até a proposição de Panaceae. A taxonomia de *Cymatoderma* e *Panus* tem sido afetada tanto pela presença de várias espécies com numerosos sinônimos heterotípicos, descritas nos séculos 19 e 20, quanto à convergência morfológica que ambos gêneros apresentam com outras famílias de Polyporales, fazendo com que sejam facilmente confundidos. Desta forma uma revisão abrangente do gênero é necessária. As espécies descritas no Brasil e aquelas com registros de ocorrência também carecem de coletas e revisões adicionais. Embora evidências moleculares tenham sido utilizadas para delimitar algumas espécies no Brasil, várias espécies ainda não foram submetidas a esse tipo de análise. Com o propósito de esclarecer a diversidade de espécies, garantir uma identificação mais precisa e realizar uma filogenia representativa de Panaceae, foram conduzidos estudos com espécies que ocorrem no Brasil. Análises morfológicas e filogenéticas (moleculares: nrITS, nrLSU, RPB1 e tef1- α) foram realizadas. Panaceae é constituída por pelo menos 18 clados, dos quais 4 são propostos neste trabalho como novas espécies, juntamente com 2 epítifícias e 4 novas combinações. *Endopandanicola thailandicus* (espécie endófita) está sendo sinonimizada e combinada no gênero *Panus*. Apresento, adicionalmente, uma chave de identificação, definições de *sensu stricto* e resoluções nomenclaturais, quando necessário, para as espécies em Panaceae. A partir do levantamento dos dados, foi possível também avaliar o estado de conservação de uma das espécies, a qual foi classificada como quase ameaçada conforme critérios da IUCN (*International Union for Conservation of Nature*).

Palavras-chave: Panaceae, *Cymatoderma* e *Panus*, *Panus velutinus*, *Endopandanicola thailandicus*, Polyporales Neotropicais.

ABSTRACT

The taxonomic revision of Panaceae, despite its relatively recent proposition, is essential due to the family's establishment based on a limited representation derived from only two taxa. The acceptance of the genera *Cymatoderma* and *Panus* within Panaceae is primarily supported by molecular phylogenetic analyses. Both *Cymatoderma* and *Panus*, although prominent and widely distributed genera, have a complex taxonomic history, and the systematic placement of these genera remained unstable until the proposal of Panaceae. The taxonomy of *Cymatoderma* and *Panus* has been impacted by the presence of numerous species with heterotypic synonyms described in the 19th and 20th centuries and by morphological convergence that both genera exhibit with other families of Polyporales, making them easily confused. Therefore, a comprehensive review of the genera is necessary. Species described in Brazil and those with occurrence records also lack additional collections and reviews. Although molecular evidence has been used to delimit some species in Brazil, several species have not yet undergone such analysis. With the aim of elucidating species diversity, ensuring more accurate identification, and conducting a representative phylogeny of Panaceae, studies were conducted with species occurring in Brazil. Morphological and phylogenetic analyses (molecular: nrITS, nrLSU, RPB1, and tef1- α) were performed. Panaceae is currently composed of at least 18 clades, with 4 of these proposed in this work as new species, along with 2 epitypifications and 4 new combinations. *Endopandanicola thailandicus* (endophytic species) is being synonymized and combined into the genus *Panus*. Additionally, I present an identification key, definitions of sensu stricto, and nomenclatural resolutions, as needed, for species in Panaceae. Based on the data compilation, it was also possible to assess the conservation status of one species, which was classified as Near Threatened according to IUCN (International Union for Conservation of Nature) criteria.

Keywords: Panaceae, *Cymatoderma* e *Panus*, *Panus velutinus*, *Endopandanicola thailandicus*, Neotropic Polyporales.

SUMÁRIO

1	INTRODUÇÃO GERAL	16
1.1	CYMATODERMA JUNGH.	17
1.2	PANUS FR.....	19
2	OBJETIVOS	21
3	REFERÊNCIAS	22
CAPÍTULO 1 – GIVE PANACEAE WHATS IS IT'S RIGHT: MOLECULAR CONFIRMATION ANDA NOMENCLATURAL ADJUSTMENTS		28
CAPÍTULO 2 – THE MOST COMPREHENSIVE PHYLOGENY OF PANUS (PANACEAE, POLYPORALES) AND REVISITED BRAZILIAN DIVERSITY		56
ANEXO A – AVALIAÇÃO DO ESTADO DE CONSERVAÇÃO DE CYMATODERMA SCLEROTIOIDES LLOYD.....		129
4	CONSIDERAÇÕES FINAIS.....	139

1 INTRODUÇÃO GERAL

Panaceae Miettinen, Justo & Hibbett é uma linhagem de Polyporales que agrupa os gêneros *Cymatoderma* Jungh. e *Panus* Fr. (Justo et al. 2017). As características determinantes para reconher os representantes de Panaceae são: presença de basidiomas pileados-estipitados com himenóforo lamelar ou liso; sistema hifal dimítico com hifas generativas fibuladas; basidiósporos de parede fina, lisa, hialinos e inamiloïdes; e cistídios de parede fina e/ou de parede grossa (Justo et al. 2017).

A proposição de agrupar os dois gêneros em Panaceae deve-se principalmente às reconstruções filogénéticas baseadas em duas amostras para os marcadores moleculares ITS, LSU e RPB1(Justo et al. 2017). No entanto, *Cymatoderma* e *Panus* também compartilham características micromorfológicas. No estudo filogenético de Yoon et al. (2003), os autores sugerem que *Panus* e *Cymatoderma* seriam táxons irmãos, contudo sem maiores discussões. Este estudo utilizou o marcador molecular SSU rRNA, e apenas uma sequência de cada gênero (*Panus* e *Cymatoderma*) foi empregada (Yoon et al. 2003). O mesmo resultado filogenético, utilizando 4 marcadores moleculares (ITS, LSU, *atp6* e mtSSU) e com uma sequência representando cada gênero, é observado no trabalho de Miettinen et al. (2012), corroborando assim o atual posicionamento adotado para estes gêneros.

Embora *Cymatoderma* e *Panus* sejam gêneros conspícuos e de ampla distribuição, possuem um histórico taxonômico problemático. Ambos podem ser facilmente confundidos em campo com outras famílias de Polyporales, por apresentarem similaridade morfológica com *Podoscypha* Pat. (Podoscyphaceae) e *Lentinus* Fr. (Polyporaceae), respectivamente.

O posicionamento sistemático de *Cymatoderma* permaneceu instável até a designação da família Panaceae. No passado, um sinônimo posterior, *Cladoderris* Pers. ex Berk., foi utilizado para se referir ao gênero (Lloyd 1913; Burt 1920). Historicamente, *Cymatoderma* sempre esteve relacionado a *Stereum* s. l. (i. e, *Aquascypha* D. A. Reid, *Cotylidia* P. Karst, *Podoscypha*, *Stereopsis* D. A. Reid, *Stereum* Hill ex Pers) ou a fungos estipitados stereoides, que faz referência a um grupo de fungos com himenóforo liso (Lloyd 1913; Talbot 1958; Reid, 1965; Sjokvist et al. 2012). No entanto, com a inclusão de caracteres microscópicos no século XX, em meados dos anos 20, e com o advento das técnicas moleculares nos anos 90 o conceito de *Stereum* foi cada vez mais reduzido.

Panus foi proposto por Fries (1838), mas por muito tempo esteve incluído no conceito amplo de *Lentinus*. Baseada exclusivamente em caracteres morfológicos, a classificação de *Panus* permeava entre a categoria gênero e de subgênero. Moser (1978), Singer (1975, 1986), Corner (1981), e Thorn et al. (2000) são exemplos de estudos que consideram *Panus* um gênero independente de *Lentinus* s.s. O trabalho mais abrangente sobre *Panus* foi realizado por Pegler (1983) que o considerou subgênero de *Lentinus* (*Lentinus* subgen. *Panus*). Foi somente com estudos moleculares que se confirmou o status de *Panus* como um gênero independente e filogeneticamente não relacionado com *Lentinus* (Hibbett e Vilgalys 1993; Grand 2004).

1.1 CYMATODERMA JUNGH.

Cymatoderma tem sido tradicionalmente caracterizado por basidioma infundibuliforme a flabeliforme, centralmente estipitado, himenóforo liso-plicado, sistema hifal dimítico, basidiósporos subcilíndricos a elipsoides, lisos e que não reagem na presença de Melzer, presença de cistídios de parede fina, raramente de parede espessa, e trama irregular (Welden 1960; Reid 1965). A maioria das espécies de *Cymatoderma* ocorrem na região Neotropical (Welden 2010).

No contexto morfológico, *Cymatoderma* não foi amplamente explorado. Além disso, as relações filogenéticas dentro do gênero não são claras. No estudo de Sjökvist et al. (2012) é possível observar que os grupos morfológicos recuperados na filogenia não compreendem agrupamentos monofiléticos, *Cymatoderma dendriticum* (Pers.) D.A. Reid e *C. pallens* Berthet & Boidin formam clados distantemente relacionados e fora do conceito filogenético de *Cymatoderma*.

Cymatoderma caperatum (Berk. & Mont.) D.A. Reid e *C. elegans* Jungh. são as espécies mais representadas em filogenias que abrangem o gênero, sendo *C. caperatum* o táxon mais coletado nas Américas Central e do Sul, segundo dados do GBIF.org (acessado em 2024). Ainda, *C. caperatum* apresenta uma distribuição disjunta com registro de poucas coletas no Japão e Austrália. O crescente número de coleções que recebe o nome de *C. caperatum*, sem uma análise precisa, sugere a possibilidade de haver uma diversidade subamostrada com táxons ainda não descritos, o mesmo ocorrendo para espécimes previamente determinados como *C. dendriticum*. A distribuição de *C. elegans* é mais representativa em partes da Oceania

e Ásia, com escassos registros para a América do Sul (GBIF, 2023), contudo é mais amplamente distribuída comparada a *C. caperatum*.

Do gênero, *Cymatoderma sclerotiooides* (Lloyd) D.A. Reid é a única espécie que foi avaliada pela IUCN (*International Union for Conservation of Nature*) (Capítulo 3 desta tese, Funez et al. 2021). Descrito a partir de espécimes do Brasil e com pouquíssimos registros de ocorrência, *C. sclerotiooides* ainda não foi amostrado em estudos moleculares. Essa é a única espécie que apresenta um esclerócio verdadeiro (daí vem a designação do epíteto) (Lloyd 1922). Dos sete registros de ocorrência de *C. sclerotiooides*, cinco deles são da região Amazônica entre Brasil, Colômbia e Peru. Vale destacar que este domínio fitogeográfico no Brasil, segundo os dados do INPE (2020), vem sofrendo com as altas taxas de incêndios e o crescente desmatamento.

Cymatoderma semiresupinatum (A.L. Welden) A.L. Welden e *C. viridan* (Lloyd) A.L. Welden são espécies descritas a partir de espécimes do Brasil e conhecidas apenas pelo holótipo. Ambas espécies são comparadas com outras de *Podoscypha*, gênero ao qual pertenciam anteriormente (Welden 2010). Além da ausência de dados moleculares, esses táxons apresentam morfologias contrastantes com as demais espécies já descritas para *Cymatoderma*, como basidioma ressupinado-reflexo, característica diagnóstica para *C. semiresupinatum*, e himenóforo totalmente liso, sem dobras obtusas, presente em *C. viridan*. Welden (2010) comenta sobre caracteres morfológicos que podem auxiliar na distinção a nível específico e genérico (neste caso, fazendo referência a *Podoscypha*), como por exemplo tamanho e forma dos basidiomas, mas sempre se questiona sobre a significância destes. A discussão sobre os caracteres que auxiliam na distinção das espécies vem desde os estudos de Lloyd (1913, como *Cladoderris*), que considerou como caracteres de valor taxonômico as dobras do himenóforo e a superfície superior do píleo (densamente ou escassamente tomentosa). É instrutivo citar as observações apontadas por Lloyd, embora seja possível constatar já nos trabalhos subsequentes (Welden 1960; Reid 1965), que devido à variação intraespecífica, a delimitação de táxons com tais caracteres pode falhar.

Com uma morfologia não resolutiva para distinção de espécies, e relações filogenéticas assumidas com base em apenas quatro espécies, *Cymatoderma* mostra-se um táxon que carece de uma abordagem molecular com inclusão de regiões informativas do DNA para melhor inferir as relações filogenéticas entre as espécies

(Bruns et al. 1991; Hibbett 1992; Hibbett e Binder 2002; Miettinen et al. 2011; Sjökvist et al. 2012), além de ampla amostragem, tentando cobrir regiões geográficas subamostradas.

1.2 *PANUS FR.*

Panus, o gênero tipo de Panaceae, é reconhecido pela combinação de basidiomas infundibuliformes a ciatiformes, central a excentricamente estipitados, himenóforo lamelar, sistema hifal dimítico (hifas esqueletais de parede espessada, tipicamente não ramificadas), basidiósporos elipsoides, lisos que não reagem na presença de Melzer, presença de cistídios de parede fina e/ou de parede grossa, e trama irregular da lamela (Corner 1981; Pegler 1983 *Lentinus* subgen. *Panus*).

Em estudos anteriores, *Panus* foi comumente observado em clados residuais ou na família Meruliaceae, contudo sem informações mais claras para o gênero (Binder et al. 2013; Zmitrovich & Malysheva 2013; Zmitrovich & Kovalenko 2016). Baseados em trabalhos essencialmente morfológicos, a taxonomia de *Panus* é instável, com espécies que possuem inúmeros sinônimos heterotípicos, sem haver consenso se são de fato sinônimos, o que dificulta saber o real número de espécies já descritas para o gênero. Desta forma faz-se necessário a revisão de *Panus*, utilizando uma abordagem integrativa, a fim de evitar a formação de mais complexos taxonômicos e contribuir com a delimitação correta das espécies.

O número relatado de espécies conhecidas de *Panus* varia entre as diferentes interpretações, Kirk et al. (2008) reconhecem 25 espécies das quais 11 são registradas na literatura como ocorrentes no Brasil (Putzke 1994; Drechsler-Santos et al. 2012; Gugliotta et al. 2015; Vargas-Isla et al. 2015). Notavelmente, há espécies descritas para o Brasil que até o momento não foram revisadas taxonomicamente.

Panus similis foi relatado como ocorrente na África, Ásia e Austrália no estudo de Pegler (1983). Grand (2004) afirma ter o primeiro registro deste táxon para as Américas, incluindo três sequências de coleções da Argentina. No entanto, não há sequências comparativas de outras regiões geográficas na filogenia para confirmar tal hipótese, e neste mesmo trabalho não há informações sobre morfologia dos espécimes. Embora Corner (1981) tenha dado uma classificação infraespécifica para *Panus similis* (*Panus fulvus* var. *similis* sensu Corner 1981), após a revisão dos materiais tipos, Pegler (1983) considerou esta espécie independente de *Panus fulvus*.

[= sinônimo de *Panus velutinus* (Fr.) Sacc. em “The genus *Lentinus*: A world monograph” Pegler 1983]. Com uma morfologia particular, como presença de um píleo finamente velutino, plicado-sulcado e lamelas amplamente espaçadas, *Panus similis* não tem registros de ocorrência no Brasil, embora existam espécimes com essa determinação em coleções brasileiras. Com o registro duvidoso para a Argentina, somado à distribuição relatada por Pegler (1983), os espécimes considerados como *Panus similis* da região neotropical possivelmente representam uma espécie distinta.

Outra espécie que carece revisão é *Panus convivalis* Corner, que embora tenha sido descrita a partir de coleções do Brasil, não apresenta registro de novas coletas deste táxon além do espécime tipo. Pegler (1983) menciona que esta espécie pode ser comparada a *Lentinus adhaerens* (Alb. & Schwein.) Fr. [= *Neolentinus adhaerens* (Alb. & Schwein.) Redhead & Ginns], mas não pôde revisar o tipo, portanto não é possível confirmar se de fato trata-se de uma espécie de *Panus*. *Panus hymenorhizus* Speg. também foi proposto a partir de material do Brasil (Spegazzini, 1889). Mas desde sua descrição, não houve novas coletas e tampouco revisão do holótipo para confirmar a posição genérica desta espécie.

Ainda, embora evidências filogenéticas baseadas em dados moleculares tenham sido utilizadas para delimitação de algumas espécies do gênero no Brasil, estas espécies nunca foram objeto desta abordagem, exceto para o reconhecimento da distinção entre *Panus lecomtei* (Fr.) Corner e *P. strigellus* (Berk) Overh. (Vargas-Isla et al. 2015).

Ainda que o gênero seja amplamente reconhecido e distribuído, os estudos mais recentes sobre *Panus* giram em torno do potencial biotecnológico de algumas espécies (e.g., *Panus lecomtei*, *P. conchatus*, Söylemez et al. 2020; Zhu et al. 2021; Peláez et al. 2023). A reconstrução filogenética mais representativa para o gênero mostra a presença de pelos menos três complexos taxonômicos (i. e., *Panus strigellus*, *Panus tephroleucus*, e *Panus velutinus*), todos estes são registrados para o Brasil (Pegler 1983; Drechsler-Santos et al. 2012; Vargas-Isla et al. 2015). Com o problemático histórico taxonômico e as relações filogenéticas intraespecíficas ainda sem definição, torna-se necessária uma revisão de *Panus* a fim de resolver os complexos presentes e revisar coleções para uma melhor compreensão da taxonomia do gênero.

2 OBJETIVOS

Esta tese teve como objetivo geral revisar taxonomicamente as espécies de Panaceae que ocorrem no Brasil, a partir de análises morfológicas e filogenéticas moleculares, e contribuir com o conhecimento da diversidade do grupo, das relações filogenéticas das espécies e da delimitação da família.

Especificamente:

- (i). Fornecer informações para identificação das espécies de *Panus* através da descrição macro e micromorfológica, ilustração e elaboração de chaves dicotômicas;
- (ii). Entender as relações dentro do grupo e com outros grupos proximamente relacionados a família Panaceae, através da obtenção de sequências de DNA de espécies ainda não incluídas em filogenias;
- (iii). Interpretar filogeneticamente, com base em dados morfológicos e moleculares, os táxons e possíveis linhagens correspondentes a novas espécies dos gêneros *Cymatoderma* e *Panus*.
- (iv). Avaliar o estado de conservação de uma espécie de Panaceae registradas no território brasileiro.

3 REFERÊNCIAS

- AGRAWAL, K., & VERMA, P. 2020. Fungal metabolites: A recent trend and its potential biotechnological applications. In New and Future Developments in Microbial Biotechnology and Bioengineering (pp. 1-14). Elsevier.
- ARAÚJO, I. F., NÓBREGA, J. P., CAVALLAZZI, J. R. P., MUNIZ, A. W., VARGAS-ISLA, R., & ISHIKAWA, N. K. 2019. Efeito do pH na atividade de lacase e na descoloração de corantes industriais por extrato enzimático de *Panus lecomtei*. Embrapa Amazônia Ocidental-Artigo em periódico indexado.
- BINDER, M.; JUSTO, A.; RILEY, R. ; SALAMOV, A.; LOPEZ-GIRALDEZ, F.; SJÖKVIST, E.; COPELAND, A; FOSTER, B.; SUN, H.; LARSSON, E.; LARSSON, K. H; TOWNSEND, J.; GRIGORIEV, I. V.; HIBBETT, D. S. 2013. Phylogenetic and phylogenomic overview of the Polyporales. *Mycologia* 105: 1350–1373.
- BURT, E. A. 1920. The Thelephoraceae of North America. XII. *Stereum*. Annals of the Missouri Botanical Garden, 7(2/3), 81-249.
- BRUNS, T. D; WHITE, T. J. & TAYLOR, J. W. 1991. Fungal molecular systematics. *Annual Reviews of Ecology and Systematics* 22: 525–564.
- CARDOSO, B.K.; LINDE, G.A.; COLAUTO, N.B.; VALLE, J.S.D. 2018. *Panus strigellus* laccase decolorizes anthraquinone, azo, and triphenylmethane dyes. *Biocatal. Agric. Biotechnol.*, 16, 558–563. [CrossRef]
- CORNER, E. J. H. 1981. The agaric genera *Lentinus*, *Panus* and *Pleurotus* with particular reference to Malaysian species. *Beih. Nova Hedw.*, v. 69, p. 1-169.
- DRECHSLER-SANTOS, E. R.; WARTCHOW, F.; COIMBRA, V. R. M.; GIBERTONI, T. B. & CAVALCANTI, M. A. Q. 2012. Studies on lentinoid fungi (*Lentinus* and *Panus*) from the semi-arid region of Brazil. *The Journal of the Torrey Botanical Society*, v. 139, p. 437-446.
- FRIES, E. M. 1838. Epicrisis systematis mycologici, seu synopsis Hymenomycetum. 1—608.Upsaliae.

- GRAND, E. A. 2004. Systematics and species concepts in the genera *Lentinus* Fr. and *Panus* Fr., with emphasis on the *Lentinus tigrinus*, *L. crinitus* and *Panus lecomtei* complexes [tese de doutorado]. Knoxville: Univ. Tennessee Press. 116 p.
- GUGLIOTTA, A. M.; GIBERTONI, T. B.; DRECHSLER-SANTOS, E. R.; SILVEIRA, R. M. B.; CHIKOWSKI, R. S.; PIRES, R. M.; MONTOYA, C. A. S.; SOUZA, J. F.; PALACIO, M.; REZENDE, D. H. C. 2015. Polyporales in Lista de Espécies da Flora do Brasil. Jardim Botânico do Rio de Janeiro. Disponível em: <<http://floradobrasil.jbrj.gov.br/jabot/floradobrasil/FB92498>>. Acesso em: 11 de Junho de 2016.
- HIBBETT, D.S. 1992. Ribosomal RNA and fungal systematics. Transactions of the Mycological Society of Japan 33: 533–556.
- HIBBETT, D. S.; VILGALYS, R. 1993. Phylogenetic Relationships of *Lentinus* (Basidiomycotina) inferred from Molecular and Morphological Characters. Systematic Botany, v. 18, p. 409-433.
- HIBBETT, DS, & BINDER, M. 2002. Evolução de morfologias complexas de frutificação e corpo em homobasidiomicetos. Proceedings of the Royal Society of London. Series B: Biological Sciences, 269 (1504), 1963-1969.
- HU, P. P., FU, S. Y., & LI, G. R. 2001. Methods of assaying laccase activity by *Panus Conchatus*. Guangzhou Chemistry, 26(4), 22-27.
- JUSTO, A.; MIETTINEN, O.; FLOUDAS, D.; ORTIZ-SANTANA, B.; SJÖKVIST, E.; LINDNER, D.; NAKASONE, K.; NIEMELÄ, T.; LARSSON, K. H.; RYVARDEN, L.; HIBBETT, D. S. 2017. A revised family-level classification of the Polyporales (Basidiomycota). Fungal Biolgy. 64p.
- KIRK, P. M.; CANNON, P. F.; MINTER, D. W.; STALPERS, J. A. 2008. Dictionary of the Fungi. 10th ed. CABI, Wallingford, UK, 771p.
- LLOYD, C. G. 1913. 'A synopsis of the genus Cladoderris', p. 1o-II, in Mycological Writings 4.

- MIETTINEN, O., LARSSON, E., SJÖKVIST, E., & LARSSON, K. H. 2012. Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimitic polypores (Polyporales, Basidiomycota). Cladistics, 28(3), 251-270.
- MOSER, M. 1978. Keys to Agarics and Boleti. London: R. Philips.
- NETO, C. B. S., CONCEIÇÃO, A. A., GOMES, T. G., DE AQUINO RIBEIRO, J. A., CAMPANHA, R. B., BARROSO, P. A. V., ... & MILLER, R. N. G. 2020. A Comparison of Physical, Chemical, Biological and Combined Treatments for Detoxification of Free Gossypol in Crushed Whole Cottonseed. Waste and Biomass Valorization, 1-11.
- PEGLER, D. N. 1983. The genus *Lentinus*: A world monograph. Kew Bull. Add. Ser., v. 10, p. 1-281.
- PELÁEZ, R. D. R., SERRA, L. A., WISCHRAL, D., CUNHA, J. R. B., MENDES, T. D., PACHECO, T. F., ... & DE ALMEIDA, J. R. M. 2023. Improvement of Laccase Activity in Co-Culture of *Panus lecomtei* and *Sporidiobolus pararoseus* and Its Application as an Enzymatic Additive in Biomass Hydrolysis and Dye Decolorization. Fermentation, 9(11), 945.
- PUTZKE, J. 1994. Lista dos fungos Agaricales (Hymenomycetes, Basidiomycotina) referidos para o Brasil. Caderno Pesquisa Série Botânica, 6:1-189.
- PUTZKE J. & PUTZKE, M. T. L. 2002. Os reinos dos fungos. Vol. 2. Editora da Universidade
- REID, D. A. 1965. A monograph of stipitate steroid fungi. Beih Nova Hedwig 18:1–382.
- RICK, J. 1938. Agaric Riograndenses. Lilloa: v. 2, p. 307- 312.
- SINGDEVSACHAN, S. K., PATRA, J. K., & THATOI, H. 2013. Nutritional and bioactive potential of two wild edible mushrooms (*Lentinus sajor-caju* and *Lentinus torulosus*) from Simlipal Biosphere Reserve, India. Food Science and Biotechnology, 22(1), 137-145.

- SINGER, R. 1975. The Agaricales in Modern Taxonomy. 3rd edn. Vaduz: J. Cramer.
- SINGER, R. 1986. The Agaricales in Modern Taxonomy. 4th edn. Königstein: Sven Koeltz Scientific Books.
- SJÖKVIST, E.; LARSSON, E.; EBERHARDT, U.; RYVARDEN, L & LARSSON, K. H. 2012. Stipitate steroid basidiocarps have evolved multiple times. *Mycologia* 104: 1046–1055.
- SOTÃO, H. M. P.; BONONI, V. L. R. & FIGUEIREDO, T. S. 1991. Basidiomycetes de manguezais da Ilha de Maracá, Brasil. *Boletim do Museu Paraense Emílio Goeldi, sér. Bot.* 7(1): 109-114.
- SOUZA-FAGUNDES, E. M., COTA, B. B., ROSA, L. H., ROMANHA, A. J., CORRÊA-OLIVEIRA, R., ROSA, C. A., ... & MARTINS-FILHO, O. A. 2010. In vitro activity of hypnophilin from *Lentinus strigosus*: a potential prototype for Chagas disease and leishmaniasis chemotherapy. *Brazilian Journal of Medical and Biological Research*, 43(11), 1054-1061.
- SOYLEMEZ, T., YAMAÇ, M., & YILDIZ, Z. 2020. Statistical optimization of cultural variables for enzymatic degradation of aflatoxin B1 by *Panus neostrigosus*. *Toxicon*, 186, 141-150.
- TALBOT, P. B. 1958. The Genera *Craterellus*, *Cymatoderma* (*Cladoderris*) and *Thelephora* in South Africa. *Bothalia*, 7(1), 117-129.
- TEIXEIRA, A. R. 1946. Himenomictos brasileiros – III. *Bragantia* 6: 165–188.
- TIBPROMMA, S., HYDE, K. D., BHAT, J. D., MORTIMER, P. E., XU, J., PROMPUTTHA, I., ... & KARUNARATHNA, S. C. 2018. Identification of endophytic fungi from leaves of Pandanaceae based on their morphotypes and DNA. Vargas-Isla, R., & Ishikawa, N. K. (2008). Optimal conditions of in vitro mycelial growth of *Lentinus strigosus*, an edible mushroom isolated in the Brazilian Amazon. *Mycoscience*, 49(3), 215.
- THORN, R. G.; MONCALVO, J-M.; REDDY, C. A.; VILGALYS, R. 2000. Phylogenetic analyses and the distribution of nematophagy support a monophyletic

- Pleurotaceae within the polyphyletic pleurotidlentinoid fungi. *Mycologia* 92: 241–252.
- VARGAS-ISLA, R., & ISHIKAWA, N. K. 2008. Optimal conditions of in vitro mycelial growth of *Lentinus strigosus*, an edible mushroom isolated in the Brazilian Amazon. *Mycoscience*, 49(3), 215-219.
- VARGAS-ISLA, R. 2012. Taxonomia, biologia e produção de semente-inóculo de *Panus strigellus*, um cogumelo comestível da Amazônia. (tese de doutorado). INPA: Manaus. 126p.
- VARGAS-ISLA, R., ISHIKAWA, N. K., & PY-DANIEL, V. 2013. Contribuições etnomicológicas dos povos indígenas da Amazônia. *Biota Amazônia* (Biote Amazonie, Biota Amazonia, Amazonian Biota), 3(1), 58-65.sequence data from southern Thailand. *MycoKeys*, (33), 25.
- VARGAS-ISLA, R.; CAPELARI, M.; MELONI, N.; NAGASAWA, E.; TOKIMOTO, K.; ISHIKAWA, N. K. 2015. Relationship between *Panus lecomtei* and *P. strigellus* inferred from their morphological, molecular and biological characteristics. *Mycoscience*. 10.1016.
- WELDEN, A. L. 1960. The genus *Cymatoderma* (Thelephoraceae) in the Americas. *Mycologia*. 52:856-876.
- WELDEN, A. L. 2010. *Stereum* s.l. *Flora Neotropica Monograph* 106:1–79.
- YAMAC, M., KANBAK, G., ZEYTINOGLU, M., BAYRAMOGLU, G., SENTURK, H., & UYANOGLU, M. 2008. Hypoglycemic effect of *Lentinus strigosus* (Schwein.) Fr. crude exopolysaccharide in streptozotocin-induced diabetic rats. *Journal of medicinal food*, 11(3), 513-517.
- YOON, S. I., KIM, S. Y., LIM, Y. W., & JUNG, H. S. 2003. Phylogenetic evaluation of steroid fungi. *Journal of microbiology and biotechnology*, 13(3), 406-414.
- ZHU, M., HAN, Y., HU, X., & REN, L. 2021. Process Development of Ergothioneine by Submerged Fermentation of a Novel Medicinal Mushroom *Panus Conchatus*.

- ZMITROVICH, I. V., & MALYSHEVA, V. F. 2013. Towards a phylogeny of *Trametes* alliance (Basidiomycota, Polyporales). *Микология и фитопатология*, 47(6), 358-380.
- ZMITROVICH, I. V., & KOVALENKO, A. E. 2016. Lentinoid and polyporoid fungi, two generic conglomerates containing important medicinal mushrooms in molecular perspective. *International Journal of Medicinal Mushrooms*, 18(1).

CAPÍTULO 1 - GIVE PANACEAE WHATS IS IT'S RIGHT: MOLECULAR CONFIRMATION ANDA NOMENCLATURAL ADJUSTMENTS

Give Panaceae whats is it's right: molecular confirmation anda nomenclatural adjustments

RESUMO

Panaceae é uma linhagem na ordem Polyporales que inclui os gêneros *Cymatoderma* e *Panus*. Ambos gêneros apresentam semelhança morfológica com outros fungos da mesma ordem. A criação da família foi baseada em uma amostragem limitada, o que leva a questionar sua validade diante da diversidade de espécies presentes. A fim de avaliar a estabilidade de Panaceae e investigar as relações entre as espécies de *Cymatoderma* e *Panus*, realizou-se a coleta e empréstimo de espécimes, seguido pela extração e sequenciamento de DNA, contemplando uma amostragem significativa de *Cymatoderma* e *Panus*. Como resultado, é apresentado uma árvore filogenética representativa de Panaceae, com a inclusão de dados moleculares inéditos, além de discussões acerca da polifilia de *Cymatoderma* e novas proposições taxonômicas.

Palavras-chave: *Cymatoderma*, *Panus*, Convergência Morfológica.

1. INTRODUÇÃO

Panaceae Miettinen, Justo & Hibbett é uma linhagem dentro da ordem Polyporales que engloba os gêneros *Cymatoderma* Jungh. e *Panus* Fr. Características chave que identificam os membros da família Panaceae incluem a presença de basidiomas pileado-estipitados, com himenóforo lamelar ou liso, um sistema hifal dimítico com hifas generativas fibuladas, basidiósporos com paredes finas, lisos, hialinos e inamiloïdes, além de cistídios com paredes finas e/ou espessas (Justo et al. 2017).

A inclusão de *Cymatoderma* e *Panus* na família Panaceae é baseada principalmente em estudos filogenéticos moleculares (e.g., Yoon et al. 2003, Miettinen

et al. 2012). No estudo filogenético conduzido por Yoon et al. (2003), sugere-se que *Panus* e *Cymatoderma* possam ser táxons irmãos, ainda que os autores não discutam este resultado. Este estudo, utilizando o marcador molecular SSU rRNA, empregou apenas uma sequência representativa de cada gênero. Resultados concordantes foram obtidos em uma análise mais recente realizada por Miettinen et al. (2012), a qual utilizou quatro marcadores moleculares (ITS, LSU, atp6 e mtSSU) e também adotou uma única amostra para cada gênero.

Apesar de *Cymatoderma* e *Panus* serem gêneros distintos e amplamente distribuídos, a taxonomia desafiadora desses fungos se deve à confusão morfológica que podem causar no campo, por conta da similaridade morfológica a outros taxa de Polyporales, como *Podoscypha* Pat. (Podoscyphaceae) e *Lentinus* Fr. (Polyporaceae), respectivamente.

A posição taxonômica de *Cymatoderma*, antes tratado em Meruliaceae, só foi definida com a criação da família Panaceae (Justo et al. 2017). Em épocas anteriores, um sinônimo posterior, *Cladoderris* Pers. ex Berk., foi empregado para referir-se ao gênero (Lloyd 1913; Burt 1920). Historicamente, *Cymatoderma* foi associado a *Stereum* s. l. [ou seja, *Aquascypha* D. A. Reid (Incertae sedis, Polyporales), *Cotylidia* P. Karst (Rickenellaceae, Hymenochaetales), *Podoscypha* (Podoscyphaceae, Polyporales), *Stereopsis* D. A. Reid (Stereopsidaceae, Stereopsidales), *Stereum* Hill ex Pers (Stereaceae, Russulales)] ou a fungos estipitados stereoides, referindo-se a um grupo de fungos com himenóforo liso (Lloyd 1913; Talbot 1958; Reid, 1965; Sjokvist et al. 2012).

Já *Panus* historicamente oscilava entre ser considerado um gênero independente e um subgênero de *Lentinus* com base na morfologia (Lloyd 1913, Talbot 1958, Welden 1960, Reid 1965, Moser 1978, Singer 1975 e 1986, Corner 1981, Pegler 1983). Os estudos de Moser (1978), Singer (1975, 1986), Corner (1981), e Thorn et al. (2000), consideravam *Panus* um gênero independente de *Lentinus* s. s., mas foi somente com estudos moleculares que *Panus* pôde ser confirmado como gênero independente e não relacionado a *Lentinus* (Hibbett e Vilgalys 1993, Thorn et al. 2000, Grand 2004, Sjokvist et al. 2012).

Essas descobertas ilustram como a taxonomia evoluiu com o uso de técnicas moleculares e aprofundou nosso entendimento da relação entre esses gêneros de

fungos na família Panaceae. Embora a proposição de Panaceae possa atualmente ter esclarecido a posição taxonômica desses gêneros, que antes estava incerta dentro de Polyporales, a criação da família baseou-se em uma amostragem bastante limitada, com apenas um representante para cada gênero. Isso nos leva a questionar a validade de uma família como Panaceae, especialmente considerando a diversidade de espécies já descritas para *Panus* e *Cymatoderma*. Diante disso, foi realizado um estudo filogenético molecular de Panaceae com a inclusão de uma amostragem significativa para ambos os gêneros *Panus* e *Cymatoderma* para testar a estabilidade deste grupo taxonômico. Além disso, novas proposições taxonômicas foram feitas a fim de esclarecer quais espécies fazem parte de Panaceae.

2. MATERIAIS E MÉTODOS

Coleções e morfologia dos espécimes

Os espécimes de Panaceae foram coletados nos domínios fitogeográficos da Amazônia (Pará e Mato Grosso), área de transição caatinga e cerrado (Piauí e Ceará), Cerrado (Mato Grosso) e Mata Atlântica (Bahia, Rio de Janeiro, São Paulo, Paraná, Santa Catarina e Rio Grande do Sul) tanto realizadas pela autora como por colaboradores. Os basidiomas coletados foram levados para o laboratório de Micologia da UFSC e em seguida mantidos por 12 a 24h em secadora para desidratação (30° a 38°C). Também foram armazenados fragmentos dos basidiomas em microtubos com sílica-gel, retirados ainda fresco, a fim de preservar o DNA para estudos moleculares.

Os exemplares coletados foram posteriormente depositados no herbário FLOR. Além disso, foram examinados espécimes de outros fungários, nomeadamente BPI, FLOR, INPA, LPS, K, SP, URM. Algumas espécies não puderam ser analisadas porque não estavam disponíveis, ou o curador não sabia onde estava, ou mesmo não houve retorno dos herbários (i. e., *Cymatoderma blumei*, *C. semiressuinatum* e *C. sclerotiooides*, *Panus convivalis*, *P. neostrigosus*, *P. tephroleucus*). As siglas dos herbários/fungários seguem Thiers (atualizadas continuamente). Nem todas as espécies amostradas na filogenia molecular foram estudadas morfologicamente.

Extração, amplificação, purificação e sequenciamento de DNA

Os dados moleculares (sequências de DNA) foram obtidos a partir do material proveniente da coleta de material em campo, material herborizado (mediante autorização dos herbários) e do banco de dados *GenBank* (<http://www.ncbi.nlm.nih.gov/genbank>). Os procedimentos de extração, amplificação e purificação foram realizados no Laboratório de Biologia Molecular do Departamento de Botânica – Lameb UFSC. A extração do DNA total dos materiais coletados seguiu a metodologia proposta por Góes-Neto et al. (2005), utilizando o tampão CTAB 2% pré-aquecido. Para amplificação (reações de PCR), as regiões nucleares ribossomais escolhidas foram ITS, LSU, RPB1 e Tef1- α . Os pares de primers empregados no procedimento foram: ITS1 e ITS4 (White et al. 1990, Gardes & Bruns 1993), LR0R e LR5 (Vilgalys & Hester 1990), RPB1-Af e RPB1-Cr (Stiller & Hall 1997, Matheny et al. 2002) e EF1-983F/EF1-2212R (Rehner 2001), respectivamente. Estes marcadores haviam sido utilizados nos estudos filogenéticos moleculares de *Panus* e *Cymatoderma* (i. e., Grand 2004; Miettinen et al. 2012; Sjokvist et al. 2012; Zmitrovich & Malysheva 2013; Vargas-Isla et al. 2015; Zmitrovich & Kovalenko 2016; Justo et al. 2017). Os produtos da amplificação foram purificados de acordo com protocolo com Polietilenoglicol (PEG; Sambrook et al. 1989) a 20% e posteriormente sequenciados através do método Sanger em sequenciador automático.

Alinhamento das sequências e análises filogenéticas moleculares

Os cromatogramas gerados foram revisados e editados manualmente no *software* Geneious versão 9.0.5 (Kearse et al. 2012). A presença de ambiguidades indicando posições heterozigotas, foram anotadas de acordo com o código do *International Union of Pure and Applied chemistry* (IUPAC).

As sequências geradas durante a realização deste estudo e de táxons relacionados depositadas em repositórios, foram agrupadas no *software* MEGA v.7 (Kumar et al. 2016) de acordo com o marcador utilizado e alinhadas no MAFFT v.7 (Katoh 2013). O alinhamento foi posteriormente revisado e editado no MEGA v.7.

Para reconstruir a hipótese filogenética de Panaceae com base em caracteres moleculares foram utilizadas a Inferência Bayesiana (IB), realizadas no MrBayes v.3.2.6 (Ronquist et al. 2012), e análise de Máxima Verossimilhança (ML) realizada no programa RAxML v.8.2.10 (Stamatakis 2014). O modelo de evolução molecular mais adequado aos dados foi obtido através do programa jModelTest2 v.2.1.11 (Darriba et

al. 2020). Ambos os métodos, modelo e programas estão disponíveis na plataforma CIPRES (<https://www.phylo.org/> Miller et al. 2010). Os programas foram utilizados pela plataforma CIPRES (<https://www.phylo.org/> Miller et al. 2010).

A análise de ML envolveu 100 buscas, cada uma a partir de uma árvore de parcimônia de adição passo a passo aleatória, sem proporção de sites invariantes e todos os outros parâmetros estimados pelo software. Após obtenção das topologias finais de ML e IB, suas congruências foram avaliadas visualmente, sendo considerados incongruentes apenas clados com configuração diferente que apresentassem suporte significativo, e em todos os casos a topologia de ML foi selecionada, e os valores de IB foram anotados. A configuração gráfica da árvore, quanto a rotação e disposição dos táxons na topologia, foi primeiro realizada no programa FigTree® v1.4.0. As árvores posteriormente foram salvas em formato PDF, e editadas graficamente no Inkscape v.1.2.2.

3. RESULTADOS

Neste estudo, foram analisados morfologicamente 154 espécimes, provenientes de coletas realizadas para este trabalho e de revisão de herbários. Foram geradas 67 sequências de DNA de 56 espécimes, especificamente 35 nrITS, 20 nrLSU, 1 RPB1 e 10 Tef1- α . O alinhamento final de 1393 pb de comprimento resultou em uma árvore filogenética (Figura 1), composta por 144 espécimes, representados por 120 nrITS, 98 nrLSU, 39 RPB1 e 42 tef1- α (Tabela 1), incluiu representantes de todas as famílias do “residual clade” conforme definido por Justo et al. (2017). A topologia IB e ML das árvores filogenéticas são consistentes, e apenas a árvore ML é apresentada (Figura 1).

As análises filogenéticas realizadas confirmaram a coesão da família Panaceae, englobando os gêneros *Panus* e *Cymatoderma*. No entanto, *Cymatoderma*, conforme sua aceitação atual, é polifilético. Sequências das espécies *Cymatoderma dendriticum* e *C. palens* formaram clados distintos, dentro do conceito filogenético de Podoscyphaceae, demonstrando uma confusa complexidade nas relações filogenéticas desse gênero. Ainda, as sequências nomeadas de

Cymatoderma dendriticum estão presentes em três distintos clados da família Podoscyphaceae.

Dados moleculares de espécies ainda não incluídas em filogenias também foram gerados, como o caso de *Cymatoderma sclerotiooides*. Cabe destacar que nem todas as espécies amostradas na filogenia foram estudadas morfologicamente, enfatizando a necessidade de integração entre abordagens moleculares e morfológicas para uma compreensão mais completa da taxonomia e filogenia desses fungos.

TAXONOMIA

***Cymatoderma sclerotiooides* (Lloyd) D.A. Reid, Kew Bulletin (3): 528 (1959).**

Figura 2.

≡ *Stereum sclerotiooides* Lloyd, Mycological Writings 7(66): 1115 (1922)

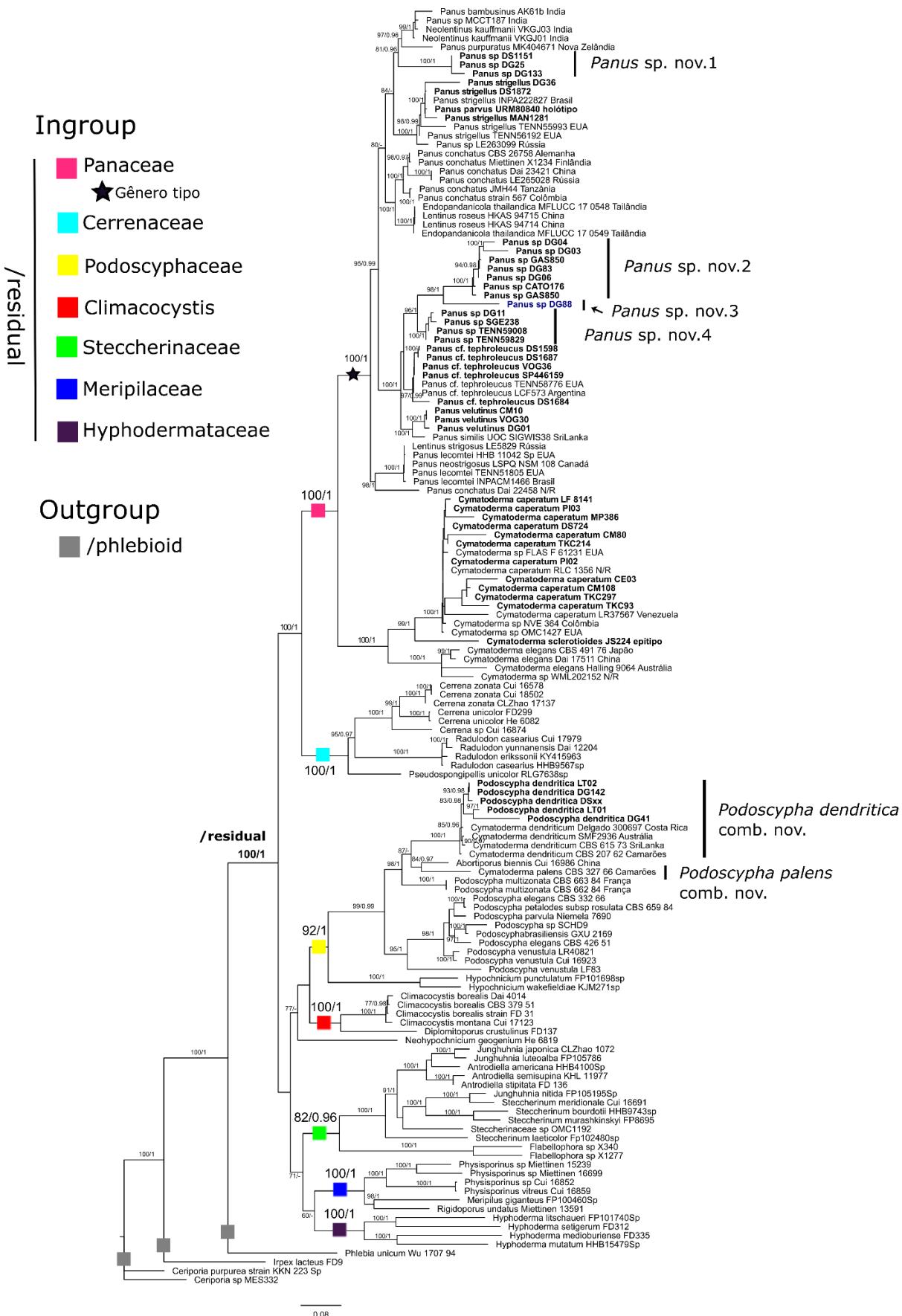
Mycobank: MB296340

Holótipo: BRASIL: 1922, Torrend, C. (BPI 329395; Catalog #: LC26679). (Ilustração do holótipo: plate 197 - figuras 2104 e 2105, Lloyd 1922)

Epítipo: BRASIL: Mato Grosso, Alta Floresta, Reserva Particular do Patrimônio Natural Cristalino, Trilha da Taboca. 20.I.2018, Simon-Cardoso, J. 224 (FLOR63606). Genbank accession numbers: ITS = to be provided ; nrLSU = to be provided; Tef1-alfa: to be provided.

Descrição : Píleo 46–70 mm diâm., infundibuliforme, coriáceo, margem apendiculada de coloração ocre a creme; superfície ornamentada com ligeiras cristas radiais cobertas por um tomento marrom avermelhado. Himenóforo liso com numerosas dobras radiais, ocre a creme; Estipe central 95–130 × 3.0–10 mm, cilíndrico, superfície tomentosa ocre a marrom; Esclerócio oval-alongado, duro, marrom-escuro, áspero, com uma massa micelial compacta esponjosa de coloração creme.

Figura 1. Árvore filogenética (Probabilidade Máxima) de Panaceae baseada em ITS, nrLSU, RPB1 e tef1. Nos ramos, os valores de suporte são indicados como BS/BPP. As sequências geradas neste estudo estão em negrito.



Fonte: Sousa-Guimarães 2024

Sistema hifal dimítico. *hifas generativas* 2.0–4.5 µm diâm., hialinas, fibuladas, de parede fina, algumas com parede mais espessa; *hifas esqueletais* 2.5–5.5 µm diâm., de parede espessa. *Basidiósporos* [30/1/1] (3.5–) 4–5.8 × 2.2–3.0 µm (Qm=1.85 µm; Q=1.3–2.3 µm; Lm= 5.0 µm; Wm= 2.5 µm), elipsóide a sub cilíndrico, hialinos, de parede fina, lisa, raramente gutulados, inamiloïdes. *Basídios* (22–) 28–40 × 4.0–6.5 µm, clavado, hialinos, de parede fina, tetraesporados. *Pleurocistídios* 30–68 × (–5.0) 7.0–12 µm, clavados, de parede fina e lisa.

Habitat e distribuição geográfica: gregário, com esclerócio. Brasil: Roraima (Macará) e Mato Grosso (Cristalino); Bolívia, Colômbia, Costa Rica, México, Panamá e Peru.

Notas: *Cymatoderma sclerotioïdes* é reconhecido por se desenvolver a partir de um esclerócio marrom escuro, rígido e fortemente estriado. Embora sua distribuição seja predominantemente tropical, há escassez de espécimes coletados, com apenas dois registros conhecidos no Brasil, ambos na região Amazônica, além do holótipo.

Propomos um epítipo deste espécime devido à excelente condição do material coletado e preservado, além de termos gerado dados moleculares inéditos para a espécie. Adicionalmente, a localização do holótipo em um herbário estrangeiro de difícil acesso (sem resposta dos curadores) nos motiva a realizar esta epitificação, visando facilitar o acesso aos dados para futuras investigações.

***Podoscypha dendritica* (D.A. Reid) Sousa-Guimarães & Drechsler-Santos, comb.
nov. Figura 3**

Mycobank:

Basônimo: *Cymatoderma dendriticum* (Pers.) D.A. Reid, Kew Bull. 13(3): 523 (1959)
[1958]

≡ *Thelephora dendritica* Pers., Botanique (Nagpur) 5: 176 (1827) [MB#471809]

Descrição: ver em Persoon 1827; e Reid 1959

Figura 2 *Cymatoderma sclerotioïdes* espécime FLOR - epítipo. **a–b.** espécime fresco
c. esclerócio. **d.** espécime desidratado. scale bar = 0.5 cm.



Fonte: Sousa-Guimarães 2024

Notas: *Podoscypha dendritica* é caracterizada por um basidioma dimidiado ou flabeliforme, profundamente lobulado, às vezes tornado-se imbricado, bege opaco a marrom claro, tornando-se esbranquiçado ou acinzentado na margem; séssil ou lateralmente estipitado, estipe curto e robusto, coberto por um tomento aveludado, marrom escuro; e himenóforo liso, com dobras bem marcadas, ramificadas e com verrugas. Esta espécie, descrita na Malásia, apresenta uma ampla distribuição e é frequentemente coletada na região neotropical. O primeiro registro *Podoscypha*

dendritica no Brasil foi feito por Saccardo (1888) como *Cladoderris dendritica*. Em nosso estudo, os materiais que corroboram a morfologia de *Podoscypha dendritica* (Reid 1959, como *Cymatoderma dendriticum*), filogeneticamente foram recuperados entre outras espécies de *Podoscypha* como linhagens distintas e aqui está devidamente combinado no gênero (Figura 1 e Figura suplementar 1).

***Podoscypha pallens* (Berthet & Boidin) Sousa-Guimarães & Drechsler-Santos,
comb. nov.**

MycoBank:

Basônimo: *Cymatoderma pallens* Berthet & Boidin, Cahiers de La Maboké 4(1): 33 (1966)

Descrição: ver em Berthet & Boidin 1966

Notas: *Podoscypha pallens* foi descrito a partir de material de Camarões, sendo reconhecido pela presença de um basidioma petaloide ou flabeliforme, imbricado, séssil, que pode atingir um raio de até 15 cm; superfície do píleo coberta por um tomento esbranquiçado; e himenóforo pruinoso, com estreitas e ramificadas nervuras. Neste estudo, a sequência designada como sendo do holótipo agrupou com espécies de *Podoscypha*, como uma linhagem distinta e aqui está devidamente combinado no gênero.

Figura 3. *Podoscypha dendritica* **a,c.** espécime DSxx (FLOR). **b.** espécime LF115 (FLOR). **d-e.** espécime LT01 (FLOR).



Fonte: Sousa-Guimarães 2024

DISCUSSÃO

O estudo representa um avanço significativo na compreensão da história evolutiva e da diversidade de espécies dentro de Panaceae. A análise, que engloba dados morfológicos e moleculares, suporta a proposição da família Panaceae feita por Justo et al. (2017).

Em um estudo anterior, Yoon et al. (2003) investigaram a história evolutiva de fungos stereoides, recuperando sequências de *Cymatoderma caperatum* e *Panus neostrigosus* (nomeado como *Panus rufus*) como um grupo irmão, proximamente relacionado a uma espécie de *Podoscypha*. Neste estudo, *Panus* fazia parte de Pleurotaceae enquanto *Cymatoderma* à família Stereaceae. Yoon et al. (2003) destacaram características micromorfológicas compartilhadas entre *Cymatoderma*, *Panus* e *Podoscypha*, como basidioma estipitado, sistema hifal dimitico com hifas esqueletais, hifas generativas fibuladas e basidiósporos inamiloïdes de parede fina. Além disso, mencionam a necessidade de uma análise mais ampla para compreender as relações filogenéticas dentro do grupo (Polyporales) (Yoon et al. 2003).

Outro estudo relevante, conduzido por Miettinen et al. (2012), ressaltou a diversidade de "políporos dimíticos". Este estudo recuperou sequências de *Cymatoderma caperatum* e *Panus conchatus*, embora não tenha fornecido uma análise detalhada desses dados além de indicar que ambos os gêneros são considerados parte da família Meruliaceae. Apesar da falta de ênfase nos dados específicos relacionados a *Panus* e *Cymatoderma*, tanto Yoon et al. (2003) quanto Miettinen et al. (2012) fortalecem a classificação atualmente aceita para esses gêneros.

Além disso, a similaridade micromorfológica entre *Cymatoderma* e *Panus* como presença de pleurocistídios e/ou queilocistídios, basidiósporos sub elipsóide a subcilíndrico, além das características já apontados por Yoon et al. (2003), também reforça a validade da proposta de classificação. Assim, ao considerar esses estudos em conjunto, percebemos não apenas a consistência nas conclusões, mas também a importância de abordagens multidisciplinares, incorporando tanto dados moleculares quanto morfológicos, para a compreensão abrangente da filogenia e classificação desses organismos.

Cymatoderma

Cymatoderma comprehende quatorze espécies segundo as bases de dados Index Fungorum (<http://indexfungorum.org>, acessado 18/01/2024) e Mycobank (<https://www.mycobank.org/>, acessado 18/01/2024), são elas: *Cymatoderma africanum* Boidin, *C. blumei* (Lév.) D. A. Reid, *C. caperatum*, *C. dendriticum*, *C. elegans*, *C. fuscum* (Cooke) D. A. Reid, *C. hainanense* Z.T Guo, *C. infundibuliforme*

(Klotzsch) Boidin, *C. pallens* Boidin, *C. plicatum* (Lloyd) D. A. Reid, *C. sclerotioides*, *C. semiresupinatum* (A. L. Welden) A. L. Welden, *C. venezuelae* D. A. Reid e *C. viridans* (Lloyd) A. L. Welden.

Concordamos com Sjokvist et al. (2012) e Justo et al. (2017) sobre *Cymatoderma* ser polifilético. Transferimos *C. dendriticum* e *C. pallens* para o gênero correto, ambas espécies pertencem a *Podoscypha* (Podoscyphaceae) e estão sendo combinadas aqui neste estudo, mas seus limites podem ser melhor estabelecidos através de estudos integrativos com materiais de referência.

Confirmamos a presença de *Cymatoderma caperatum*, *C. elegans* e *C. sclerotioides* em *Cymatoderma*. Outras espécies do gênero, descritas no Brasil, como *Cymatoderma semiressupinatum* e *C. viridans* (ambas com distribuição restrita à localidade do tipo) não puderam ser confirmadas em *Cymatoderma* pela dificuldade de acesso aos materiais tipo. No protólogo, *Cymatoderma semirressupinatum* apresenta a condição resupinada-reflexa, única dentro do gênero, enquanto *C. viridans* possui longos pileocistídios (um tipo de dermatocistídios), característica relatada no gênero após a inclusão desta espécie em *Cymatoderma* (Welden 2010). Essas particularidades levantam questionamentos sobre a estabilidade taxonômica dessas duas espécies dentro de *Cymatoderma*.

Não foi possível localizar o tipo de *Cymatoderma fuscum* através das bases de dados que indicavam o herbário Kew. No entanto, as características descritas no protólogo confirmam sua inclusão no gênero, evidenciadas pela presença de basidioma dimidiado a flabeliforme, textura esponjoso-coriácea radialmente rugosa, com tomento abundante no centro diminuindo em direção à margem. Os espécimes podem ser sésseis ou estipitados, apresentando um himenóforo liso e plicado (Cooke 1882).

Cymatoderma africanum, *C. blumei*, *C. hainanense*, *C. infundibuliforme*, *C. plicatum* e *C. venezuelae* não foram objetos deste estudo por não haver registro de ocorrência no Brasil.

Após essa análise, são reconhecidas dez espécies descritas para o gênero *Cymatoderma*, a saber: *Cymatoderma africanum*, *C. blumei*, *C. caperatum*, *C. elegans*, *C. fuscum*, *C. hainanense*, *C. infundibuliforme*, *C. plicatum*, *C. sclerotioides* e *C. venezuelae*. Dentre essas, *C. caperatum*, *C. elegans*, *C. fuscum* e *C. sclerotioides* são encontradas no Brasil. No entanto, 70% das espécies de *Cymatoderma* carecem

de dados moleculares e/ou de revisões morfológicas atualizadas, e cerca de 40% são conhecidas apenas por meio do espécime tipo (*C. fuscum*, *C. hainanense*, *C. plicatum*, *C. venezuelae*). Portanto, é necessário realizar novas pesquisas, especialmente aquelas que envolvam os espécimes-tipo e incluam sequenciamento adicional de DNA, a fim de avançar nos estudos e determinar a presença ou ausência de outras espécies de *Cymatoderma*.

Panus

Panus é o gênero mais representativo, em número de espécies, de Panaceae. Neste estudo foram recuperados pelo menos 10 clados de espécies conhecidas, além de 4 novos clados com novidades científicas.

Sousa-Guimarães et al. (2024), apresenta a filogenia abrangente de *Panus* e discute diversas implicações taxonômicas e nomenclaturais. São propostas, *P. capelariae*, *P. pachysporus*, *P. speciosus* e *P. stipitonotatus* como novidades científicas. *Panus campinensis* e *P. thailandicus* (uma espécie endofítica) como novas combinações no gênero, com base em uma revisão morfológica e evidência filogenética de seus tipos, respectivamente. Além disso, são discutidos dados de ocorrência, delimitação de sensustricto e aspectos nomenclaturais de espécies com registro de ocorrência para o Brasil. Uma avaliação abrangente que traz mais estabilidade para o gênero e contribui para o conhecimento da real diversidade de espécies no Brasil (Sousa-Guimarães et al. 2024).

Toda discussão relacionada a *Panus* como número de espécies, novidades científicas, complexos taxonômicos, são tratadas no capítulo 2 deste trabalho.

4. REFERÊNCIAS

- BERTHET, P.; BOIDIN, J. 1966. Observations sur quelques Hyménomycètes récoltés en République Camerounaise. Cahiers de la Maboké. 4(1):27-54.
- CORNER, E. J. H. 1981. The agaric genera *Lentinus*, *Panus* and *Pleurotus* with particular reference to Malaysian species. Beih. Nova Hedw., v. 69, p. 1-169.

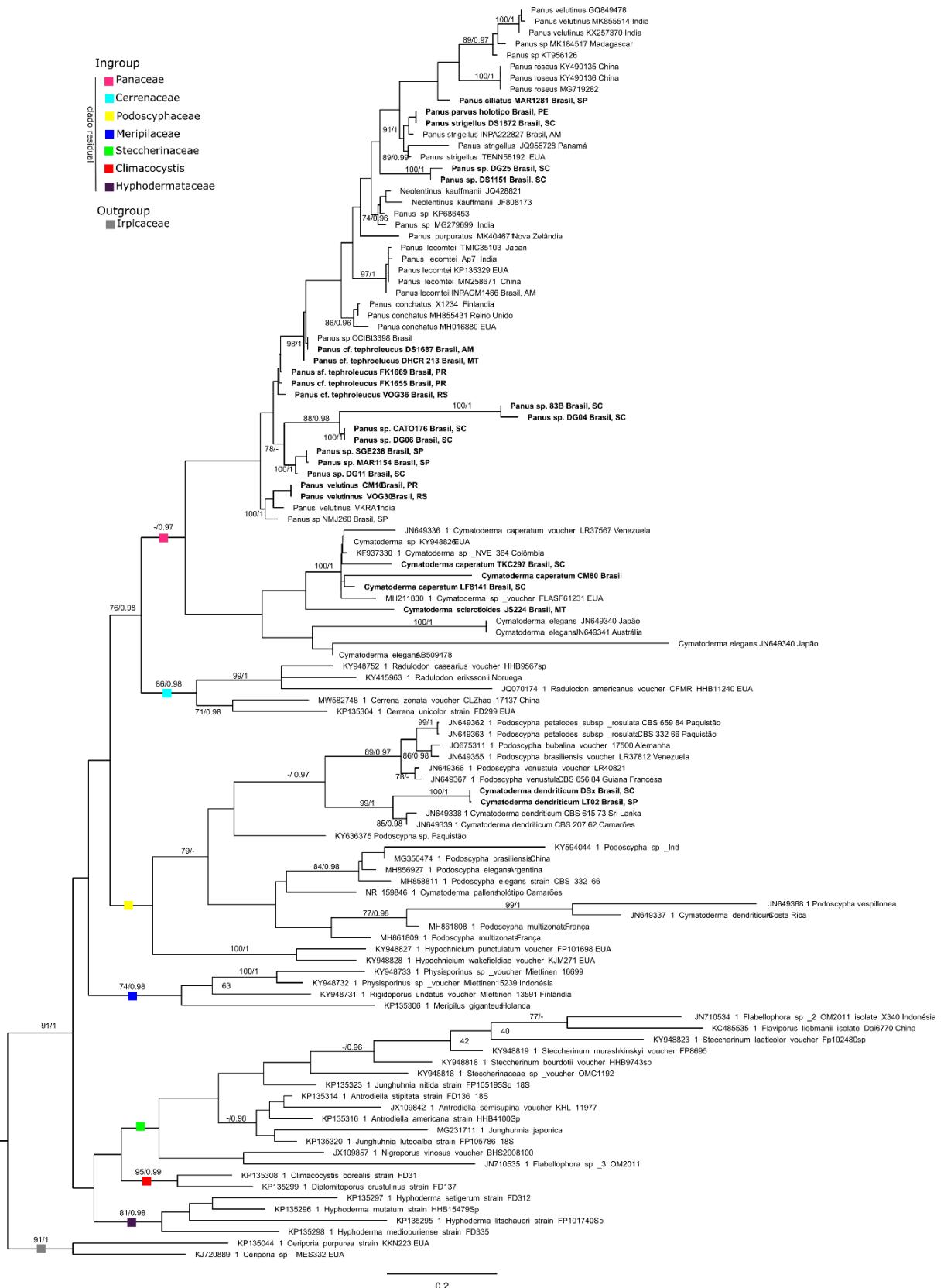
- DARRIBA, D., POSADA, D., KOZLOV, A.M., STAMATAKIS, A., MOREL, B. & FLOURI, T. 2020. ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. *Molecular Biology and Evolution* 37 (1): 291–294. <https://doi.org/10.1093/molbev/msz189>
- GARDES, M. & BRUNS, T. D. 1993. ITS primers with enhanced specificity for basidiomycetes application to the identification of mycorrhizae and rusts. *Mol Ecol* 2:113–118.
- GÓES-NETO, A.; LOGUERCIO-LEITE, C.; GUERRERO, R.T. 2005. DNA extraction from frozen field-collected and dehydrated herbarium fungal basidiomata: performance of SDS and CTAB-based methods. *Biotemas* 18(2): 19-32.
- GUINDON, S.; DUFAYARD, J.F.; LEFORT, V.; ANISIMOVA, M.; HORDIJK, W.; GASCUEL, O. 2010. New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. *Systematic Biology*, 59(3):307-21.
- GRAND, E. A. 2004. Systematics and species concepts in the genera *Lentinus* Fr. and *Panus* Fr., with emphasis on the *Lentinus tigrinus*, *L. crinitus* and *Panus lecomtei* complexes [tese de doutorado]. Knoxville: Univ. Tennessee Press. 116 p.
- HIBBETT, D. S.; VILGALYS, R. 1993. Phylogenetic Relationships of *Lentinus* (Basidiomycotina) inferred from Molecular and Morphological Characters. *Systematic Botany*, v. 18, p. 409-433.
- JUSTO, A.; MIETTINEN, O.; FLOUDAS, D.; ORTIZ-SANTANA, B.; SJÖKVIST, E.; LINDNER, D.; NAKASONE, K.; NIEMELÄ, T.; LARSSON, K. H.; RYVARDEN, L.; HIBBETT, D. S. 2017. A revised family-level classification of the Polyporales (Basidiomycota). *Fungal Biolgy*. 64p.
- KATOH, S. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30: 772-780.
- KEARSE, M.; MOIR, R.; WILSON, A.; STONES-HAVAS, S.; CHEUNG, M.; STURROCK, S.; BUXTON, S.; COOPER, A.; MARKOWITZ, S.; DURAN, C.;

- THIERER, T.; ASHTON, B.; MENTJIES, P.; DRUMMOND, A. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*, 28(12): 1647-1649.
- KUMAR, S.; STECHER, G.; TAMURA, K. 2016. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for bigger datasets. *Molecular Biology and Evolution*, msw 054.
- LLOYD, C. G. 1913. A synopsis of the genus *Cladoderris*. na.
- LLOYD, C. G. 1922-1925. Index of the Mycological Notes of C. G. Lloyd (Vol. 7).
- MATHENY, P. B.; LIU, Y. J.; AMMIRATI, J. F. & HALL, B. D. 2002. Using RPB1 sequences to improve phylogenetic inference among mushrooms (*Inocybe*, Agaricales). *Am J Bot* 89: 688–698.
- MIETTINEN, O., LARSSON, E., SJÖKVIST, E., & LARSSON, K. H. 2012. Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimitic polypores (Polyporales, Basidiomycota). *Cladistics*, 28(3), 251-270.
- MILLER, M. A.; PFEIFFER, W.; SCHWARTZ, T. 2010. Creating the CIPRES science gateway for inference of large phylogenetic trees. In: *Proceedings of the Gateway Computing Environments Workshop (GCE)*.
- MOSER, M. 1978. Keys to Agarics and Boleti. London: R. Philips.
- PEGLER, D. N. 1983. The genus *Lentinus*: A world monograph. *Kew Bull. Add. Ser.*, v. 10, p. 1-281.
- POSADA, D. 2008. ModelTest: phylogenetic model averaging. *Molecular Biology and Evolution* 25: 1253-1256.
- REHNER S. 2001. Primers for Elongation Factor 1- α (EF1- α). <http://ocid.NACSE.ORG/research/deephyphe/EF1primer.pdf>
- REID, D. A. 1965. A monograph of stipitate stereoid fungi. *Beih Nova Hedwig* 18:1–382

- RONQUIST, F., TESLENKO, M., VAN DER MARK, P., AYRES, D. L., DARLING, A., HÖHNA, S., ... & HUELSENBECK, J. P. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic biology*, 61(3), 539-542.
- SACCARDO, P. A. 1888. Em *Sylloge fungorum* 6: 1-928. (reimpresso por Edwards Brothers, Inc., Michigan, U. S. A. 1944).
- SINGER, R. 1975. The Agaricales in Modern Taxonomy. 3rd edn. Vaduz: J. Cramer.
- SINGER, R. 1986. The Agaricales in Modern Taxonomy. 4th edn. Königstein: Sven Koeltz Scientific Books.
- SJÖKVIST, E.; LARSSON, E.; EBERHARDT, U.; RYVARDEN, L & LARSSON, K. H. 2012. Stipitate steroid basidiocarps have evolved multiple times. *Mycologia* 104: 1046–1055.
- STAMATAKIS, A. 2014. RAxML Version 8: A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies. *Bioinformatics Advance Access*.
- STILLER, J. W. & HALL, B. D. 1997. The origin of red algae: implications for plastid evolution. *Proc Natl Acad Sci USA*. 94:4520–4525.
- TALBOT, P. B. 1958. The Genera *Craterellus*. *Cymatoderma* (*Cladoderris*) and *Thelephora* in South Africa. *Bothalia*, 7(1), 117-129.
- THORN RG, MONCALVO J-M, REDDY CA, VILGALYS R. 2000. Phylogenetic analyses and the distribution of nematophagy support a monophyletic Pleurotaceae within the polyphyletic pleurotidlentinoid fungi. *Mycologia* 92: 241–252.
- VARGAS-ISLA, R.; CAPELARI, M.; MELONI, N.; NAGASAWA, E.; TOKIMOTO, K.; ISHIKAWA, N. K. 2015. Relationship between *Panus lecomtei* and *P. strigellus* inferred from their morphological, molecular and biological characteristics. *Mycoscience*. 10.1016.

- VILGALYS, R. & HESTER, M. 1990. Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. J Bacteriol 172:4238–4246.
- WELDEN, A. L. 1960. The genus *Cymatoderma* (Thelephoraceae) in the Americas. Mycologia. 52:856-876
- WHITE, T. J.; BRUNS, T.; LEE, S.; TAYLOR, J. W. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (eds), PCR protocols: a guide to methods and applications. Academic Press Inc, New York, p. 315 e 322.
- YOON, S. I., KIM, S. Y., LIM, Y. W., & JUNG, H. S. 2003. Phylogenetic evaluation of steroid fungi. Journal of microbiology and biotechnology, 13(3), 406-414.
- ZMITROVICH, I. V., & MALYSHEVA, V. F. 2013. Towards a phylogeny of *Trametes* alliance (Basidiomycota, Polyporales). *Микология и фитопатология*, 47(6), 358-380.
- ZMITROVICH, I. V., & KOVALENKO, A. E. 2016. Lentinoid and polyporoid fungi, two generic conglomerates containing important medicinal mushrooms in molecular perspective. International Journal of Medicinal Mushrooms, 18(1).

Figura Suplementar 1. Reconstrução filogenética de Panacea (ML) usando um conjunto de dados nrITS. Nas filiais, os valores de suporte são fornecidos como BS / BPP. O hífen (“-”) indica um valor inferior a 70% BS ou 0,95 BPP. Sequências em negrito foram geradas.



Fonte: Sousa-Guimarães 2024

TABELA

Tabela 1. Espécies, coleções e sequências utilizadas nas análises filogenéticas e seus números de acesso no Genbank. Novas sequências geradas neste estudo estão destacadas em negrito.

Táxon	Número Genbank					
	Voucher	País	ITS	LSU	RPB1	Tef1
<i>Abortiporus biennis</i>	Cui 16986	China	ON417150	ON417198	ON424664	ON424822
<i>Antrodiella americana</i>	HHB4100Sp	EUA	KP135316	KP135196	KP134885	N/A
<i>Antrodiella semisupina</i>	KHL 11977	Noruega	JX109842	N/A	N/A	JX109896
<i>Antrodiella stipitata</i>	FD_136	EUA	KP135314	N/A	KP134886	KP135197
<i>Ceriporia purpurea</i>	KKN-223-Sp	EUA	KP135044	KP135203	KP134788	N/A
<i>Cerrena sp</i>	MES332	EUA	KJ720889	KJ720891	N/A	N/A
<i>Cerrena sp</i>	Cui 16874	Porto Rico	ON682357	ON680809	ON688462	ON688504
<i>Cerrena unicolor</i>	FD-299	EUA	KP135304	KP135209	KP134874	N/A
<i>Cerrena unicolor</i>	He6082	China	OM100740	OM083972	N/A	N/A
<i>Cerrena zonata</i>	CLZhao 17137	China	MW582748	N/A	N/A	N/A
<i>Cerrena zonata</i>	Cui 16578	Austrália	ON417153	ON417203	ON424673	ON424826
<i>Cerrena zonata</i>	Cui 18502	China	ON417154	ON417204	ON424674	ON424827
<i>Climacocystis borealis</i>	Dai 4014	China	KJ566627	KJ566637	ON688463	KJ566644
<i>Climacocystis borealis</i>	FD-31	EUA	KP135308	KP135210	KP134882	N/A
<i>Climacocystis borealis</i>	CBS:379.51	Áustria	MH856909	MH868431	N/A	N/A

Táxon	Número Genbank					
	Voucher	País	ITS	LSU	RPB1	Tef1
<i>Climacocystis montana</i>	Cui 17123	China	ON682360	ON680812	ON688467	ON688506
<i>Cymatoderma caperatum</i>	CE03	Brasil	N/A	this work	N/A	N/A
<i>Cymatoderma caperatum</i>	CM80	Brasil	this work	N/A	N/A	this work
<i>Cymatoderma caperatum</i>	CM108	Brasil	this work	N/A	N/A	N/A
<i>Cymatoderma caperatum</i>	DS724	Brasil	this work	N/A	N/A	N/A
<i>Cymatoderma caperatum</i>	TKC 297	Brasil	this work	N/A	N/A	this work
<i>Cymatoderma caperatum</i>	MP386	Brasil	this work	N/A	N/A	this work
<i>Cymatoderma caperatum</i>	TKC93	Brasil	this work	N/A	N/A	N/A
<i>Cymatoderma caperatum</i>	RLC_1356	Equador	N/A	OQ913044	N/A	N/A
<i>Cymatoderma caperatum</i>	LR37567	Venezuela	JN649336	N/A	N/A	N/A
<i>Cymatoderma caperatum</i>	LF_8141	Brasil	this work	N/A	N/A	this work
<i>Cymatoderma caperatum</i>	TKC214	Brasil	this work	this work	N/A	N/A
<i>Cymatoderma caperatum</i>	PI02	Brasil	N/A	this work	N/A	N/A
<i>Cymatoderma caperatum</i>	PI03	Brasil	N/A	this work	N/A	N/A
<i>Cymatoderma dendriticum</i>	SMF2936	Austrália	OL771705	OL771764	N/A	N/A
<i>Cymatoderma dendriticum</i>	CBS 207.62	Camarões	JN649339	N/A	N/A	N/A

Táxon	Número Genbank					
	Voucher	País	ITS	LSU	RPB1	Tef1
<i>Cymatoderma dendriticum</i>	CBS 615.73	Sri Lanka	JN649338	N/A	N/A	N/A
<i>Cymatoderma dendriticum</i>	Delgado_300697	Costa Rica	JN649337	N/A	N/A	N/A
<i>Cymatoderma elegans</i>	CBS 491.76	Japão	JN649340	N/A	N/A	N/A
<i>Cymatoderma elegans</i>	Dai 17511	China	ON417155	ON417205	N/A	N/A
<i>Cymatoderma elegans</i>	Halling9064	Austrália	JN649341	N/A	N/A	N/A
<i>Cymatoderma palens</i>	CBS 327.66	Camarões	JN649342	N/A	N/A	N/A
<i>Cymatoderma sclerotiooides</i>	JS 224	Brasil	this work	this work	N/A	N/A
<i>Cymatoderma</i> sp	OMC1427	EUA	KY948826	KY948872	KY948971	N/A
<i>Cymatoderma</i> sp	NVE_364	Colômbia	KF937330	N/A	N/A	N/A
<i>Cymatoderma</i> sp	FLAS-F-61231	EUA	MH211830	N/A	N/A	N/A
<i>Cymatoderma</i> sp	WML2021_5_2	-	OK586734	K586660.	N/A	N/A
<i>Diplomitoporus crustulinus</i>	FD-137	EUA	KP135299	KP135211	KP134883	N/A
<i>Endopandanico la thailandica</i>	MFLUCC_17_05 48	Tailândia	MG646964	N/A	N/A	N/A
<i>Endopandanico la thailandica</i>	MFLUCC_17_05 49	Tailândia	MG646963	N/A	N/A	N/A
<i>Flabellophora</i> sp	X340	Indonésia	JN710534	N/A	N/A	N/A
<i>Flabellophora</i> sp	X1277	Indonésia	JN710535	N/A	N/A	N/A

Táxon	Número Genbank					
	Voucher	País	ITS	LSU	RPB1	Tef1
<i>Hypoderma litschaueri</i>	FP-101740-Sp	EUA	KP135295	KP135219	KP134868	N/A
<i>Hypoderma medioburiense</i>	FD-335	EUA	KP135298	KP135220	KP134869	N/A
<i>Hypoderma mutatum</i>	HHB15479Sp	EUA	KP135296	KP135221	KP134870	N/A
<i>Hypoderma setigerum</i>	FD-312	EUA	KP135297	KP135222	KP134871	N/A
<i>Hypochnicium punctulatum</i>	FP101698sp	EUA	KY948827	KY948860	KY948932	N/A
<i>Hypochnicium wakefieldiae</i>	KJM271sp	EUA	KY948828	N/A	KYT948933	N/A
<i>Irpea lacteus</i>	FD9	EUA	KP135026	KP135224	KP134806	N/A
<i>Junghuhnia japonica</i>	CLZhao 1072	-	MG231711	N/A	N/A	N/A
<i>Junghuhnia luteoalba</i>	FP-105786	EUA	KP135320	N/A	N/A	N/A
<i>Junghuhnia nitida</i>	FP-105195-Sp	EUA	KP135323	KP134964	KP134888	N/A
<i>Lentinus roseus</i>	HKAS 94715	China	KY490135	KY490137	N/A	N/A
<i>Lentinus roseus</i>	HKAS 94714	China	KY490136	KY490138	N/A	N/A
<i>Lentinus strigosus</i>	LE5829	Rússia	KM411451	N/A	N/A	N/A
<i>Meripilus giganteus</i>	FP100460Sp	Holanda	KP135306	N/A	N/A	N/A
<i>Neohypochnici um geogenium</i>	He_6819	China	OM039282	OM039182	N/A	N/A
<i>Neolentinus kauffmanii</i>	VKGJ01	Índia	JF808173	N/A	N/A	N/A
<i>Neolentinus kauffmanii</i>	VKGJ03	Índia	JQ428821	N/A	N/A	N/A
<i>Panus bambusinus</i>	AK61b	Índia	MW453097	N/A	N/A	N/A

	Táxon		Número Genbank				
	Voucher	País	ITS	LSU	RPB1	Tef1	
<i>Panus conchatus</i>	LE265028	Rússia	N/A	LE265028	N/A	N/A	
<i>Panus conchatus</i>	Dai 23421	China	N/A	ON417226	N/A	N/A	
<i>Panus conchatus</i>	CBS 26758	Alemanha	MH857778	N/A	N/A	N/A	
<i>Panus conchatus</i>	Dai 22458	-	OL477381	OL477382	N/A	N/A	
<i>Panus conchatus</i>	JMH44	Tanzânia	N/A	N/A	N/A	OM037805	
<i>Panus conchatus</i>	strain 567	Colômbia	N/A	MZ424282	N/A	N/A	
<i>Panus conchatus</i>	Miettinen X1234	Finlândia	JN710579	N/A	N/A	N/A	
<i>Panus cf. tephroleucus</i>	DS1684	Brasil	this work	this work	N/A	N/A	
<i>Panus cf. tephroleucus</i>	VOG36	Brasil	MT669124	N/A	N/A	N/A	
<i>Panus cf. tephroleucus</i>	TENN58776	EUA	N/A	AY615996	N/A	N/A	
<i>Panus cf. tephroleucus</i>	LCF573	Argentina	N/A	AY615997	N/A	N/A	
<i>Panus cf. tephroleucus</i>	DS1598	Brasil	MT669120	N/A	N/A	N/A	
<i>Panus cf. tephroleucus</i>	DS1687	Brasil	MT669122	this work	N/A	N/A	
<i>Panus cf. tephroleucus</i>	SP446159	Brasil	MT669123	N/A	N/A	KM411496	
<i>Panus lecomtei</i>	HHB_11042_Sp	EUA	KP135328	N/A	ON424716	ON424855	
<i>Panus lecomtei</i>	INPACM1466	Brasil	JQ955730	N/A	N/A	N/A	
<i>Panus lecomtei</i>	TENN51805	EUA	N/A	AY615994	N/A	N/A	
<i>Panus neostrigosus</i>	LSPQ_NS108	Canadá	KU761236	KU761116	N/A	N/A	

Táxon			Número Genbank			
	Voucher	País	ITS	LSU	RPB1	Tef1
<i>Panus parvus</i>	URM80840	Brasil	MT669125	this work	N/A	this work
<i>Panus purpuratus</i>	MK404671	Nova Zelândia	N/A	MK404671	N/A	N/A
<i>Panus similis</i>	UOC_SIGWIS38	Sri Lanka	KR818820	N/A	N/A	N/A
Panus sp.	DG 88	Brasil	N/A	this work	N/A	this work
<i>Panus</i> sp.	TENN59829	Argentina	N/A	AY615999	N/A	N/A
<i>Panus</i> sp.	TENN59008	Argentina	N/A	AY616000	N/A	N/A
<i>Panus</i> sp.	DG11	Brasil	this work	this work	N/A	N/A
<i>Panus</i> sp.	SGE238	Brasil	this work	N/A	N/A	this work
<i>Panus</i> sp.	MCCT187	Índia	MG279699	N/A	N/A	N/A
<i>Panus</i> sp.	DS1151	Brasil	MT669130	N/A	KP134877	N/A
<i>Panus</i> sp.	DG25	Brasil	MT669129	this work	N/A	N/A
<i>Panus</i> sp.	DG133	Brasil	N/A	this work	N/A	N/A
<i>Panus</i> sp.	CATO176	Brasil	MT669131	N/A	N/A	N/A
<i>Panus</i> sp.	GAS850	Brasil	MT669132	MT669152	N/A	N/A
<i>Panus</i> sp.	DG03	Brasil	this work	this work	N/A	N/A
<i>Panus</i> sp.	DG04	Brasil	this work	N/A	N/A	N/A
<i>Panus</i> sp.	DG06	Brasil	MT669133	this work	N/A	N/A
<i>Panus</i> sp.	DG83	Brasil	this work	this work	N/A	N/A
<i>Panus strigellus</i>	MAN1281	Brasil	this work	N/A	N/A	N/A
<i>Panus strigellus</i>	DG36	Brasil	MT669135	N/A	N/A	N/A
<i>Panus strigellus</i>	DS1872	Brasil	MT669136	N/A	N/A	N/A
<i>Panus strigellus</i>	INPA222827	Brasil	JQ955722	N/A	N/A	N/A
<i>Panus strigellus</i>	TENN55993	EUA	JQ955728	N/A	N/A	N/A

Táxon			Número Genbank			
	Voucher	País	ITS	LSU	RPB1	Tef1
<i>Panus strigellus</i>	TENN56192	EUA	JQ955727	N/A	N/A	N/A
<i>Panus velutinus</i>	LE263099	Rússia	N/A	N/A	N/A	KM411498
<i>Panus velutinus</i>	CM10	Brasil	MT669138	N/A	N/A	N/A
<i>Panus velutinus</i>	DG01	Brasil	this work	this work	N/A	N/A
<i>Panus velutinus</i>	VOG30	Brasil	MT669139	this work	N/A	N/A
<i>Phlebia unicum</i>	Wu 1707_94	China	N/A	MZ637102	N/A	N/A
<i>Physisporinus</i> sp	Miettinen 15239	Indonésia	KY948732	KY948867	KY948946	N/A
<i>Physisporinus</i> sp	Miettinen 16699	EUA	KY948733	KY948863	KY948947	N/A
<i>Physisporinus</i> sp	Cui_16852	Porto Rico	ON417179	ON417229	ON424719	ON424858
<i>Physisporinus</i> vitreus	Cui_16859	Porto Rico	ON417180	ON417230	ON424720	ON424859
<i>Podoscypha dendritica</i>	LT02	Brasil	N/A	this work	N/A	this work
<i>Podoscypha dendritica</i>	DSXX	Brasil	this work	N/A	N/A	N/A
<i>Podoscypha dendritica</i>	LT01	Brasil	N/A	this work	N/A	N/A
<i>Podoscypha dendritica</i>	DG 41	Brasil	this work	N/A	N/A	this work
<i>Podoscypha dendritica</i>	DG142	Brasil	this work	N/A	N/A	N/A
<i>Podoscypha elegans</i>	CBS:332.66	-	MH858811	MH870450	N/A	N/A
<i>Podoscypha elegans</i>	CBS:426.51	Argentina	MH856927	MH868453	N/A	N/A
<i>Podoscypha multizonata</i>	CBS:662.84	França	MH861808	MH861808	N/A	N/A

Táxon	Número Genbank					
	Voucher	País	ITS	LSU	RPB1	Tef1
<i>Podoscypha multizonata</i>	CBS:663.84	França	MH861809	MH873501	N/A	N/A
<i>Podoscypha parvula</i>	Niemela 7690	Quênia	N/A	NL677690	N/A	N/A
<i>Podoscypha petalodes</i> <i>subsp rosulata</i>	CBS:659.84	Paquistão	JN649362	MH873498	N/A	N/A
<i>Podoscypha</i> sp	SCHD9	Índia	KY594044	KY594043	N/A	N/A
<i>Podoscypha venustula</i>	LF83	Brasil	this work	N/A	N/A	N/A
<i>Podoscypha venustula</i>	LR40821	Venezuela	JN649366	N/A	MZ748358	MZ913705
<i>Podoscypha venustula</i>	Cui_16923	Porto Rico	ON417181	ON417231	ON424722	ON424860
<i>Podoscyphabra siliensis</i>	GXU_2169	China	MG356474	N/A	KY948733	N/A
<i>Pseudospongip ellis unicolor</i>	RLG7638sp	EUA	KY948751	N/A	ON417179	N/A
<i>Radulodon casearius</i>	HHB9567sp	EUA	KY948752	N/A	ON417180	N/A
<i>Radulodon casearius</i>	Cui 17979	China	ON417185	ON417236	ON424727	ON424868
<i>Radulodon erikssonii</i>	KY415963	Noruega	KY415963	N/A	N/A	N/A
<i>Radulodon yunnanensis</i>	Dai 12204	China	OM971916	N/A	N/A	OM982705
<i>Rigidoporus undatus</i>	Miettinen 13591	Finlândia	KY948731	KY948870	N/A	N/A
<i>Steccherinacea e</i> sp	OMC1192	EUA	KY948816	KY948865	KY949047	N/A
<i>Steccherinum bourdotii</i>	HHB9743sp	EUA	KY948818	N/A	KY949043	N/A

Táxon	Número Genbank					
	Voucher	País	ITS	LSU	RPB1	Tef1
<i>Steccherinum laeticolor</i>	Fp102480sp	EUA	KY948823	KY948868	KY948948	N/A
<i>Steccherinum meridionale</i>	Cui 16691	Austrália	ON417195	ON417247	ON424743	ON424882
<i>Steccherinum murashkinskyi</i>	FP8695	EUA	KY948819	N/A	KY948945	N/A

Fonte: Sousa-Guimarães 2024

**CAPÍTULO 2 –THE MOST COMPREHENSIVE PHYLOGENY OF PANUS
(PANACEAE, POLYPORALES) AND REVISITED BRAZILIAN DIVERSITY**

**The most comprehensive phylogeny of *Panus* (*Panaceae*, *Polyporales*) and
revisited Brazilian diversity**

Mycological Progress (2024) 23:19 <https://doi.org/10.1007/s11557-024-01955-3>

Received: 16 October 2023 / Revised: 23 January 2024 / Accepted: 25 January 2024

Denyse Kalyne Sousa-Guimarães^{a,b}, Genivaldo Alves-Silva^{a,b}, Felipe Bittencourt^{a,b},
Olga Camacho^a, Nelson Menolli Jr^{c,d}, Aristóteles Góes-Neto^e, Gerardo L. Robledo^{f,g,h},
Elisandro Ricardo Drechsler-Santos^{a,b,*}

*Corresponding author: drechslersantos@yahoo.com.br

^aUniversidade Federal de Santa Catarina, Campus Universitário Trindade, PPG
Biologia de Fungos, Algas e Plantas, Departamento de Botânica, Centro de
Ciências Biológicas, CEP: 88040-900, Florianópolis-SC, Brazil

^bMIND.Funga (Monitoring and Inventorying Neotropical Diversity of Fungi) -
MICOLAB, Brazil

^cIFungiLab, Instituto Federal de Educação, Ciência e Tecnologia de São Paulo
(IFSP), Campus São Paulo (SPO), Departamento de Ciências da Natureza e
Matemática (DCM), Subárea de Biologia (SAB) CEP: 01109-010, São Paulo-SP,
Brazil

^dPós-graduação em Biodiversidade Vegetal e Meio Ambiente, Instituto de
Pesquisas Ambientais, Av. Miguel Estefano, 3687, Água Funda, CEP: 04301-012,
São Paulo-SP, Brazil

^eUniversidade Federal de Minas Gerais, Instituto de Ciências Biológicas,
Departamento de Microbiologia, CEP:31270-901, Belo Horizonte-MG, Brazil

^fUniversidad Nacional de Córdoba, Facultad de Ciencias Agropecuarias, Ing. Agr.
Félix Aldo Marrone 746 – CP 5000, Córdoba, Argentina

^gCONICET, Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina.

^hFundación FungiCosmos, www.fungicosmos.org, Córdoba, Argentina

ABSTRACT

The genus *Panus* and many of its species have a wide geographic distribution, and in-depth up-to-date taxonomic review is needed that includes critical review of type materials within a phylogenetic frame. In order to recover the phylogenetic relationships within *Panus* species, their morphological boundaries and to critically analyze the diversity recorded for Brazil, we carried out fieldwork in poorly explored areas in the country and morphological and literature revisions of fungarium specimens, including several type materials. We present a comprehensive phylogeny of *Panus* and discuss several taxonomic and nomenclatural implications in order to achieve stability for species of the genus. Four new species are proposed, *P. capelariae*, *P. pachysporus*, *P. speciosus*, and *P. stiptonotatus*. *Panus campinensis* and *P. thailandicus* (an endophytic species) are proposed as new combinations in the genus, based on a morphological revision and phylogenetic evidence of their types, respectively. Additionally, *Endopandanicola* is synonymized within *Panus*, and *P. parvus* is synonymized within *P. strigellus*. The occurrence of *P. conchatus*, *P. convivalis*, *P. fulvus*, *P. similis*, and *P. tephroleucus* in Brazil is rejected due to morphological and phylogenetic evidences. For *P. conchatus* and *P. similis* we present bases for the recognition of its *sensu stricto* status. We also discuss nomenclatural issues surrounding the *Lentinus velutinus* complex, that include the basionym elucidation, its *sensu stricto* delimitation, and an epitypification based on a new sequenced specimen from the type locality. Our comprehensive assessment of *Panus* in Brazil has led to the confirmation of ten species supported by morphological and/or molecular data, which are critically discussed, and an identification key is presented.

Keywords: *Lentinus*, Neotropical, Funga, wood-rotting fungi, taxonomy, 4 new

taxa, 2 new combinations

INTRODUCTION

Panus Fr. was proposed by Fries (1838) and encompasses wood-inhabiting species characterized by centrally to eccentrically stipitate basidiomata, infundibuliform to cyathiform pilei, and a hymenophore with decurrent lamellae. Species are distinguished by a dimitic hyphal system featuring unbranched skeletal hyphae, cystidia ranging from thin to thick-walled, and ellipsoid, smooth, thin-walled basidiospores (Corner 1981). *Panus* exhibits remarkable diversity and wide geographic distribution, with many species described during the 19th century (Fries 1821; 1830; Leveillé 1844; Berkeley and Curtis 1869; Berkeley and Broome 1873; Corner 1981). However, the genus remains underrepresented in molecular phylogenetic studies, and its phylogenetic relationships remain poorly understood. Only a limited number of species have molecular data available, with the majority of them having been recently described, such as *P. subfasciatus* Thongbai, Karun., C. Richt. & K.D. Hyde, *P. roseus* (Karun., K.D. Hyde & Zhu L. Yang) N. Vinjusha & T.K.A. Kumar, and *P. paraibensis* V. Galvão, Koroiva & Wartchow (Tibpromma et al. 2017; Vinjusha and Kumar 2022; Galvão et al. 2023, respectively). Furthermore, little or nothing is known about the species diversification and biogeographical patterns, character evolution, or their ecology.

Panus was previously classified as an infrageneric taxon of *Lentinus* Fr. (Pegler 1971, 1972, 1983), viz. *Lentinus* subg. *Panus* (Fr.) Pegler and, consequently, many *Panus* species remain under *Lentinus*. Therefore, those taxa should be revised, including the type material reexamination, in order to assess their taxonomic limits and generic position. There are ca. 150 names of *Panus* listed in Index Fungorum

(<http://indexfungorum.org>, accessed 01/05/2023), of which most of their type specimens and information (morphological, molecular, and locality) are not easily accessible. This is mainly because around 95% of these names were proposed between the 18th and 20th centuries. Consequently, they exhibit challenges such as poor preservation and small size, rendering them less amenable to loan requests (Dayarathne et al. 2016).

Few studies have explored the diversity of *Panus* in the Neotropics, with the majority of them describing new species solely based on morphological data. In Brazil, 12 *Panus* species have been recorded: *Panus ciliatus* (Lév.) T.W. May & A.E. Wood (e.g., Rick 1907), *P. conchatus* (Bull.) Fr. (Spegazzini 1889), *P. convivalis* Corner (Corner 1981), *P. fulvus* (Berk.) Pegler & R.W. Rayner (<https://specieslink.net/>, accessed 01/05/2023), *P. hymenorhizus* Speg. (Spegazzini 1889), *P. neostrigosus* Drechsler-Santos & Wartchow (e.g., Spegazzini 1889; Rick 1907; Pegler 1983; Drechsler-Santos et al. 2012; Vargas-Isla et al. 2015; Sanuma et al. 2016), *P. paraibensis* (Galvão et al. 2023), *P. parvus* Drechsler-Santos & Wartchow (Drechsler-Santos et al. 2012), *P. similis* (Berk. & Broome) T.W. May & A.E. Wood (e.g., Teixeira 1946; Meijer 2006; Cavalcante et al. 2021), *P. strigellus* (Berk.) Chardón & Toro (e.g., Rick 1930; Pegler 1983; Sanuma et al. 2016; Cavalcante et al. 2021), *P. tephroleucus* (Mont.) T.W. May & A.E. Wood (e.g., Pegler 1983, 1997), and *P. velutinus* (Fr.) Fr. (e.g., Fries 1830; Berkeley 1843; Spegazzini 1889; Teixeira 1946; Batista et al. 1966; Pegler 1983; Sanuma et al. 2016; Cavalcante et al. 2021).

Among those species, only *P. neostrigosus*, *P. paraibensis*, and *P. strigellus* have reliable and verified molecular data, alongside detailed morphological descriptions (Vargas-Isla et al. 2015; Galvão et al. 2023). For a few other *Panus*

species reported in Brazil, molecular data exist from other countries (e.g., *P. conchatus*, *P. similis*, and *P. velutinus*). However, these data still require verification to serve as references for their respective taxa, ensuring taxonomic and phylogenetic stability for future research on the genus. *Panus strigellus* and *P. tephroleucus* were originally described from Cuba (Berkeley and Curtis 1869) and Suriname (Pegler 1983), respectively, and their presence in Brazil may indeed reflect their true distributional range (Maia et al. 2015; Vargas-Isla et al. 2015). However, for other species recorded in Brazil, such as *P. ciliatus* (type from Indonesia), *P. conchatus* (type from Sweden), and *P. fulvus* and *P. similis* (both types from Sri Lanka), their wider distribution raises questions and could potentially involve misidentifications (Putzke 1994; Maia et al. 2015; Putzke and Putzke 2002).

Multiple studies have shown that *Agaricomycetes* species with occurrences on multiple continents, usually referred to as "cosmopolitan species", often consist of several species with restricted distribution ranges that represent a species-complex (Palacio et al. 2017; Peintner et al. 2019; Motato-Vásquez et al. 2020; Olou et al. 2020; Liu et al. 2021). Among the species described based on Brazilian specimens, *P. velutinus* has been widely recorded worldwide and its delineation remains ambiguous, leading to suggestions that it constitutes a species-complex (Pegler 1983; Douanla-Meli and Langer 2010). In light of these uncertainties, a taxonomic revision of *Panus* in Brazil is warranted, and species with broad and disjointed distributions should be subjected to further study to ascertain their taxonomic status and potentially unveil undescribed species in the Neotropics.

To ensure a comprehensive phylogenetic analysis and to provide an in-depth assessment of *Panus* diversity in Brazil, we conducted field expeditions in poorly explored regions of the Brazilian Atlantic Forest. We performed detailed

morphological examinations of both newly collected specimens and specimens from fungarium collections. Furthermore, we conducted molecular phylogenetic analyses utilizing DNA sequences from both ITS and nrLSU regions. In addition to proposing new taxa, we reevaluated the boundaries of several *Panus* species and conducted a thorough review of all recorded occurrences of *Panus* names in Brazil.

MATERIAL AND METHODS

Specimens and morphological descriptions

Specimens were collected during field surveys in the Atlantic Rainforest of Southern Brazil [classification according to Oliveira-Filho (2015)]. They were subsequently deposited at the FLOR herbarium. Additionally, we examined specimens from other herbaria, namely BAFC, IAC, FLOR, LISU, LPS, K, SP, TENN, UPS, and URM. Herbarium acronyms follow Thiers (continuously updated). Color determinations follow Küppers (1994). For the observation and description of microscopic characteristics, we manually prepared sections and mounted them in a solution of 5% potassium hydroxide with aqueous phloxine 1%. We also employed Melzer's reagent (IKI) to assess the amiloidicity reaction. The hyphal system was described based on Teixeira (1995). The terminology for the basidia, pleurocystidia, and cheilocystidia shapes follows Vellinga and Noordeloos (2001). The description of pileipellis follows Pegler (1983). Microscopic structures were measured ($N = 20$) using a micrometer ruler eyepiece attached to an optical microscope (Olympus CX22LED OM). In basidiospore measurements, the "[a/b/c]" at the beginning indicates "a" number of basidiospores measured from "b" number of basidiomata taken from "c" number of collections. Basidiospores were measured in lateral view, with a minimum of 20 basidiospores for each basidioma. The terminology used to describe the

basidiospore shapes follows Largent et al. (1977). The Q value represents the length-to-width quotient interval for all measured basidiospores; Qm represents the average of all calculated Q values for all measured basidiospores, while Lm and Wm represent the average lengths and widths of all measured basidiospores, respectively.

DNA extraction, amplification, and sequencing methods

Genomic DNA was extracted from dried materials stored in silica gel using a CTAB protocol (Góes-Neto et al. 2005). The primer pairs ITS1F-ITS4 (White et al. 1990; Gardes and Bruns 1993) and LR0R-LR5 (Vilgalys and Hester 1990) were used to amplify the nuc rDNA internal transcribed spacer region ITS1-5.8S-ITS2 (ITS) and the nuc rDNA 28S (nrLSU), respectively. Amplification parameters for each region were as follows: ITS – 94 °C for 5 min, followed by 35 cycles 94 °C for 3 min, 50 °C for 30 sec, and 72 °C for 1 min, and a final extension at 72 °C for 10 min; and nrLSU – 94 °C for 5 min, followed by 35 cycles 94 °C for 1 min, 50 °C for 1 min 20 sec, and 72 °C for 1 min 30 sec, and a final extension at 72 °C for 10 min. The PCR products were purified with Polyethylene Glycol according to Sambrook et al. (1989). The sequencing of both markers was conducted with the same primers used in the amplification, and it was done by capillary electrophoresis in an ABI3730 device, using BigDye 3.1 polymer (Myleus Biotechnology, Belo Horizonte, Brazil).

Phylogenetic analyses

The generated chromatograms were manually verified with Geneious 9.0.5 (Kearse et al. 2012) and the final sequences were deposited at GenBank (<https://www.ncbi.nlm.nih.gov/>). GenBank accession numbers for newly provided sequences and additional downloaded sequences for the analyses are listed in Table

S1. Sequences of *Cerrena unicolor* (Bull.) Murrill were used as outgroups based on Justo et al. (2017). The sequences were aligned in MAFFT 7 with strategy Q-INS-i for ITS and G-INS-i for nrLSU (Katoh 2013), and then manually edited using MEGA 7 (Kumar et al. 2016).

We carried out phylogenetic analyses based on two datasets: ITS+nrLSU combined and only ITS. From the combined dataset, a total of 208 ingroup specimens were included. All phylogenetic analyses were performed online using the CIPRES Science Gateway (Miller et al. 2010). Phylogenetic tree of only the ITS dataset was reconstructed based on Maximum Likelihood analysis. All of the following methods were applied to the combined dataset. We defined partitions *a priori* (ITS+nrLSU) to estimate the best-fit partition scheme and substitution models in PartitionFinder 2 (Guindon et al. 2010; Lanfear et al. 2017) under the linked model of branch lengths, greedy search algorithm (Lanfear et al. 2012), and Akaike information criterion for model selection.

The Maximum Likelihood (ML) analyses were carried out in RAxML 8.2.9 (Stamatakis 2014). For each partition, GTR+G model was applied. The analysis initially included 1000 rapid bootstrap inferences, followed by a thorough ML search. To assess node reliability, we conducted rapid bootstrapping replicates, with the program employing an extended majority rule (MRE)-based bootstopping criterion (Pattengale et al. 2009).

The Bayesian Inference (BI) was performed in MrBayes 3.2.6 (Ronquist et al. 2012). For each partition, we employed partition-specific models determined as the best-fit models. In these partitioned mixed-model analyses, the substitution matrix, base frequencies, and gamma shape parameter were unlinked between data

partitions, and the rate prior was set to variable [prset applyto = (all), ratepr = variable], allowing for variations in rates among partitions. We set to execute two independent runs, each initiated from random trees, employing four simultaneous independent chains. The analysis spanned 5,000,000 generations, with tree sampling occurring at every 1000th generation. Convergence diagnostics were computed every 10,000th generation. We assessed the minimal effective sample sizes (ESS > 200) and checked for convergence between runs using Tracer 1.7 (Rambaut et al. 2018). To ensure robust results, we discarded the initial 25% of sampled trees as burn-in. The remaining trees were used to construct a 50% majority-rule consensus tree and to estimate Bayesian Posterior Probabilities (BPPs) for the branches.

Clades with BPP values above 0.95 and Bootstrap (BS) values above 70% were considered moderately supported, and those with BPP = 0.99–1 and BS = 99–100% were considered highly or fully supported (Felsenstein 1985; Hillis and Bull 1993; Soltis and Soltis 2003; Huelsenbeck and Rannala 2004). Only both moderately and highly/fully supported clades were deemed for taxonomic decisions. The recovered topology in the phylogenetic trees were organized in clades both moderately and highly supported main clades, being most inclusive as possible in order to reflect the phylogenetic relationships of the infrageneric lineages. In cases where a clade represents a single species, it was retained unless closely related clades lacked substantial support. The alignments and trees were deposited at Harvard Dataverse (Sousa-Guimarães et al. 2022).

RESULTS

In this study, we incorporated 57 newly acquired sequences, comprising 34 ITS and 23 nrLSU sequences, as outlined in Table S1. The resultant combined dataset featured a final alignment spanning 1576 base pairs (716 bp for ITS and 860 bp for nrLSU). Among these, 963 were invariable, 198 were variable parsimony-uninformative, and 405 were parsimony-informative.

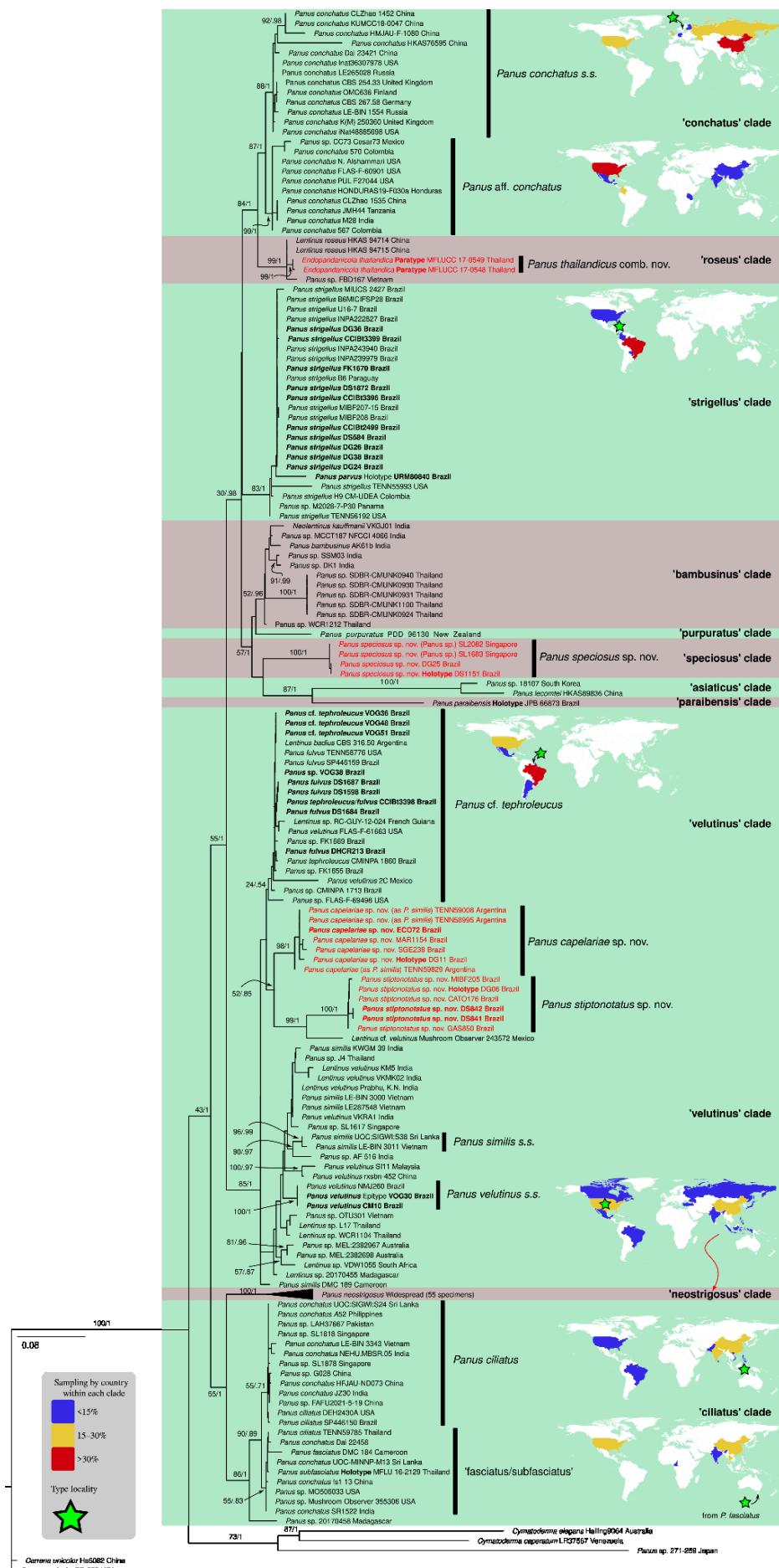
The optimal evolutionary models were determined through AIC (Akaike Information Criterion) selection, resulting in the following models: GTR+I+G for ITS and GTR+I+G for nrLSU. In BI analyses, the runs converged to stable likelihood values, specifically $-\ln L = 10,688.12$ and $10,700.54$. After discarding the initial 25% of trees as burn-in, 7,501 trees were used to compute a 50% majority-rule consensus tree and to estimate the BPP. During ML searches, the combined alignment revealed 775 distinct patterns, with a proportion of gaps and undetermined characters totaling 48.44%. The bootstrapping criteria in RAxML indicated that 550 pseudoreplications sufficed to determine internal branch support, with the final ML optimization likelihood recorded as $-\ln L = 10,571.85$.

No significant topological conflicts were detected between the ML and BI analyses, thereby allowing us to superimpose both BS and BPPs onto the best-scoring ML tree for the combined ITS+nrLSU dataset (Fig. 1). The topology derived from ITS+nrLSU (Fig. 1) and solely ITS (SUPPL. Fig. 1) trees were congruent and the main clades are as follows. Eleven primary clades have been identified and designated from bottom to top in Fig. 1 and SUPPL. Fig. 1. From Fig. 1, the clades and their respective support values (BS/BPP) are as follows: ‘ciliatus’ (BS = 86/BPP = 1), ‘neostrigosus’ (100/1), ‘velutinus’ (85/1), ‘paraibensis’ (100/1), ‘asiaticus’

(100/1), ‘speciosus’ (100/1), ‘purpuratus’ (100/1), ‘bambusinus’ (52/0.96), ‘strigellus’ (83/1), ‘roseus’ (100/1), and ‘conchatus’ (87/1) clades.

In the following clades, two or more phylogenetic species were recovered: ‘ciliatus’, ‘velutinus’, ‘asiaticus’, ‘bambusinus’, ‘strigellus’, ‘roseus’, and ‘conchatus’. Most of the eleven main clades, which encompass specimens from multiple countries, exhibit a predominantly Pantropical distribution. Notably, this includes the clades ‘ciliatus’, ‘speciosus’, and the subclade *Panus* aff. *conchatus* (Fig. 1 and Table S1). In contrast, the ‘neostrigosus’ clade displays a widespread distribution, while specimens from other clades tend to be more geographically restricted (Fig. 1 and Table S1). Specifically, specimens from the ‘asiaticus’, ‘bambusinus’, and ‘roseus’ clades primarily inhabit Asian regions, while the subclade *Panus* cf. *tephroleucus* (within the ‘velutinus’ clade) and the ‘strigellus’ clade are concentrated in the Neotropical region. Additionally, the subclade *Panus conchatus* s.s. is distributed within the Temperate region of the Northern Hemisphere (Fig. 1 and Table S1).

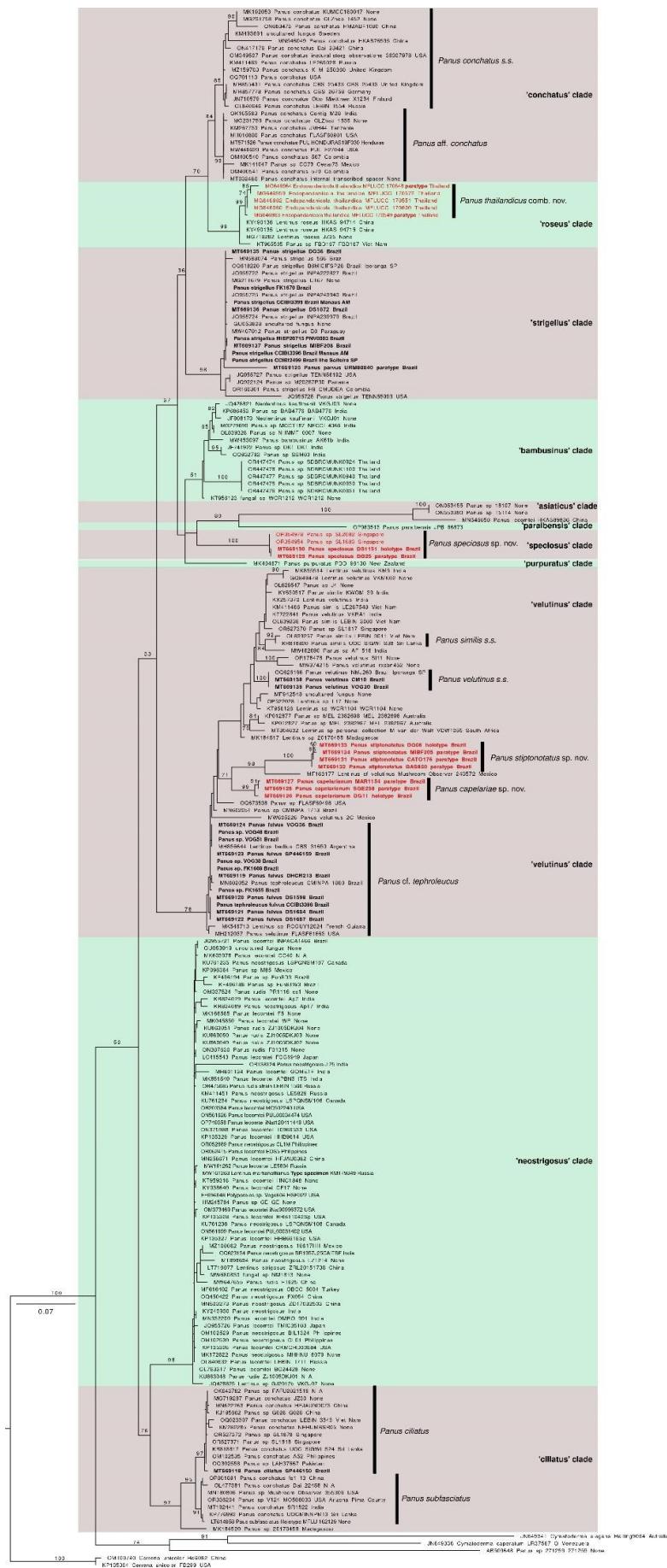
Fig. 1 Phylogenetic tree (Maximum Likelihood) of *Panus* based on ITS and nrLSU. On branches, support values are given as BS/BPP. The black circles in the branches are BS \geq 99 and BPP \geq 0.99. The sequences generated in this study are in bold. Sequences in red are those taxa newly proposed. The different colors in the maps distinguish the specimens sampled by country within each clade. Blue indicates countries with up to 15% from the clade sampling; yellow indicates 15–30% and red indicates more than 30% of the specimens in such a clade occur in a unique country.



Brazilian specimens represent at least nine phylogenetic species distributed as follows: *P. ciliatus* (SP446150) in the ‘ciliatus’ clade; *P. neostrigosus* (CC40, Fun81W3, Fun8D3, and INPACM1466) in the ‘neostrigosus’ clade; *P. capelariae*, *P. cf. tephroleucus*, *P. stipitonotatus*, and *P. velutinus* s.s. in the ‘velutinus’ clade; *P. paraibensis* in the ‘paraibensis’ clade; *P. speciosus* in the ‘speciosus’ clade; and *P. strigellus* in the ‘strigellus’ clade. *Panus capelariae*, *P. stipitonotatus*, and *P. speciosus* are newly proposed species, as detailed in the Taxonomy section.

Furthermore, we propose *P. pachysporus* as a new species and combine *Lentinus campinensis* Teixeira into the *Panus* genus, both of which are grounded in morphological data. Our study also revealed the presence of four endophytic samples located within *Panus*, spanning two distinct clades: KF496188 and KF496194 from Brazilian specimens in the ‘neostrigosus’ clade, and the paratypes of *Endopandanicola thailandica* Tibpromma & K.D. Hyde from Thailand, that we now treat as an independent species closely related to *P. roseus*. This scenario leads us to combine *E. thailandica* in *Panus* as *P. thailandicus*. We have also conducted a comprehensive revision of the list of *Panus* species found in Brazil and provide an identification key for the species that occur in the country with certainty.

Supplementary Fig. 1 Phylogenetic tree (Maximum Likelihood) of *Panus* based on ITS. On branches, only BS support values are given. The sequences generated in this study are in bold. Sequences in red are those taxa newly proposed.



Type revision and type localities

We morphologically analyzed the following holotypes that were loaned [the list is as follows: “species (type: type locality)”: *Lentinus campinensis* (IAC 4376: Brazil), *Panus fasciatus* (Berk.) Singer [K(M) 153553: Tasmania, Australia], *P. hymenorhizus* [LPS16800: Brazil], *P. guaraniticus* Speg. [LPS19295: Paraguay], *P. parvus* [URM80840: Brazil], *P. strigellus* [K(M) 153658: Cuba; syntype: K(M) 179354]. Additionally, we had access to photos of the holotypes of *L. blepharodes* Berk. & M. A. Curtis [K(M) 1436369: Cuba], *L. pseudociliatus* Raithelh. [BAFC52304: Argentina], *L. thomensis* Cout. [LISU63038: São Tomé and Príncipe], *P. fulvus* [K(M) 179387: Sri Lanka], *P. similis* [syntype: K(M) 179352: Sri Lanka], and *P. velutinus* (UPS F-012409: Brazil).

Furthermore, the following holotypes were not located or not confirmed at herbaria as cited by Pegler (1983) or confirmed as lost by the curatorships. *Lentinus coelopus* Lév. (PC: USA), *L. natalensis* Van der Byl (PREM: South Africa), *Panus ciliatus* (PC0093414: Indonesia), and *P. tephroleucus* (PC0737995: Suriname) were not confirmed by the curatorship at those herbaria as we have not received an answer from them. *Panus conchatus* [K(M) or UPS: Sweden] and *P. neostrigosus* [K(M): USA] are probably lost as K staff could not find them and we did not locate *P. conchatus* type in the UPS catalog (<http://webdev.its.uu.se/evomus/botanik/home.php>, accessed 02/10/2023). In addition, *Lentinus castaneus* Ellis & T. Macbr. (ISC: Nicaragua), *L. fallax* Speg. (LPS1271: Paraguay), and *P. convivalis* (K: Brazil) were confirmed as lost by the curatorship. Additionally, given the *Panus* circumscription the protologue of *P. convivalis* is inconclusive (Corner 1981).

The type of *Lentinus velutinus* Fr. was not found in UPS and was never studied by Pegler (1983) who, instead, provides a description based on *Agaricus velutinus* Fr. [=*Panus velutinus* (Fr.) Fr.]. The type of *Lentinus velutinus* Fr. should represent another lentinoid species and seems to be lost.

TAXONOMY

Panus campinensis (Teixeira) Drechsler-Santos & Robledo, comb. nov. Fig. 2

MycoBank: 804004

Basionym: *Lentinus campinensis* Teixeira, Bragantia 6:169. 1946.

Complete description: See Teixeira (1946).

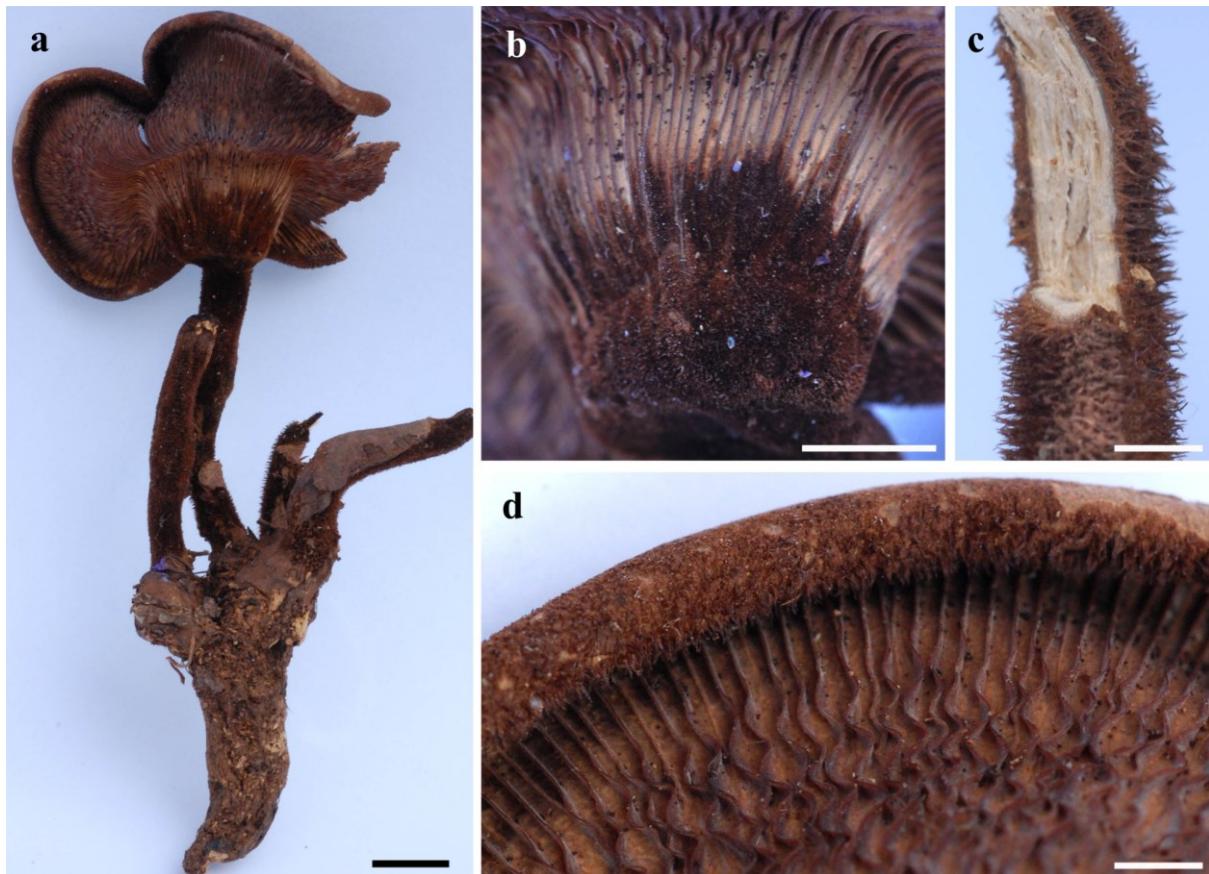
Material examined: BRAZIL. SÃO PAULO: Campinas, Bosque dos Jequitibas, 2 December 1943, F.P. Bastos s/n (IAC 4376!, **holotype**).

Notes: As outlined by Teixeira (1946), *Lentinus campinensis* displays distinctive characteristics, including a lateral to eccentric stipe and a reniform pileus [see Fig. b from plate III in Teixeira (1946)]. The upper or external surfaces of both the pileus and stipe exhibit a velutinate to villose texture (see Fig. 2c). Under microscopic examination, it has a dimictic hyphal system composed of hyaline to pale brown, unbranched skeletal hyphae and hyaline, clamped generative hyphae, it presents pleurocystidia and lacks hyphal pegs. This combination of features corresponds to the morphological circumscription of *Panus* (Corner 1981; Hibbett and Vilgalys 1993; Drechsler-Santos et al. 2012) and, hence, the new combination is proposed.

Fig. 2 *Panus campinensis* (holotype: IAC 4376 of *Lentinus campinensis*). **a.**

basidioma overview, scale bar = 1 cm. **b.** detail of the lamellae and their insertion into

the stipe, scale bar = 0.5 cm. **c.** surface detail and context of the stipe, scale bar = 0.2 cm. **d.** detail of lamellae and margin of incurvation, scale bar = 0.2 cm.



FONTE: Sousa-Guimarães et al. 2024

This name had been previously regarded as a synonym of *Lentinus velutinus* due to the rather broad morphological concept of *L. velutinus* (Pegler 1983). However, upon conducting a detailed morphological analysis of the type specimen, significant distinctions were uncovered. Notably, the lateral to eccentric stipe, along with the reniform pileus that curves inwards from the margin should be regarded as additional diagnostic characteristics [see Figs. 2a, 2d and also refer to plate III in Teixeira (1946)]. *Lentinus velutinus* sensu Pegler (1983) is a species characterized by a more or less slender basidiomata, with an elongated stipe and a circular, infundibuliform pileus that typically folds in a distinctive manner when mature or dried

(typically midway between the margin and the center of the pileus). Moreover, the holotype of *L. campinensis* has short ellipsoid basidiospores, $5.0\text{--}6.0 \times 2.5\text{--}3.0 \mu\text{m}$ ($n = 40$, $Q_m = 1.50$). In contrast, basidiospores of *L. velutinus* are oblong-cylindric to ellipsoid, $5.0\text{--}7.0(8.0) \times 3.0\text{--}3.7 \mu\text{m}$ ($Q_m = 1.87$) according to Pegler (1983), or $6.0\text{--}7.0 \times 2.5\text{--}3.0 \mu\text{m}$ according to Teixeira (1946). It is worth to mention that the presence or absence of a pseudosclerotium could be considered a diagnostic character. However, it is important to note that the type specimen might have been collected without the pseudosclerotium, rendering this feature inconclusive for differentiation.

Panus capelariae Sousa-Guimarães, Menolli & Drechsler-Santos, sp. nov. Figs. 1, 3a–c, 4

Mycobank: 850307

Typification: BRAZIL. SANTA CATARINA: Florianópolis, Parque Municipal da Lagoa do Peri, 11 December 2016, Sousa-Guimarães, D. K. DG11 (**holotype** FLOR 73885). Genbank accession numbers: ITS = MT669126; nrLSU = MT669146.

Etymology: “capelariae”, named in honor of Dr. Marina Capelari, a Brazilian mycologist who contributed to the taxonomy of Brazilian mushrooms and also collected one of the specimens examined.

Diagnosis: *Panus capelariae* is recognized for the radially plicate-sulcate pileus surface, subdistant lamellae and narrowly utriform and thin-walled pleurocystidia.

Description: *Pileus* 24–35 mm diam., infundibuliform to cyathiform, chestnut to dark brown (N₈₀Y₇₀M₆₀), radially plicate-sulcate, almost glabrous to slightly velutinate, glabrous towards the center, margin curved downwards and slightly sulcate.

Lamellae decurrent, beige ($N_{40}Y_{60}M_{40}$), subdistant, margin entire, with lamellulae.

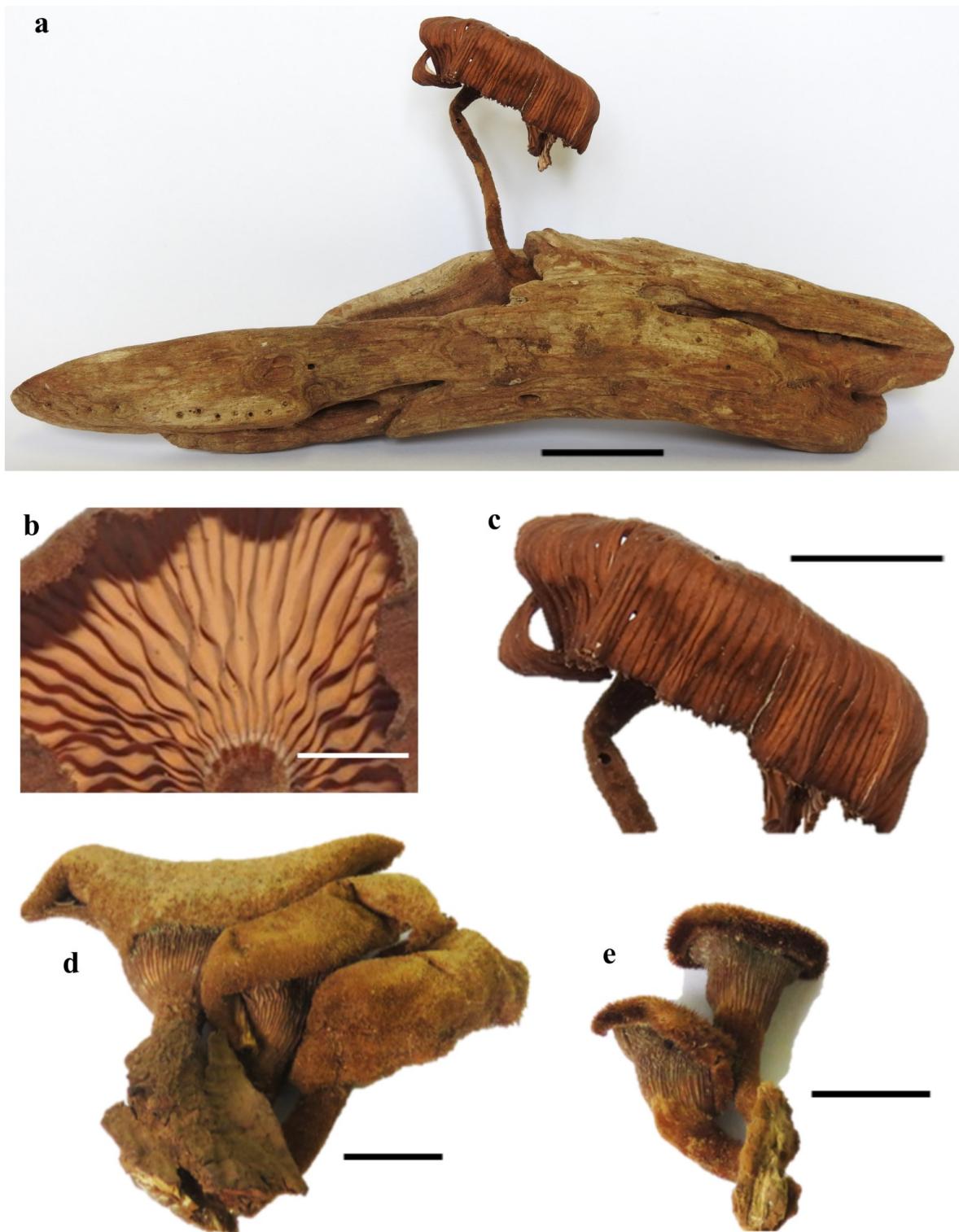
Stipe central, $25\text{--}40 \times 2\text{--}4$ mm, mostly cylindric, villose to tomentose, concolorous with the pileus surface or slightly darker, slightly enlarged at the base, arising from a small to large pseudosclerotium.

Hyphal system dimitic. *Generative hyphae* $2.0\text{--}4.0 \mu\text{m}$ diam., hyaline, branched, clamped, thin-walled to rarely thick-walled. *Skeletal hyphae* $2.5\text{--}5.0 \mu\text{m}$ diam., hyaline to pale brown, unbranched, thick-walled. *Basidiospores* ellipsoid to cylindric, [70/7/7] $5.0\text{--}8.1 \times 2.5\text{--}4.3 \mu\text{m}$ ($Q_m = 1.94$; $Q = 1.6\text{--}2.5$; $L_m = 6.87 \mu\text{m}$; $W_m = 3.12 \mu\text{m}$), hyaline, thin-walled, smooth, rarely with guttulae, IKI-. *Basidia* cylindrical-clavate, $17\text{--}32 \times 5.0\text{--}6.2 \mu\text{m}$, hyaline, thin-walled, 4-sterigmate, clamped at the base. *Pleurocystidia* $20\text{--}37(47) \times 3.7\text{--}7.5$ of two types: (1) flexuous, thin-walled, smooth; (2) conical to narrowly conical, thick-walled ($1.0\text{--}2.5 \mu\text{m}$ thick).

Cheilocystidia $19\text{--}26 \times 3.0\text{--}6.0 \mu\text{m}$, flexuous, smooth, thin to thick-walled.

Hymenophoral trama irregular, hyaline, similar in structure to the context. *Pileipellis* an epicutis composed of erect to loose fascicles of brown, thick-walled, and clamped generative hyphae.

Fig. 3 *Panus capelariae* (a and c FLOR 73885, holotype). **a.** overview of the basidioma. **b.** detail of the subdistant lamellae (SP446152, paratype). **c.** detail of the pileus surface. Macroscopic view of *P. pachysporus* (SP60914, holotype). **d** and **e** overview of the basidioma. Scale bars = 1cm.



FONTE: Sousa-Guimarães et al. 2024

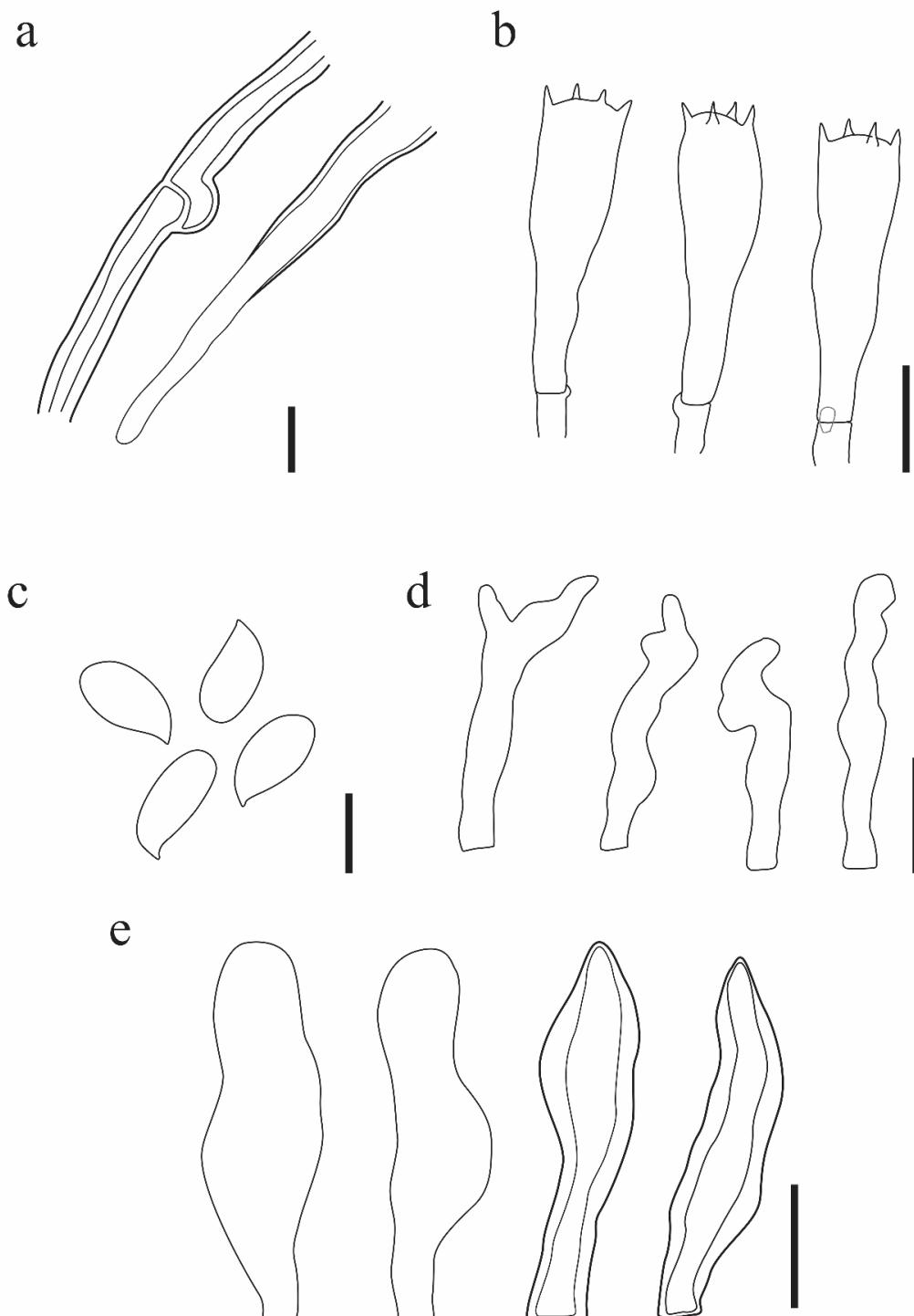
Habit, habitat, and known distribution: Solitary, rarely gregarious, with a pseudosclerotium. Growing on fallen dead logs. Currently known from Southern South America, in Tropical Broadleaved Forest from Brazil and Argentina.

Additional specimens examined: BRAZIL. SÃO PAULO: São Paulo, 2008, Capelari, M. 4365 (SP446152); Caraguatatuba, Parque Estadual Serra do Mar, 19 January 2016, Elias, S. G. SGE238 (FLOR 73887); *ibid.*, 20 January 2016, Reck, M. A. MAR1154 (FLOR 73888); *ibid.*, July 2016, Copini, E. EC72 (FLOR 73889); RIO GRANDE DO SUL: Araricá, 23 November 2017, Palacio, M. MP296 (FLOR 73890); SANTA CATARINA: Florianópolis, UCAD, trilha principal, 2012, Drechsler-Santos, E. R., DS840 (FLOR73886).

Notes: *Panus capelariae* is primarily characterized by its radially plicate-sulcate pileus, utriform and thin-walled pleurocystidia, the presence of small to large pseudosclerotia, and its distribution in the Neotropical region. In terms of macroscopic features, it bears a striking resemblance to *P. similis* due to their shared radially plicate-sulcate pileus and subdistant lamellae. However, *P. similis*, typified by a collection from Sri Lanka, distinguishes by smaller basidiospores 5.0–6.2 × 2.5–3.2 µm, conical to narrowly conical pleurocystidia with thick walls, and an Asian distribution with putative records in Africa, as documented by Pegler (1983).

Phylogenetically, *P. capelariae* was recovered as sister (Fig. 1: unsupported, SUPPL. Fig. 1: 71) to a clade with a new species described below and another Mexican phylogenetic species (Fig. 1, SUPPL. Fig. 1). For morphological comparison, see hereafter. Also, *P. capelariae* does not cluster with the *P. similis sensu stricto* subclade, which comprises sequences from collections in Sri Lanka (Ediriweera et al. 2021) and Vietnam. Corner (1981) considered *P. similis* as a variety of *P. fulvus* [*Panus fulvus* var. *similis* (Berk. & Broome) Corner]. However, based on morphology, the independence between the species *P. similis* and *P. fulvus* is supported. *Panus fulvus* can be distinguished from *P. capelariae* by its erect fasciculate hairs on the pileus and by moderately spaced lamellae, as shown by

Fig. 4 Microcharacters of *Panus capelariae* (FLOR 73885). **a.** thick-walled generative hyphae, scale bar = 5 µm. **b.** basidia. **c.** basidiospores, scale bar = 5 µm. **d.** pleurocystidia. **e.** cheilocystidia. Scale bars =10 µm.



Corner (1981). Within the clade associated with *P. capelariae* there are three sequences from Argentinean collections that were previously labeled as *P. similis*; however, these collections represent *P. capelariae*, as shown by our phylogenetic results, thus expanding the distribution of this species to Argentina.

Panus pachysporus Sousa-Guimarães, Menolli & Drechsler-Santos, sp. nov. Figs. 3d,e, 5.

Mycobank: 850309

Typification: BRAZIL. RIO GRANDE DO SUL: Gramado, Várzea Grande, 07 May 1961, Costa-Neto, J. P. (holotype SP60914).

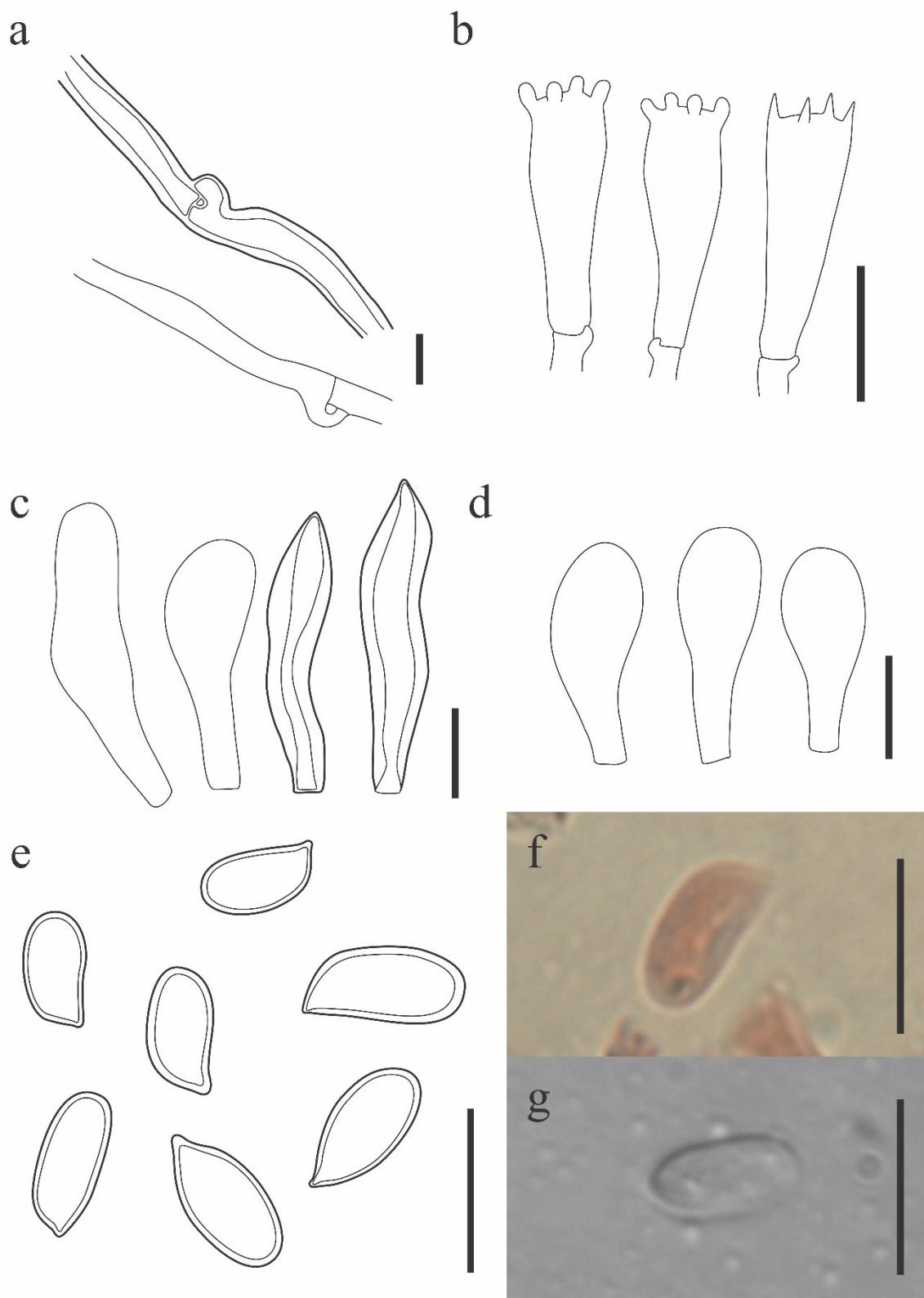
Etymology: from the Greek ‘pachy’ = thick and ‘sporus’ = basidiospore, referring to the thick-walled basidiospores.

Diagnosis: *Panus pachysporus* is distinguished by its large, thick-walled basidiospores.

Description: *Pileus* 11–40 mm diam., infundibuliform to cyathiform, coriaceous, chestnut brown to dark brown ($N_{60}A_{60}M_{50}$) when dry, slightly striate, villous to tomentose, margin thin. *Lamellae* decurrent, vinaceous brown ($N_{60}A_{30}M_{40}$), moderately to densely crowded, margin entire, with lamellulae. *Stipe* central, 13–24 × 3–5 mm, cylindric, slightly enlarged at the base, surface villous to tomentose, chestnut brown, concolorous with the pileus surface.

Fig. 5 Microcharacters of *Panus pachysporus* (SP60914, holotype). **a.** generative hyphae, scale bar = 5 µm. **b.** basidia. **c.** pleurocystidia. **d.** cheilocystidia. **e.** basidiospores. **f-g:** light microscopy of basidiospores, showing the thickened wall; **f.** basidiospore under Congo Red reagent using standard light microscopy; **g.**

basidiospore under Differential Interference Contrast (DIC) light microscopy in grayscale. Scale bars = 10 μm .



FONTE: Sousa-Guimarães et al. 2024

Hyphal system dimitic. *Generative hyphae* 2.0–4.5 µm diam., hyaline, clamped, thin-walled, some thick-walled. *Skeletal hyphae* 2.5–6.0 µm diam., hyaline, thick-walled, IKI–. *Basidiospores* ellipsoid to cylindric, [30/1/1] 6.5–11.5(12.0) × 4.0–5.5(6.0) µm (Qm = 1.97, Q = 1.6–2.4, Lm = 10 µm, Wm = 5.0 µm), hyaline, thick-walled, smooth, some with guttulae, IKI–. *Basidia* cylindric-clavate, 17.0–26 × (5.5)6.0–8.0 µm, hyaline, thin-walled, 4-sterigmated, clamped at the base.

Pleurocystidia of two types: (1) clavate, (22)25–32 × 5.5–7.0 µm, thin-walled, smooth; (2) narrowly conical 23–46 × 4.0–7.5 µm, narrowly thick-walled (1.0–2.0 µm thick), smooth. *Cheilocystidia* clavate (18.0)21–28 × 4.0–7.5 µm, smooth, thin-walled.

Hymenophoral trama irregular, of radiate construction, consisting of a dimitic hyphal system with skeletal hyphae. *Pileipellis* a trichodermium composed of erect generative hyphae, with thick- and brown-walls, with clamp connections.

Habit, habitat, and known distribution: Gregarious, without a pseudosclerotium. Known only from the type locality in the Tropical Broadleaved Forest of the state of Rio Grande do Sul, Brazil.

Notes: The macromorphological description provided above is based on a dehydrated specimen dating back to 1961. *Panus pachysporus* is notably characterized by presenting the largest and thick-walled basidiospores of the genus. *Panus velutinus* and *P. pachysporus* share several similarities, including a coriaceous, chestnut brown, and velutinate pileus, which is marked with striations, and lamellae that are moderately to densely crowded. However, *P. velutinus*, can be distinguished by presenting a pseudosclerotium, larger basidiomata (pilei up to 160 mm diam. and stipe 35–205 × 2.0–8.0 mm), larger cheilocystidia (22)25–36(40) × 5.0–8.5 µm, and thin-walled and smaller basidiospores that typically measure 4.5–7.0 × 3.0–4.0 µm.

Panus speciosus Sousa-Guimarães & Drechsler-Santos, sp. nov. Figs. 6a–c, 7

Mycobank: 850308

Typification: BRAZIL, SANTA CATARINA: Florianópolis, Universidade Federal de Santa Catarina, 01 November 2013, Drechsler-Santos, E. R. DS1151 (**holotype** FLOR 68417). Genbank accession numbers: ITS = MT669130; nrLSU = MT669150.

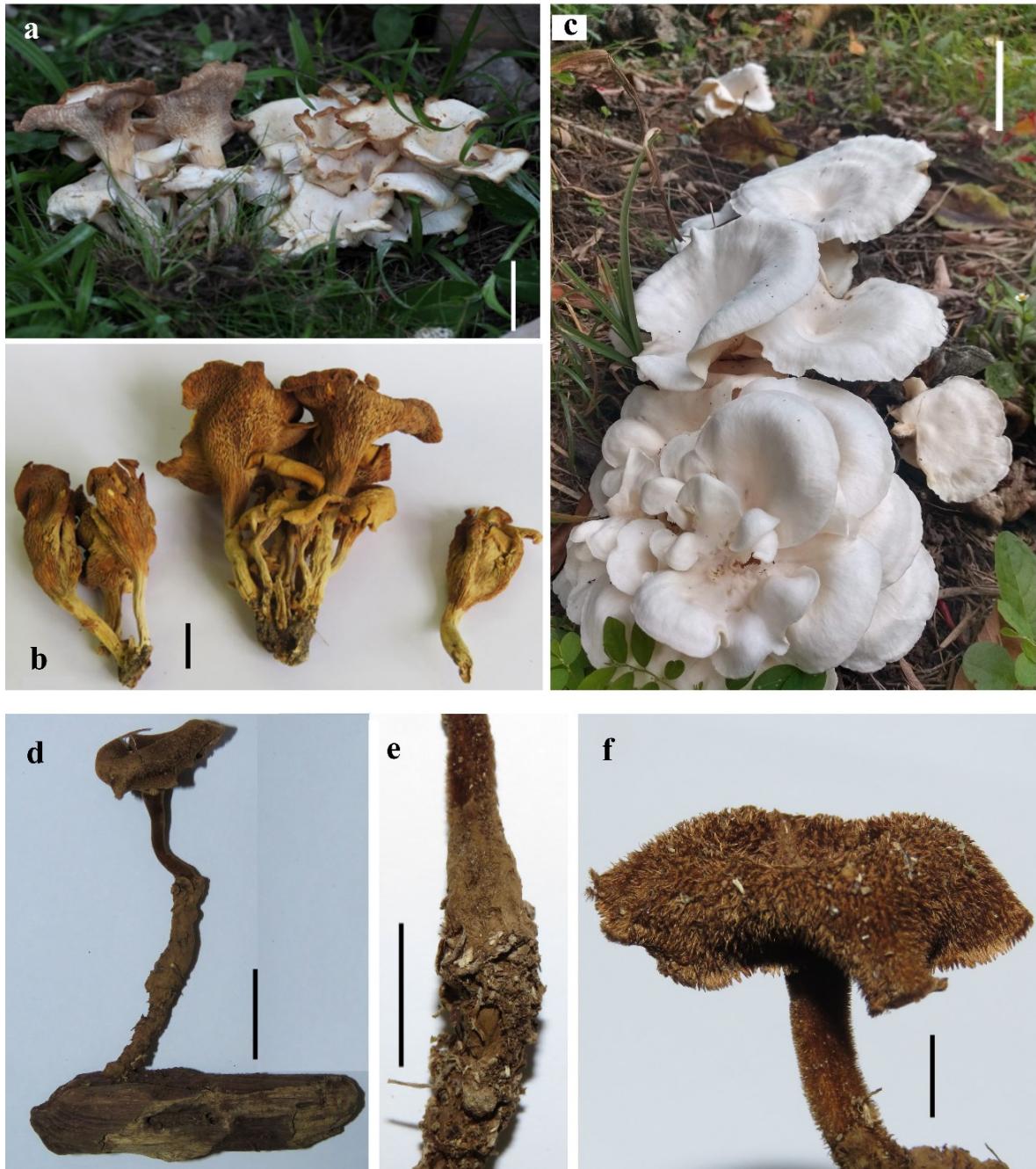
Etymology: from Latin “speciosus” = handsome, referring to the beauty of this *Panus* species.

Diagnosis: *Panus speciosus* is distinguished by the soft, white to cream pileus, the mostly glabrous pileus surface and a fibrillose stipe.

Description: *Pileus* 18–50 mm diam., applanate when young, infundibuliform at maturity, surface white to cream ($N_{10}A_{20}M_{10}$) when fresh, then slightly darkening to beige when dry ($N_{10}A_{30}M_{20}$), hairy-squamose only at the center, margin involute, glabrous. *Lamellae* decurrent, beige to pinkish brown when fresh ($A_{50}M_{40}C_{30}$), then brownish ($A_{80}M_{50}C_{30}$) when dry, crowded, anastomosed near the stipe, margin entire, with lamellulae. *Stipe* central to eccentric, 28–45 × 5 mm, flexuous, flattened, slightly enlarged towards the apex, beige ($N_{10}A_{30}M_{20}$), surface glabrescent, fibrillose.

Hyphal system dimitic. *Generative hyphae* 2.0–5.0 µm diam., hyaline, clamped, thin- to thick-walled. *Skeletal hyphae* 2.5–5.5 µm diam., thick-walled. *Basidiospores* ellipsoid to cylindric, [60/3/3] (4.0)5.0–7.5 × 2.5–3.5 (Qm = 1.91; Q = 1.6–2.2; Lm = 6.0 µm; Wm = 3.0 µm), hyaline, thin-walled, smooth, rarely gutted, IKI–. *Basidia* cylindric-clavate, (18)21–35(49) × 4.5–9.0 µm, hyaline, thin-walled, 4-sterigmated, clamped at the base. *Pleurocystidia* of two types: (1) narrowly clavate to clavate, 30–45 × 6.0–9.0 µm, thin-walled; (2) narrowly utriform, 22–64 × 6.0–12.0 µm, thick-

Fig. 6 Macroscopic view of *Panus speciosus* and *P. stipitonotatus*. *Panus speciosus* (a–c). a, b. FLOR 68417, holotype. c. FLOR 68419, paratype. *Panus stipitonotatus* (d–f). d, e. FLOR 68422, holotype, scale bar d = 2 cm. f. FLOR 68424, paratype. Scale bars = 1cm.



FONTE: Sousa-Guimarães et al. 2024

walled (1.5–3.0 µm thick), almost smooth. *Cheilocystidia* clavate, 22–39(42) × 6.5–12.0 µm, smooth, thin-walled. *Hymenophoral trama* irregular, of radiate construction, consisting of a dimitic hyphal system with skeletal hyphae. *Pileipellis* an epicutis composed of radially to parallel arranged generative hyphae, with slightly thick and brown walls, septated, clamp connections not observed.

Habit, habitat, and known distribution: Gregarious, without pseudosclerotium. On fallen dead logs. Currently known from Brazil, in the Tropical Broadleaved Forest in the urban area of Florianópolis, Santa Catarina state and in Singapore.

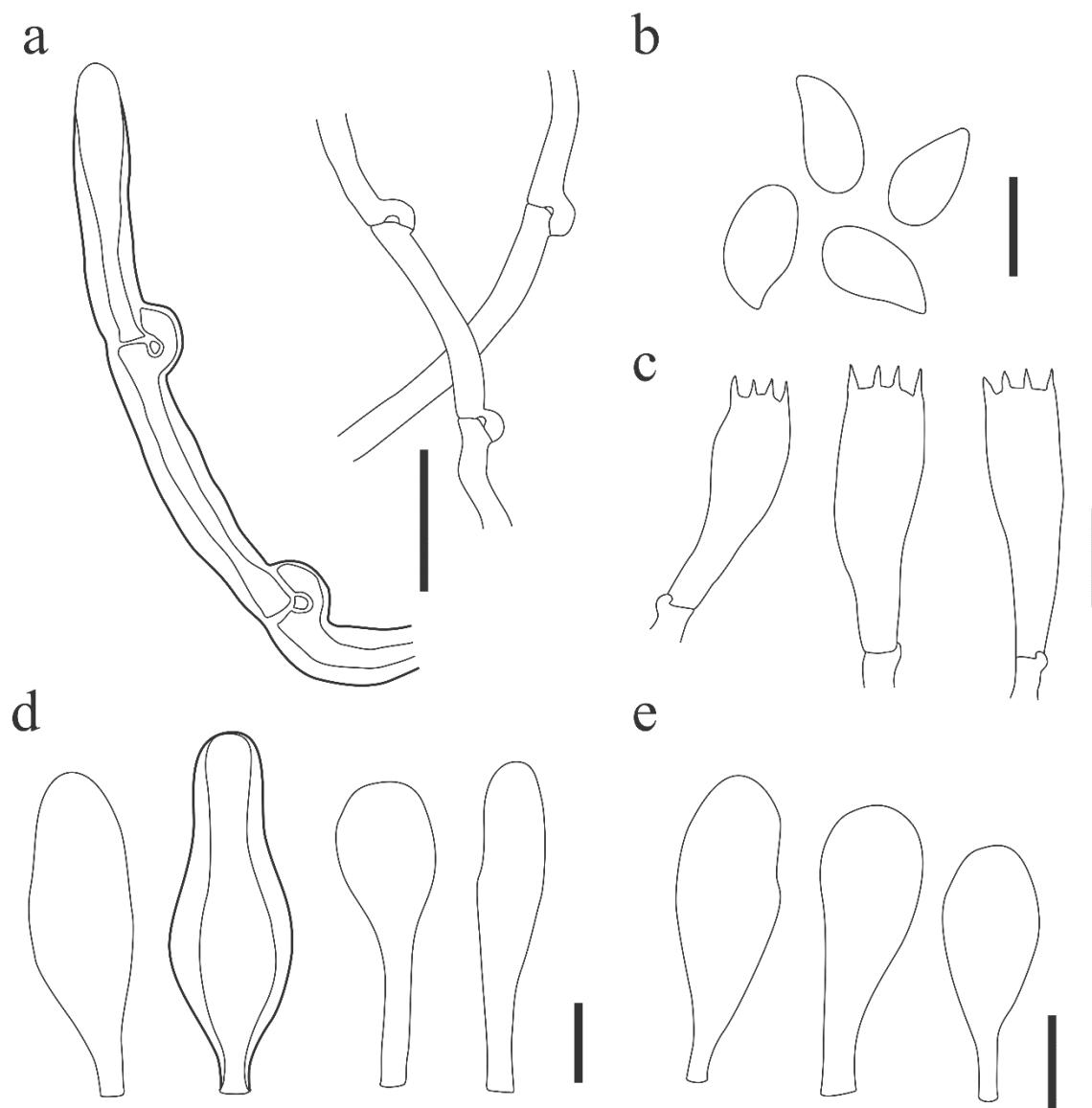
Additional specimens examined: BRAZIL. SANTA CATARINA: Florianópolis, Universidade Federal de Santa Catarina, 18 October 2016, *Sousa-Guimarães*, D. K. DG25 (FLOR 68418); *ibid.*, 02 December 2017 *Sousa-Guimarães*, D. K. DG68 (FLOR 68419).

Notes: *Panus speciosus* is characterized by its whitish and glabrous pileus, featuring a squamose central area, and a stipe that varies from fibrillose to glabrescent. *Panus hirtiformis* (Murril) Drechsler-Santos & Wartchow, described from Belize, also has a glabrous pileus, which appears pinkish ochraceous when fresh (Pegler 1983). However, it distinguishes from *P. speciosus* by exhibiting a brown ochraceous pileus, smaller basidia 15–19 × 3.5–4.5 µm, and longer pleurocystidia 28–80 × 5.0–9.0 µm (Pegler 1983).

Panus caespiticola (Pat. & Har.) Drechsler-Santos & Wartchow also presents an applanate and pale ochraceous to cream-colored pileus. Nevertheless, it differs from *P. speciosus* in having slightly longer and differently shaped pleurocystidia (fusoid to lageniform, 35–54 µm long) and shorter cheilocystidia 24–33 × 7.0–9.0 µm,

with a cylindrical-lanceolate to ventricose-fusoid morphology (Pegler 1983; Drechler-Santos et al. 2012).

Fig. 7 Microcharacters of *Panus speciosus* (FLOR 68417). **a.** generative hyphae. **b.** basidiospores, scale bar = 5 µm. **c.** basidia. **d.** pleurocystidia. **e.** cheilocystidia. Scale bars = 10 µm.



FONTE: Sousa-Guimarães et al. 2024

Phylogenetically, *P. speciosus* was recovered in the 'speciosus' clade nested within at least four phylogenetic species that exhibit shared morphological features. These species are discussed hereafter in the 'speciosus' clade.

Panus stiptonotatus Sousa-Guimarães & Drechsler-Santos, sp. nov. Figs. 1, 6d–f,
8

MycoBank: 850310

Typification: BRAZIL. SANTA CATARINA: Florianópolis, Parque Municipal do Córrego Grande, 04 June 2016, *Sousa-Guimarães, D. K. DG06* (**holotype** FLOR 68422). Genbank accession numbers: ITS = MT669133; nrLSU = MT669153.

Etymology: "Stipto" from Latin = stipe; from Latin "notatus" = marked, notable, referring to the marked nodulose portions of the stipe.

Diagnosis: *Panus stiptonotatus* is distinguished by having nodular portions on the stipe and pleurocystidia that are partially immersed in the hymenium.

Description: *Pileus* 22–30 mm diam., infundibuliform, dark brown (N₉₀A₇₀M₁₀) when dry, surface hispid strigose with short and erect hairs, margin involute, hairy. *Lamellae* decurrent, brown (N₆₀A₅₀M₅₀) when dry, moderately crowded, anastomosed near the stipe, margin entire, with lamellulae. *Stipe* central to eccentric, 38–65 × 5 mm, sometimes with nodules extending over the entire surface of the stipe or disposed on the middle portion or on the base and then, nodulose portion up to 9 mm diam., cylindric to flexuous, surface pilose, velutinate and tomentose from base to apex, brown, concolorous with the pileus surface, arising from a pseudosclerotium.

Hyphal system dimitic. *Generative hyphae* 1.5–5.0 µm diam., hyaline, clamped, thin-walled, some thick-walled. *Skeletal hyphae* 2.5–5.0 µm diam., thick-walled.

Basidiospores ellipsoid to oblong ellipsoid, [70/7/7] 4.0–5.5(6.0) × 2.0–3.0 µm (Qm = 1.82, Q = 1.6–2.0, Lm = 5.0 µm, Wm = 2.5 µm), hyaline, thin-walled, smooth, rarely gutted, IKI–. *Basidia* cylindrical-clavate, 17.0–22(24) × 4.5–7.0 µm, hyaline, thin-walled, 4-sterigmate, clamped at the base. *Pleurocystidia* of two types: (1) flexuous with subcapitate apex to clavate, 40–62 × 5.0–9.0 µm, thin-walled, smooth, almost totally immersed in the hymenium, projecting (3.5–8.0 µm) from the initial portion of the hymenophoral trama; (2) fusiform, 17.0–24 × 5.0–8.0 µm, narrowly thick-walled (1.0–1.5 µm thick). *Cheilocystidia* flexuous, (11.0)13.0–22.0 × 3.5–7.0 µm, smooth, thin-walled. *Hymenophoral trama* irregular, hyaline consisting of a dimitic hyphal system with skeletal hyphae. *Pileipellis* an epicutis composed of erect, loosely arranged fascicles of unbranched, brown, thick-walled, clamped generative hyphae.

Habit, habitat, and known distribution: Solitary, rarely gregarious, with pseudoesclerotium. Growing on fallen dead logs. Currently known from Southern Brazil, in Tropical Broadleaved Forest, in the states of Santa Catarina and Rio Grande do Sul.

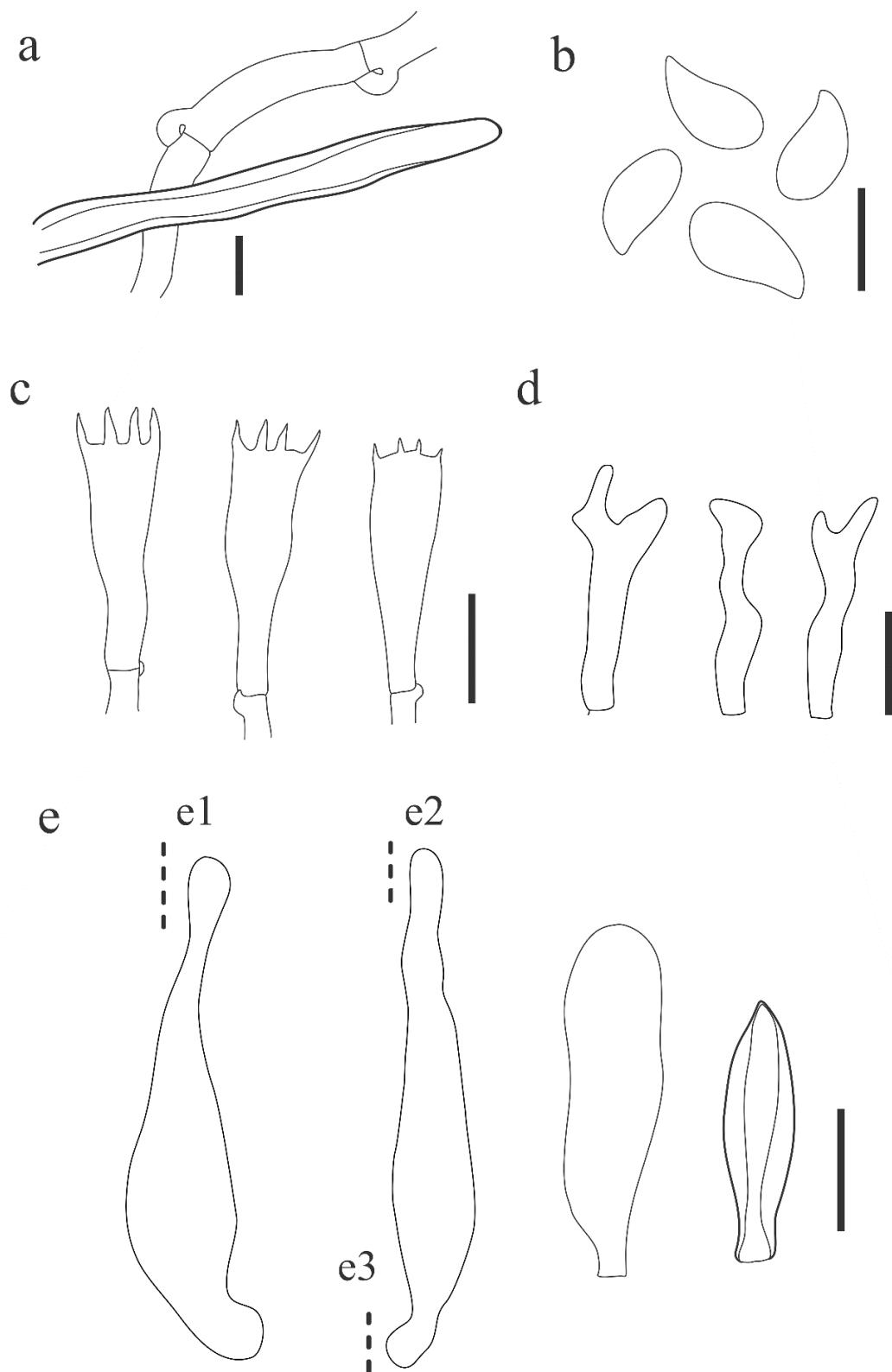
Additional specimens examined: BRAZIL. SANTA CATARINA: Santo Amaro da Imperatriz, Plaza Caldas da Imperatriz, 21 March 2014, J. Menezes Prata JP0048 (FLOR 68424); *ibid.*, Florianópolis, PBP0002 (FLOR 68425); *ibid.*, Unidade de Conservação Ambiental Desterro - UCAD, 28 March 2017, Oliveira, C. A. T. CATO176 (FLOR 68423). RIO GRANDE DO SUL: Porto Alegre, Morro Santana, 27 July 2016, Alves-Silva, G. GAS850 (FLOR 68420); *ibid.*, GAS851 (FLOR 68421).

Notes: *Panus stipitonotatus* is characterized by the presence of nodular portions in the stipe and flexuous pleurocystidia, which are partially embedded in the hymenium, showcasing a visible subcapitate apex. *Panus caespiticola*, described from Mali (Africa), also presents a nodulose-like stipe (Pegler 1983), but it can be readily distinguished by its slightly larger basidiospores ($5.5\text{--}7.0 \times 3.0\text{--}4.5 \mu\text{m}$) and longer cheilocystidia ($24\text{--}33 \mu\text{m}$ long) that are cylindrical-lanceolate to ventricose-fusoid (Pegler 1983).

Panus velutinus and *P. pachysporus* also exhibit velutinate, chestnut brown pileus surfaces and lamellae that are moderately to densely crowded. However, *P. velutinus* is distinguished by smaller [(22)25–31 \times 5.5–9.0 μm] and differently shaped pleurocystidia, which are clavate and thin-walled. Conversely, *P. pachysporus* differs mainly by larger basidiospores, $6.5\text{--}11.5(12) \times 4.0\text{--}5.5(6.0) \mu\text{m}$.

In a phylogenetic context (Fig. 1, SUPPL. Fig. 1), *P. stipitonotatus* forms a sister group (Fig. 1: 100/1, SUPPL. Fig. 1: 98) to a specimen from Mexico identified as *Lentinus cf. velutinus* and *P. capelariae* as sister to them (Fig. 1: unsupported, SUPPL. Fig. 1: 71). This specimen, *Lentinus cf. velutinus*, is not related to *P. velutinus* s.s., as we define it here (see below) and, in a broad sense, *P. velutinus* is different to *P. stipitonotatus* as discussed above. *Panus capelariae* differs from *P. stipitonotatus* by having radially plicate-sulcate pileus surface and subdistant lamellae.

Fig. 8 Microcharacters of *Panus stipitonotatus* (FLOR 68422). **a.** generative hyphae, scale bar = 5 μm . **b.** basidiospores, scale bar = 5 μm . **c.** basidia. **d.** cheilocystidia. **e.** pleurocystidia: **e1**, **e2**. projection on the hymenium; **e3**. projection in the lamellar trama. Scale bars = 10 μm .



FONTE: Sousa-Guimarães et al. 2024

Panus thailandicus (Tibpromma & K.D. Hyde) Menolli, Alves-Silva, Sousa-Guimarães & Drechsler-Santos, comb. nov. Fig. 1

MycoBank: 850311

Basionym: *Endopandanicola thailandica* Tibpromma & K.D. Hyde, MycoKeys 33: 32 (2018)

Description: See Tibpromma et al. (2018).

Notes: *Panus thailandicus* was initially characterized based on cultures of endophytic fungi found in association with the leaves of *Pandanaceae* (Tibpromma et al. 2018). Hitherto, the morphology of its basidioma, or whether the species is capable of producing it, remains uncharted. In terms of phylogenetic positioning, it was recovered related to *P. roseus* (Fig. 1), within a distinct lineage (see SUPPL. Fig. 1) among other *Panus* species but not as a distinct genus. Consequently, we have formally combined *Endopandanicola thailandica* into *Panus* and *Endopandanicola* must be considered a synonym of *Panus*.

Panus velutinus (Fr.) Fr. Epicrisis: 398 (1838), non (Fr.) Sacc. 1887, Figs. 1, 9, 10

≡ *Agaricus (Omphalia) velutinus* Fr. Linnaea 5: 508 (1830), non *Lentinus velutinus* Fr. Linnaea 5: 510 (1830)

MycoBank: MB178816

Holotype: BRAZIL: December 1830, *Sic Beyrich* (UPS F-012409). (Fig. 9a)

Epitype: BRAZIL: RIO GRANDE DO SUL: Canela, 09 October 2016, *Garcia, V. O. VOG30* (FLOR 75655). Genbank accession numbers: ITS = MT669139; nrLSU = MT669155. (Fig. 8b-d, 9).

*Description based on Brazilian specimens, including the epitype designated here and the holotype of **Agaricus velutinus** Fr.: Pileus* 90–160 mm diam., deeply umbilicate to broadly infundibuliform to cyathiform, coriaceous, pale brown or chestnut to cinnamon brown ($N_{70}M_{50}C_{40}$), uniformly velutinous to short hispid, margin thin and involute. *Lamellae* decurrent, buff pale brown ($N_{60}M_{50}C_{30}$), moderately to densely crowded, margin entire, with lamellulae. *Stipe* central, 35–205 × 2.0–8.0 mm, cylindrical, uniformly velutinous, slender, elongate, concolorous with the pileus surface, expanding slightly at both apex and base, arising from a hard pseudosclerotium.

Hyphal system dimitic. *Generative hyphae* 2.0–4.5 µm diam., hyaline, clamped, thin- to rarely thick-walled. *Skeletal hyphae* 2.5–5.0 µm diam., hyaline, thick-walled. *Basidiospores* ellipsoid to cylindrical, [80/1/4] 4.5–7.0 × 3.0–4.0 µm ($Q_m = 1.78$; $Q = 1.5$ –2.1; $L_m = 6.0$ µm; $W_m = 3.25$ µm), hyaline, thin-walled, smooth, rarely gutted, IKI^- . *Basidia* cylindrical-clavate, 22–25 × 4.0–5.5 µm, hyaline, thin-walled, 4-sterigmate, clamped at the base. *Pleurocystidia* of two types: (1) clavate (22)25–31 × 5.5–9.0 µm thin-walled, smooth; (2) clavate to fusiform, 28–50 × 4.0–7.0 µm, narrowly thick-walled (1.5–2.0 µm thick). *Cheilocystidia* clavate to fusiform, (22)25–36(40) × 5.0–8.5 µm, smooth, thin-walled. *Hymenophoral trama* irregular, hyaline consisting of a dimitic hyphal system with skeletal hyphae. *Pileipellis* a trichodermium composed of erect, clamped generative hyphae, with thick- and brown-walls.

Fig. 9 *Panus velutinus*. **a.** basidioma overview [holotype UPS F-012409 of *Agaricus (Omphalia) velutinus*]. **b–d.** Epitype FLOR 75655 of *P. velutinus* **b.** basidioma overview, scale bar = 2 cm. **c.** detail of the lamellae and their insertion into the stipe, scale bar = 0.5 cm. **d.** detail of pileus surface and margin involute. Scale bars = 1 cm.



FONTE: Sousa-Guimarães et al. 2024

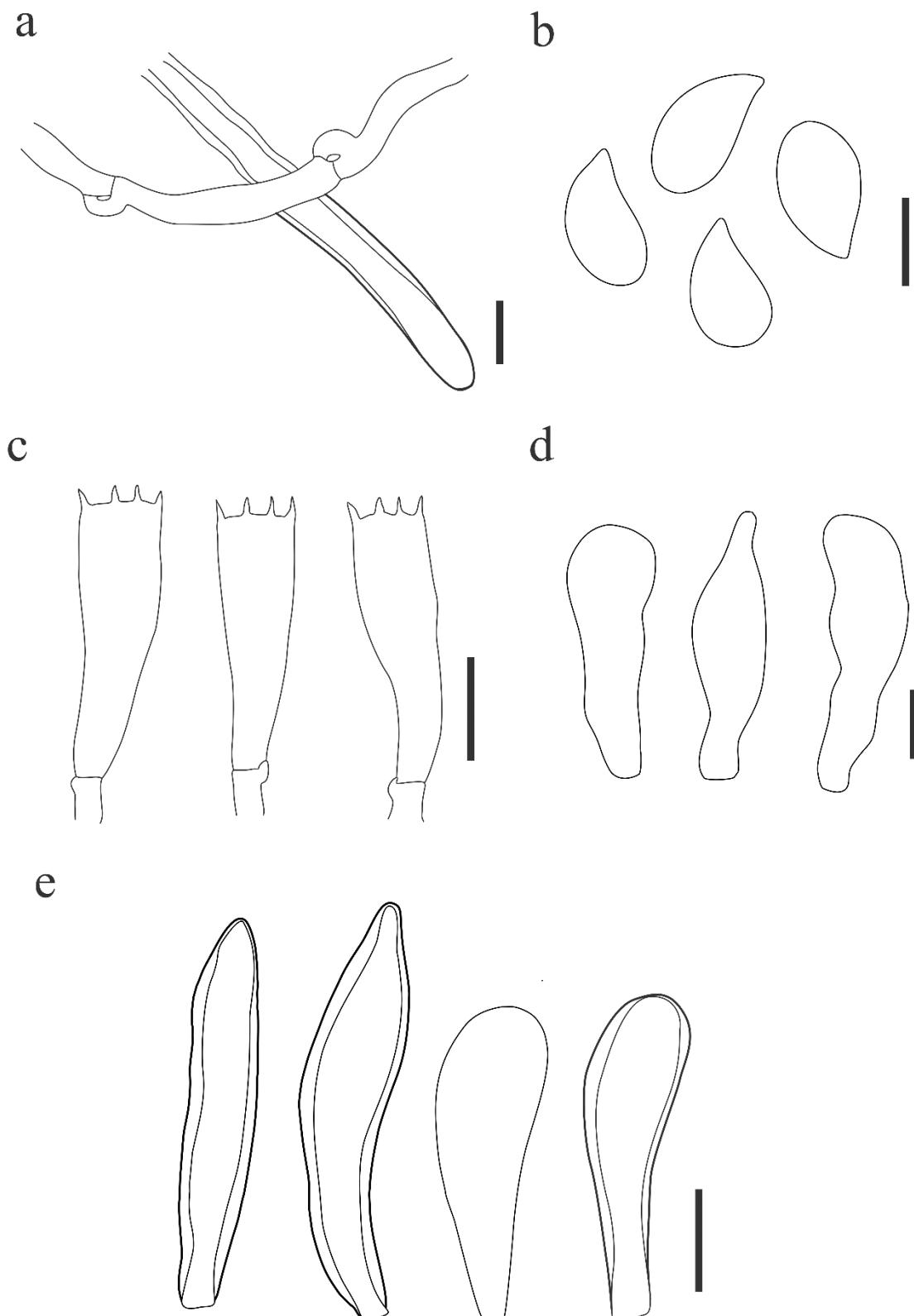
Habit, habitat, and known distribution: Solitary, rarely 2–3 basidiomata together, with pseudosclerotium. Dead fallen trunk. Hitherto and based on our results, it is considered a Neotropical species. Paleotropical records must be confronted by molecular analyses.

Additional specimens examined: BRAZIL, PARANÁ: Piraí do Sul, localidade Corpo Seco, 30 July 2016, *Comin, M.*, CM10 (FLOR 75657); *ibid.*, Foz do Iguaçu, Parque Nacional Iguaçu, Trilha do Hidrômetro, 7 November 2010, *Karstedt, F.* FK1659 (SP446146). SÃO PAULO: Santo André, Estação Biológica de Paranapiacaba, November 1959, *Gomes, A.* (SP46390); São Paulo, Parque Estadual das Fontes do Ipiranga, 30 May 1984, *Romaniec-Neto, S.* (SP193686). SANTA CATARINA: Florianópolis, 27 August 2014, *Freire, F. M.* FMF261 (FLOR 75658); *ibid.*, 19 April 2016 *Freire, F. M.* DG01 (FLOR 75659); *ibid.*, 5 November 2017, *Drechsler-Santos, E. R.* DS2116 (FLOR 75660); *ibid.*, Lagoa do Peri, Início trilha da Gurita, Neves, 18 August 2018, *Neves, M.A.*, MAN1270 (FLOR 75661). RIO GRANDE DO SUL: Entre Ijuís, 03 August 2019, *Palacio, M.*, MP446 (FLOR 75656).

Notes: *Panus velutinus* stands out due to its distinctive macromorphology (Fig. 9), characterized by a uniformly velutinate to short hispid upper surface, a deeply umbilicate to broadly infundibuliform or cyathiform pileus, and a cylindrical, slender, and elongated stipe featuring a characteristic pseudosclerotium. Morphologically, the most closely related species within the ‘velutinus’ clade is *P. stipitonotatus*, which possesses velutinate, chestnut brown pileus surfaces and lamellae that are moderately to densely crowded. However, the stipe of *P. stipitonotatus* is distinctly different, characterized by nodules and a flexuous appearance. Other species within the same phylogenetic group exhibit significant differences in both macro and micro features, e.g. *P. similis* (see Pegler 1983; Ediriweera et al. 2021), *P. tephroleucus* (see Pegler 1983), and *P. capelariae* (this study).

Fig. 10 Microcharacters of *Panus velutinus* (FLOR 75655, epitype) a. thin-walled generative hyphae and fragment of a thick-walled skeletal hyphae, scale bar = 5 µm.

b. basidia c. basidiospores, scale bar =5 µm.. d. cheilocystidia. e. pleurocystidia. Scale bars =10 µm.



The epithet 'velutinus' within the genus *Panus* is associated with three names based on different authorities: *P. velutinus* (Fr.) Fr. (Fries 1838), *P. velutinus* (Fr.) Sacc. (Saccardo 1887), and *P. velutinus* (Fr.) Overh. (Overholts 1930). *Panus velutinus* (Fr.) Overh., as cited by Pegler (1983), does not exist. Overholts (1930) merely mentioned "*Panus velutinus* Fr." in his work, referencing the principal study "Epicr. Syst. Myc. 398. 1838" by Fries (1838). In this context, Fries (1838) validly combined *Agaricus (Omphalia) velutinus* Fr. (Fries 1830, on page 508) into *Panus*, leading to the legitimate *P. velutinus* (Fr.) Fr. *Panus velutinus* (Fr.) Sacc. was also based on *Agaricus velutinus* Fr. by Saccardo (1887), however, this name is illegitimate (Art. 53.1; Turland et al. 2018) due to being a posterior homonym of *Panus velutinus* (Fr.) Fr. Pegler (1983) incorrectly addressed the name *Lentinus velutinus* Fr. in his description based on the type specimen of *Agaricus (Omphalia) velutinus* Fr., leading to further confusion of what species he was referring to. This is further confirmed by comparing the morphological description made by Pegler (1983) and the holotype of *Agaricus velutinus* (UPS F-012409), as well as the collection date (december). Thus, the combination made by Fries (1838), *P. velutinus* (Fr.) Fr. is the correct name for this species.

Furthermore, it is essential to address heterotypic synonyms of *P. velutinus* (Pegler 1983). Some of these synonyms, upon our examination of type specimens and protogues, appear morphologically distinct and should be recognized as independent species. For instance, *Lentinus campinensis*, now combined into *Panus*, is one such case. In addition, we do not agree with the synonymy of *L. blepharodes* from Cuba (Berkeley and Curtis 1869), *L. fastuosus* Kalchbr. & MacOwan from South Africa (Kalchbrenner 1881), *L. fissus* Henn. from Togo (Hennings 1897), *L. holumbrinus* De Seynes from Dem. Rep. of Congo (Seynes 1897), *L. nepalensis*

Berk. from Nepal (Berkeley 1854), and *L. thomensis* from São Tomé and Príncipe (Coutinho 1925) with *Panus velutinus*. In general, all these species, based on our revision (from protologue and/or type specimen, see Results), present whitish basidiomata and anastomosed lamellae, which is completely different from the *sensu stricto* circumscription of *P. velutinus* proposed in this study. Additionally, none of those species present neither a deeply umbilicate to broadly infundibuliform or cyathiform pileus, nor a slender and elongated stipe.

Regarding other heterotypic synonyms, we found challenges in our attempts to study them. It has been confirmed that the types of *L. fallax* from Paraguay and *L. castaneus* from Nicaragua are missing (pers. comm. with curators of LPS and ISC herbaria, respectively). Additionally, *L. pseudociliatus* from Argentina (Raithelhuber 1974) has only fragments of the stipe, rendering it impossible to analyze. Lastly, for *L. natalensis* from South Africa, we were unable to ascertain its existence at PREM herbarium, as our inquiries were not answered by the curatorship.

To prevent further ambiguity surrounding *P. velutinus*, maintain a nomenclatural stability, and establish a phylogenetic concept, we have chosen an epitype (FLOR 75655) from a recently collected Brazilian specimen found in the type locality with DNA sequences.

DISCUSSION

Global Phylogeny of Panus and the taxonomic/nomenclatural implications

Our study addressed critical gaps in the phylogenetic understanding of *Panus* and highlights the need for taxonomic revisions within the group. By incorporating newly collected *Panus* specimens from Brazil and encompassing all available *Panus*

sequences from the GenBank database, we have assembled the most comprehensive phylogenetic analysis of this genus to date. Our investigations have unveiled several noteworthy findings, including the identification of previously unknown lineages, some of which have been proposed as new species.

Previous *Panus* phylogenetic analyses have recovered three to five main clades (Grand 2004; Douanla-Meli and Langer 2010; Zmitrovich and Malysheva 2013; Vargas-Isla et al. 2015; Zmitrovich and Kovalenko 2016; Vinjushan and Kumar 2021). In contrast, our analyses revealed the existence of at least 11 well-supported main clades within the genus. In particular, below we have focused on discussing several of these clades, as follows.

'conchatus' clade

This clade encompasses two distinct groups of specimens labeled as *Panus conchatus* (see Fig. 1 and SUPPL. Fig. 1). One group (*Panus* aff. *conchatus*) was retrieved with specimens pantropically distributed (including Colombia, Honduras, India, Mexico, Tanzania, China, and the USA), while the other (*Panus conchatus* s.s.) comprises specimens particularly found in temperate regions of the Northern Hemisphere (including China, Finland, Germany, Russia, Sweden, USA, and the United Kingdom) (Fig. 1, SUPPL. Fig. 1 and Table S1). Moreover, we observed that certain specimens previously named as *P. conchatus* are also located within the 'ciliatus' clade, demonstrating a lack of clear morphological criteria in the circumscription of *P. conchatus*.

The systematics of *P. conchatus*, originally proposed based on a specimen from Sweden by Bulliard (1787), holds particular significance as it is the type species for the genus *Panus*. Based on the geographic distribution of both subclades within

the ‘conchatus’ clade and the topotype of *P. conchatus*, we recognize the clade consisting of specimens distributed in the north temperate regions to represent the *sensu stricto* status for *P. conchatus*. This clarification could significantly contribute to stabilizing the taxonomy of the species. However, it is crucial to verify the existence and current location of the original *P. conchatus* type specimen.

In the event that the type specimen is confirmed as lost, the designation of a lectotype or neotype may become necessary. Additionally, an epitype could be considered to establish a phylogenetic concept for the entity, thereby linking it to a nomenclatural type. Until these steps are taken, specimens identified as *P. conchatus* that cluster within the ‘ciliatus’ clade (discussed below) and the Pantropics distributed clade, named here as *Panus* aff. *conchatus* should be treated as distinct species different from *P. conchatus* s.s. It is possible that some of these specimens represent new species, while others may correspond to previously named ones, given the extensive list of synonyms associated with *P. conchatus* (<https://www.mycobank.org/>, accessed 01/05/2023). Future studies are required for *P. conchatus*, since we do not have access to their respective type specimens and DNA sequences from reference specimens do not exist.

‘roseus’ clade

The ‘roseus’ clade comprises exclusively species described or recorded from Asia, consisting of specimens previously identified as *Lentinus roseus* Karun., K.D. Hyde & Zhu L. Yang along with the paratypes of *Endopandanicola thailandica*. Notably, while *L. roseus* had previously been combined in *Panus* by Vinjusha and Kumar (2022), *E. thailandica* has now been integrated into the genus *Panus* as *P. thailandicus* (see Taxonomy section). It is worth mentioning that *Endopandanicola* was originally

described as a monospecific genus based on cultured endophytic specimens recovered from *Pandanaceae* leaves (Tibpromma et al. 2018). Based on our phylogenetic analyses (Fig. 1, SUPPL. Fig. 1), we propose the synonymization of *Endopandanicola* with *Panus*, with *P. thailandicus* identified as the sister taxon of *P. roseus*.

Additionally, it is essential to draw attention to the case of *P. roseus* because there are neither DNA sequences of its type specimen nor sequences from specimens from the type locality in Thailand. Furthermore, *L. roseus* specimens from China did not form a single phylogenetic species (see SUPPL. Fig. 1), highlighting the complexity surrounding the taxonomic status of this species.

'strigellus' clade

The 'strigellus' clade groups American specimens identified as *P. strigellus*, *Panus* sp., and *P. parvus*, including the holotype of the latter. Interestingly, *P. parvus* did not emerge clearly as a distinct lineage in our analyses; instead, it weakly clustered (Fig. 1: 41/0.87, SUPPL. Fig. 1: 51) together with South American sequences named as *P. strigellus* (except those from Colombia).

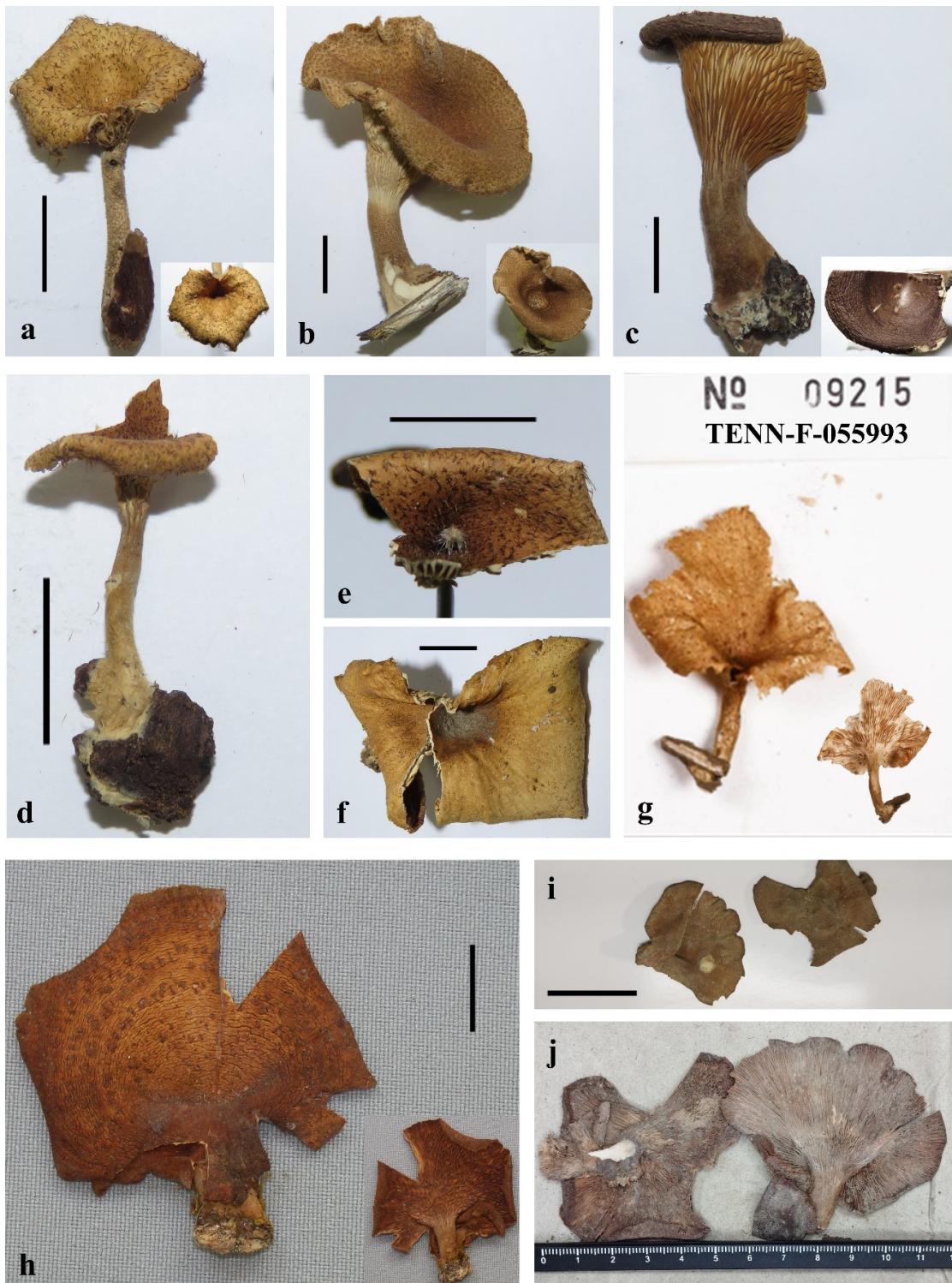
In accordance with the original description, *P. parvus* could be distinguished from *P. strigellus* primarily by its smaller and more slender basidiomata, the presence of more abundant and irregularly distributed pileal squamules (in contrast to the scarce and concentric distribution of them in *P. strigellus*), and the pale buff pileus color of dried specimens (as opposed to the dark reddish-brown color in *P. strigellus*) (Drechsler-Santos et al. 2012). While not explicitly mentioned in Pegler (1983), the presence of elongate-clavate cheilocystidia was observed in the holotype of *P. strigellus* (K-M 153658!) by Drechsler-Santos et al. (2012), and similar

pleurocystidia were also recorded by Vargas-Isla et al. (2015) in specimens from Brazil and the USA. Vargas-Isla et al. (2015) noted the villose to hispid pileus surface in young basidiomata, a feature not cited by Pegler (1983), even though he examined young specimens of its synonym *L. tubarius* Lloyd (Pegler 1983). Additionally, we examined the holotype of *P. guaraniticus* (LPS19295!), one of the seven heterotypic synonyms of *P. strigellus* listed by Pegler (1983), which displayed a similar pileus surface to *P. parvus* (Drechsler-Santos et al. 2012), although we did not observe cylindrical, thick-walled pleurocystidia.

In light of these findings, we consider two possible scenarios. One with the whole ‘strigellus’ clade potentially being treated as a single species, *P. strigellus*, with *P. parvus* regarded as an additional synonym. This interpretation, which we are assuming conservatively at the moment, suggests that *P. strigellus* encompasses a broad distribution across the American continent, featuring considerable macro and micromorphological variation (Fig. 11). This variation encompasses differences in basidioma size, pileus color, distribution of squamules on the pileus surface, and the presence or absence of cylindrical, thick-walled pleurocystidia and cheilocystidia.

The other scenario recognizes that the morphological and phylogenetic evidence presented in our analyses hints the existence of a much more intricate lineage within it, likely consisting of multiple species with distinct distribution patterns and morphological characteristics. To fully elucidate this complexity, additional sampling, morphological assessments, phylogenetic analyses (including the use of additional DNA markers and sequences from type localities specimens), and a comprehensive taxonomic revision of the names listed as synonyms of *P. strigellus* by Pegler (1983) are necessary.

Fig. 11 *Panus strigellus* **a.** specimen FLOR 75673. **b.** specimen FLOR 75675. **c.** specimen FLOR 75674. **d–e.** holotype of *Panus parvus* (URM80840), scale bar **e** = 0.5 cm. **f.** specimen FLOR 75676. **g.** specimen TENN-F-055993. **h.** holotype of *Panus strigellus* (K-M 153658). **i–j.** holotype of *Panus guaraniticus* (LPS19295), scale bar **i** = 5 cm. Scale bars = 1 cm.



FONTE: Sousa-Guimarães et al. 2024

'speciosus' clade

Phylogenetically, *P. speciosus* was recovered in a clade moderately supported (57/1) nested within at least four phylogenetic species in the 'bambusinus', 'purpuratus', 'asiaticus', and 'paraibensis' clades, including two species unequivocally identified as *P. purpuratus* G. Stev. and *P. paraibensis* (Stevenson 1964; Galvão et al. 2023). Additionally, when including those specimens labeled as *P. bambusinus* (T.K.A. Kumar & Manim.) N. Vinjusha & T.K.A. Kumar and treating them as *P. bambusinus*, all these species share common characteristics, such as pinkish lamellae and white, pale cream to pinkish basidiomata. The *P. lecomtei* specimen recovered in the 'asiaticus' clade is a misidentification, as we discuss below. *Panus bambusinus* stands out due to its 15–200 mm diam. and striated pileus, tomentose to strigose stipe, and versiform cheilocystidia (Kumar and Manimohan 2005; Vinjushan and Kumar 2021). *Panus paraibensis* differs by having pleurotoid basidiomata and smaller basidiospores (4.4–5.5 × 2–2.9), and *P. purpuratus* by its smaller basidiospores (5–6 × 2–2.5).

Our phylogenetic analyses (Fig. 1) evidence that *P. speciosus* may have a Pantropical distribution as sequences from Singapore specimens grouped as conspecific with those from Brazil. Therefore, those specimens from Singapore should be studied to better understand the morphological concept of the species.

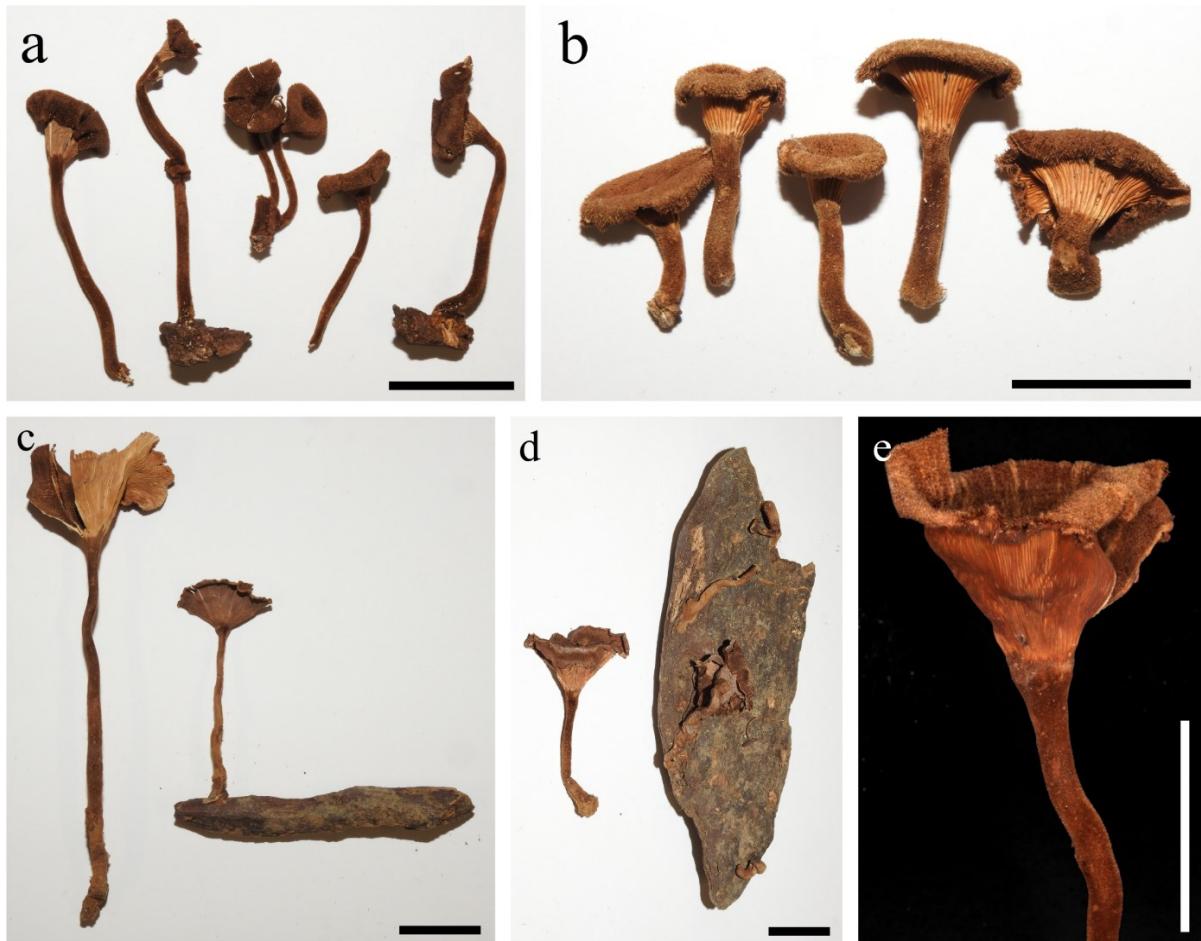
'velutinus' clade

The 'velutinus' clade exhibits a complex composition, encompassing a diverse array of species. Many specimens named as *P. similis* and *P. velutinus* could lead to interpret these taxa as polyphyletic. It also includes *P. capelariae* and *P. stipptonotatus*, which are independent lineages, proposed here as new species (see

Taxonomy). And, additionally, it also includes several other unsupported lineages in the phylogeny and without taxonomic stability based on the different names attributed to the sampled sequences. One of those lineages could confirm the occurrence of *P. tephroleucus* (type is from Suriname) or *P. fulvus* (type is from Sri Lanka) in Brazil. However, the unsupported subclade named as *Panus cf. tephroleucus* (Fig. 1, SUPPL. Fig. 1) exhibits significant morphological variation (Fig. 12). Due to the unavailability of sequences from the types or from specimens at the type locality associated with the names within this clade, confidently assigning a name to the Brazilian specimens under consideration becomes impossible. In this case, future studies are required for *P. tephroleucus*, since we do not have access to the type specimen or DNA sequences of any reference specimen. Our attempts to gather information from PC curatorship yielded no results, without feedback from PC herbarium.

The position of *P. similis* in the phylogeny (Fig. 1) raises noteworthy considerations. Specimens identified as *P. similis* from Argentina, Cameroon, India, Sri Lanka, and Vietnam were recovered as four phylogenetic species. Given that the type locality of *P. similis* is Sri Lanka (Berkeley and Broome 1873), we propose that the core represented by the specimens from Sri Lanka (UOC SIGWI S38) and Vietnam (LE-BIN 3011) should be treated as *P. similis* s.s. (Fig. 1). Additionally, morphological and molecular data provided by Ediriweera et al. (2021) also support the Sri Lanka specimen to be a representative of *P. similis* s.s. Moreover, sequences of TENN59008, TENN58995, and TENN59829 from Argentina, previously identified as *P. similis*, correspond to the new species, *P. capelariae*. In conclusion, *P. similis* is indeed an Asian species, and morphologically similar Neotropical specimens represent *P. capelariae*.

Fig. 12 Macromorphological diversity of *Panus cf. tephroleucus* **a.** specimen FLOR 75678. **b.** specimen FLOR 75683. **c.** specimen FLOR 75679. **d.** specimen FLOR 75680. **e.** SP446147. Scale bars = 2 cm.



FONTE: Sousa-Guimarães et al. 2024

Panus fulvus could be a similar case as *P. similis*, occurring exclusively in Asia or instead, being Pantropical. But there are no available sequences from specimens from Asia and as presented above, all the specimens labeled as *P. fulvus* are from the American continent, raising questions about the Pantropical distribution of *P. fulvus*. Further investigation is needed regarding *P. tephroleucus* vs. *P. fulvus* in America.

Regarding the systematics of *P. velutinus*, several critical points warrant attention and some of them have been presented in the taxonomic notes of the species (see Taxonomy). Based on the morphology of holotype UPS F-012409 (see Taxonomy and Figs. 9 and 10) and the acceptance of *Agaricus (Omphalia) velutinus* (Fries 1830, on page 508) as the correct basionym for the species, contrary to what was traditionally assumed by Pegler (1983), we realized the necessity of choosing an epitype (FLOR 75655) from a new Brazilian specimen collected in the type locality (Fries 1830), in order to have also a phylogenetic stability.

'neostrigosus' clade

The 'neostrigosus' clade stands as the sister group to the 'ciliatus' clade and consists of a single species, *P. neostrigosus*, notable for its extensive distribution across different continents, with records from Brazil, Canada, China, India, Japan, Mexico, Philippines, Russia, the USA (including Hawaii and Puerto Rico), and Turkey (Fig. 1; SUPPL. Fig. 1; Table S1). Among *P. neostrigosus* synonyms, *P. lecomtei* (Fr.) Corner and *P. rufis* Fr. are the labels associated with the majority of specimens recovered in this clade. It is noteworthy that the type of *Lentinus martianoffianus* Kalchbr., as already synonymized in *P. neostrigosus* by Psurtseva et al. (2021).

A certain degree of confusion between *P. neostrigosus* and the morphologically similar species *P. strigellus* (as discussed earlier), prompted further investigation by Vargas-Isla et al. (2015). They displayed a combination of morphological, molecular, and mating compatibility tests data to clarify this situation. Their phylogenetic analysis unequivocally established the distinctiveness of the two species. Nonetheless, concerns arose about the validity of the name *P. neostrigosus* vs. *P. lecomtei*.

To address those concerns, *P. neostrigosus* was proposed as a new name, allowing for the proper combination of *Lentinus strigosus* Fr. into *Panus* and avoiding a homonym (Drechsler-Santos et al. 2012). *Lentinus strigosus* and *L. lecomtei* are synonyms and share equal naming priority because both were described by Fries (1825). Vargas-Isla et al. (2015) argued that, within *Panus*, *P. lecomtei* (Fr.) Corner should be the correct name for this taxon because the epithet *strigosus* was already occupied within *Panus* by another species, viz. *Panus strigosus* Berk. & M.A. Curtis. However, as pointed out by Sanuma et al. (2016), the International Code of Nomenclature for Algae, Fungi, and Plants (Turland et al. 2018) in Art. 11.5 states that when a choice exists between legitimate names of equal priority, the first such choice to be effectively published establishes the priority of the selected name. In the case where *L. strigosus* was intentionally preferred over the synonym *L. lecomtei* by Murrill (1915) and later by Pegler (1972), the priority between these two names was set when they were still classified under *Lentinus*. Consequently, the correct name for this species is *P. neostrigosus*.

'ciliatus' clade

The 'ciliatus' clade is characterized by the presence of at least three distinct phylogenetic species (Fig. 1, SUPPL. Fig. 1). One of these species remains unnamed and hails from a sequence (MK184520) from Madagascar, while the other two consist of specimens previously identified as *P. conchatus*, *P. subfasciatus*, *P. fasciatus*, and *P. ciliatus* (Fig. 1, SUPPL. Fig. 1). *Panus conchatus* actually belongs to a separate and unrelated lineage (see above). These *P. conchatus* specimens are misidentifications. *Panus subfasciatus* holotype, in turn, grouped together specimens assigned to *P. fasciatus*. It suggests further investigation needed in order to elucidate whether both taxa are conspecific or distinct species, as proposed by Tibpromma et

al. (2017). Furthermore, concerning specimens labeled as *P. ciliatus*, one, from Thailand was recovered in the '*Panus subfasciatus*' clade and another two from Brazil and USA in the '*Panus ciliatus*' clade. The Brazilian specimen (SP446150 = FK1890), the unique specimen we had access to the morphology, resembles *P. ciliatus* morphologically.

As Pegler's (1983) description of *Panus ciliatus*, the Brazilian specimen (SP446150, Fig. 13) presents a densely crowded, vinaceous-colored lamellae, a radially striated but not sulcate pileus that is finely hispid, velutinate, and display concentric zoning, ellipsoid to cylindric basidiospores $5.5\text{--}7.0 \times 2.5\text{--}3.5 \mu\text{m}$, and pleurocystidia measuring $22\text{--}36 \times 5.0\text{--}8.0 \mu\text{m}$, which are clavate and thin- to rarely thick-walled ($1.0\text{--}2.0 \mu\text{m}$ thick).

This evidence also support us to indicate *P. ciliatus* is pantropically distributed. It was described based on an Indonesian specimen by Léveillé (1844) and the type was already phylogenetically tested and confirmed in previous analysis by Dr. Jaya Seelan (Univ. of Malaysia Sabah) as part of the subclade here named '*Panus ciliatus*', together with Brazilian specimens as well (J. Seelan. pers. comm., unpublished data).

Brazilian diversity of Panus

In our comprehensive evaluation, we considered various sources of data, including morphological and molecular information, to assess the occurrences of *Panus* species in Brazil. We have confirmed the occurrence of *P. ciliatus* (Pantropical distribution), *P. neostrigosus* (widespread), *P. paraibensis* (endemic to Brazil), *P. strigellus* (American distribution with *P. parvus* as a synonym), and *P. velutinus*

(Neotropical distribution with Pantropical distribution to be confirmed), and we introduced *P. capelariae* (southern South America distribution), *P. speciosus*

Fig. 13 *Panus ciliatus* (SP446150). **a.** fresh basidioma overview **b.** detail of the pileus surface. **c.** detail of the densely crowded lamellae **d.** dehydrated basidioma overview. Scale bars = 1 cm.



FONTE: Sousa-Guimarães et al. 2024

(Pantropical distribution), and *P. campinensis*, *P. pachysporus*, and *P. stipitonotatus*, all three as endemic species to Brazil, comprising ten species confirmed in the Brazilian ecosystems. Additionally, we rejected the occurrence in Brazil of *P.*

conchatus (putatively restricted to the North Temperate region), *P. convivalis* (no quality data is available), *P. fulvus* (Asiatic distribution but with Pantropical occurrences to be confirmed), *P. hymenorhizus* (not a *Panus* species, since it was described as growing on small twigs and having free lamellae; Spegazzini 1889; LPS16800!), *P. similis* (an Asiatic species), and *P. tephroleucus* (probably with Neotropical distribution, but quality data is lacking).

In conclusion, our comprehensive assessment of *Panus* in Brazil has led to the confirmation of ten species supported by morphological and/or molecular data. However, we acknowledge that further research, particularly involving type specimens and additional DNA sequencing, is important to continue the studies in order to determine the presence or absence of other *Panus* species in Brazil. To aid in the accurate identification of these confirmed species, we present below an identification key.

Identification key for *Panus* species occurring in Brazil

1. Basidioma with pseudosclerotium 2

1'. Basidioma without pseudosclerotium or without distinct information on pseudosclerotium presence 5

2 Basidioma large and robust, pileus up to 160 mm diam., stipe slender up to 205 mm long *Panus velutinus*

2' Basidioma smaller, pileus up to 80 mm diam., stipe up to 90 mm 3

3 Pileus almost glabrous, radially plicate-sulcate; lamellae spaced *P. capelariae*

- 3' Pileus velutinate to hispid-strigose with short hairs, not sulcate; lamellae moderately to densely crowded 4
- 4 Lamellae moderately crowded, anastomosed at the stipe, brown; stipe cylindric with nodules extending over the entire surface of the stipe or present on the middle portion or on the base *P. stipitonotatus*
- 4' Lamellae densely crowded, not anastomosed at the stipe, with a vinaceous hue; stipe cylindric without nodules..... *P. ciliatus*
- 5 Basidioma pleurotoid, convex plane *P. paraibensis*
- 5' Basidioma agaricoid, cyathiform or infundibuliform 6
- 6 Pileus and stipe equally velutinate to villose *P. campinensis*
- 6' Pileus glabrous or densely hairy 7
- 7 Pileus glabrous, squamules restricted to the center *P. speciosus*
- 7' Pileus with few isolated hairs to densely hairy 8
- 8' Basidiospores 6.5–12 µm long, thick-walled *P. pachysporus*
- 8' Basidiospores up to 7.0 µm long, thin-walled 9
- 9 Pileus densely villous to hispid-strigose; gloeocystidia absent *P. neostrigosus*
- 9' Pileus glabrous, with blackish spiniform squamules, to finely striate; gloeocystidia present *P. strigellus*

ACKNOWLEDGMENTS

Acknowledgements We are grateful to all the protected areas and their directors for permission to sample collections; the curators of mentioned fungaria for the loan of specimens (FLOR, IAC, SP, URM); the fungaria curatorship that readily sent photos and support us with type specimen data (BAFC, ISC, LISU, LPS, K, TENN, UPS); the Laboratório Multusuário de Estudos em Biologia (LAMEB/UFSC) for providing infrastructure to carry out the molecular studies; J. Prado, C. Bicudo, and F. Wartchow for nomenclatural discussion on *Panus neostrigosus* versus *Panus lecomtei*; Dra. Fernanda Karstedt for pictures of *Panus ciliatus*; Dra. Viviane de Oliveira Garcia and colleagues from MICOLAB-UFSC for specimen collections; Dr. Diogo Henrique Costa-Rezende and Kelmer Cunha for assistance in analyses and discussion of species and pictures, respectively; and Dr. Jaya Seelan Sathiya Seelan (Univ. of Malaysia Sabah) for generating ITS and nrLSU sequences from some Brazilian specimens loaned from the herbarium SP. This research is part of the MIND.Funga research group: <https://mindfunga.ufsc.br/>. Author contribution Conceptuali.

DECLARATIONS

Availability of data and material

All data used in this study are either directly cited (nomenclature) or are available through the cited references (underlying phylogeny and sequence data) or through the cited repositories (MycoBank registration numbers, molecular data at Dataverse).

Competing interests

The authors declare no competing interests.

Funding

The authors thank Coordenação de Aperfeiçoamento Pessoal de Nível Superior (CAPES) for providing a master and PhD scholarships to DKSG and FB; the

PPGFAP/UFSC; the FONCYT (PICT 0830 to GR) and Fundación FungiCosmos for partial financing of the research; the Society of Systematic Biologists for the Mini-ARTS award to FB, allowing type revisions at LPS. NMJr. thanks the ‘Fundação de Amparo à Pesquisa do Estado de São Paulo’ (FAPESP), (grant #18/15677-0). AGN, ERDS, NMJr. and GAS are supported by CNPq (Grants No. 308880/2022-6, 310150/2022-1, 314236/2021-0 and 153025/2022-0, respectively).

LITERATURE CITED

- Alves-Silva G, Reck MA, da Silveira RM, Bittencourt F, Robledo GL, Góes-Neto A, Drechsler-Santos ER (2020) The Neotropical *Fomitiporia* (Hymenochaetales, Basidiomycota): the redefinition of *F. apiahyna* s.s. allows revealing a high hidden species diversity. Mycol Progress 19:769–790.
<https://doi.org/10.1007/s11557-020-01593-5>
- Batista AC, Falcão RGS, Peres GEP, Moura NR (1966) Fungi Paraenses (Revisão da Coleção de Paul C. Hennings, do Museu Paraense Emílio Goeldi). Instituto de Micologia 506:10–290.
- Berkeley MA (1843) Notices of Fungi in the Herbarium of the British Museum. Ann Mag Nat Hist 10:369–385.
- Berkeley MJ (1854) Decades of fungi. Decades XLI- XLIII. Indian fungi. Hooker's Journal of Botany and Kew Garden Miscellany 6:129–143.
- Berkeley MJ, Broome CE (1873) Enumeration of the Fungi of Ceylon. Part II., containing the remainder of the Hymenomycetes, with the remaining established tribes of Fungi. J Linn Soc, Bot 14(73):29–140. <http://dx.doi.org/10.1111/j.1095-8339.1873.tb00301.x>

Berkeley MJ, Curtis MA (1869) Fungi Cubenses (Hymenomycetes). J Linn Soc, Bot 10:280–320.

Bulliard P (1792) Herbier de la France; ou, Collection complete des plantes indigenes de ce royaume; avec leurs propriétés, et leurs usages en medecine, vol 12. Bulliard, Didot, Debure, and Belin, Paris.

Cavalcante FSA, Campos MCC, de Lima JPS (2021) New Occurrences of Macrofungi (Basidiomycota) in Southern Amazonas, Brazil. Ci e Nat 43:e46.
<https://doi.org/10.5902/2179460X44026>

Cooke M C (1882) A Quarterly Record of Cryptogamic Botany and its Literature - Exotic Fungi. Grevillea (no. 56) v. 10, p 123.

Corner, E J H (1981) The agaric genera *Lentinus*, *Panus* and *Pleurotus* with particular reference to Malaysian species. Beih Nova Hedw 69:1–169.

Coutinho A X P.(1925). Florae mycologicae Insulae St. Thomae. Anais do Instituto Superior de Agronomia da Universidade Técnica de Lisboa 2:1-26.

Dayarathne MC, Boonmee S, Braun U, Crous PW, Daranagama DA, Dissanayake AJ, Ekanayaka H, Jayawardena R, Jones EB, Maharachchikumbura SS, Perera RH (2016) Taxonomic utility of old names in current fungal classification and nomenclature: Conflicts, confusion & clarifications. Mycosphere 7:1622–1648.
<https://doi.org/10.5943/mycosphere/7/11/2>

Douanla-Meli C, Langer E (2010) Reassessment of phylogenetic species relationship of some lentinoid fungi with velutinate basidiomes based on partial 28S ribosomal RNA gene sequencing. Sydowia 62(1):23–35.

Drechsler-Santos ER, Wartchow F, Coimbra VRM, Gibertoni TB, Cavalcanti MAQ (2012) Studies on lentinoid fungi (*Lentinus* and *Panus*) from the semi-arid region of Brazil. J Torrey Bot 139:437–446.

- Drechsler-Santos ER, Robledo GL, Lima-Junior NC, Malosso E, Reck MA, Gibertoni TB, Cavalcanti MA, Rajchenberg M (2016) *Phellinotus*, a new neotropical genus in the Hymenochaetaceae (Basidiomycota, Hymenochaetales). *Phytotaxa* 261(3):218–39. <https://doi.org/10.11646/phytotaxa.261.3.2>
- Ediriweera SS, Nanayakkara CM, Weerasena OV, Karunarathna SC, Wijesundara RL, Piyatissa MA (2021) Morphology and phylogeny reveal nine new records of polypores from dry zone of Sri Lanka. *Chiang Mai J Sci* 48(3):893–908.
- Felsenstein J (1985) Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* 39(4):783–791.
- Fries EM (1821) *Systema mycologicum I*. Officina Berlingiana, Lundae.
- Fries EM (1825) *Systema orbis vegetabilis*. Lundae.
- Fries EM (1830) *Eclogae fungorum, praecipue ex herbarus germanorum de scriptorum*. Linnaea 5:497–553.
- Fries E (1838) *Epicrisis systematis mycologici seu synopsis Hymenomycetum*. Typographia Academica, Uppsala. <https://doi.org/10.1080/00222934009512452>
- Galvão VIP, Koroiva R, Wartchow F (2023) A new species of *Panus* (Panaceae, Polyporales) from Paraíba, Brazil. *Phytotaxa* 514(3):17. <https://doi.org/10.11646/phytotaxa.619.2.5>
- Gardes M, Bruns TD (1993) ITS primers with enhanced specificity for basidiomycetes-application to the identification of mycorrhizae and rusts. *Mol Ecol* 2 (2):113–118. <https://doi.org/10.1111/j.1365-294X.1993.tb00005.x>
- Góes-Neto A, Loguerio-Leite C, Guerrero RT (2005) DNA extraction from frozen field-collected and dehydrated herbarium fungal basidiomata: performance of SDS and CTAB-based methods. *Biotemas* 18(2):19–32.

Grand EA (2004) Systematics and species concepts in the genera *Lentinus* Fr. and *Panus* Fr., with emphasis on the *Lentinus tigrinus*, *L. crinitus* and *Panus lecomtei* complexes. Thesis, University of Tennessee.

Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Syst Biol* 59(3):307–321.

<https://doi.org/10.1093/sysbio/syq010>

Hennings P (1897) Fungi camerunenses II. Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie 23:537–558.

Hibbett DS, Vilgalys R (1993) Phylogenetic Relationships of *Lentinus* (Basidiomycotina) inferred from Molecular and Morphological Characters. *Syst Bot* 18:409–433. <https://doi.org/10.2307/2419417>

Hillis DM, Bull JJ (1993) An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Syst Biol* 42(2):182–92.

<https://doi.org/10.2307/2992540>

Huelsenbeck JP, Rannala B (2004) Frequentist properties of Bayesian posterior probabilities of phylogenetic trees under simple and complex substitution models. *Syst Biol* 53(6):904–913. <https://doi.org/10.1080/10635150490522629>

Justo A, Miettinen O, Floudas D, Ortiz-Santana B, Sjökvist E, Lindner D, Nakasone K, Niemelä T, Larsson KH, Ryvarden L, Hibbett DS (2017) A revised family-level classification of the Polyporales (Basidiomycota). *Fungal Biol* 121(9):798–824.

<https://doi.org/10.1016/j.funbio.2017.05.010>

Kalchbrenner C (1881) Fungi Macowaniani. *Grevillea* 9(52):131–137.

Katoh S (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol* 30:772–780.

<https://doi.org/10.1093/molbev/mst010>

- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Mentjies P, Drummond A (2012) Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* 28(12):1647–1649. <https://doi.org/10.1093/bioinformatics/bts199>
- Kumar TA, Manimohan P (2005) A new species of *Lentinus* from India. *Mycotaxon* 92:119–123.
- Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for bigger datasets. *Mol Biol and Evol* 33(7):1870–1874. <https://doi.org/10.1093/molbev/msw054>
- Küppers H (1994) *Atlas de los colores*. Naturart, Barcelona.
- Lanfear R, Calcott B, Ho SY, Guindon S (2012) PartitionFinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Mol Biol and Evol* 29(6):1695–1701. <https://doi.org/10.1093/molbev/mss020>
- Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B (2016) PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. *Mol Biol and Evol* 34(3):772–773. <https://doi.org/10.1093/molbev/msw260>
- Largent DL, Johnson D, Watling R (1977) How to identify mushrooms to genus III: microscopic features. Eureka, California: Mad River Press, pp 148.
- Leveille JH (1844) Champignons exotiques. *Ann Nat Sci, Bot Ser* 3(2):167–221.
- Maia LC et al. (2015) Diversity of Brazilian fungi. *Rodriguésia* 66(4):1033–1045. <https://doi.org/10.1590/2175-7860201566407>
- Meijer AAR (2006) Preliminary list of the macromycetes from the Brazilian State of Paraná. *Bol Mus Bot Mun* 68:1–59.

Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES science gateway for inference of large phylogenetic trees. Proceedings of the Gateway Computing Environments Workshop (GCE). IEEE Press, New Orleans, Louisiana.

<https://doi.org/10.1109/GCE.2010.5676129>

Motato-Vásquez V, Gugliotta AM, Rajchenberg M, Catania M, Urcelay C, Robledo G (2020) New insights on *Bjerkandera* (Phanerochaetaceae, Polyporales) in the Neotropics with description of *Bjerkandera albocinerea* based on morphological and molecular evidence. *Plant Ecol Evol* 153(2):229–245.

<https://doi.org/10.5091/plecevo.2020.1667>

Murrill WA (1915) (Agaricales) Polyporaceae. *North Amer Fl* 9:201–296.

Oliveira-Filho AT (2015) Um sistema de classificação fisionômico-ecológico da vegetação neotropical: segunda aproximação. In: Eisenlohr PV, Felfili JM, de Melo MMRF, de Andrade LA, Meira-Neto JAA (eds) *Fitossociologia no Brasil: métodos e estudos de casos*, v2. UFV, Viçosa, pp 385–411.

Overholts LO (1930) Eu-Basidiomycetes. In: Chardon CE, BA Toro. *Mycological explorations of Colombia*. *J Agric Univ P R* 14:195–353.

<https://doi.org/10.46429/jaupr.v14i4.14223>

Palacio M, Robledo GL, Reck MA, Grassi E, Góes-Neto A, Drechsler-Santos ER (2017) Decrypting the *Polyporus dictyopus* complex: Recovery of *Atroporus* Ryvarden and segregation of *Neodictyopus* gen. nov. (Polyporales, Basidiomycota). *PLOS ONE* 12(10):e0186183.

<https://doi.org/10.1371/journal.pone.0186183>

Pattengale ND, Alipour M, Bininda-Emonds ORP, Moret BME, Stamatakis A (2009) How Many Bootstrap Replicates Are Necessary?. In: Batzoglou, S. (eds) *Research in Computational Molecular Biology. RECOMB 2009. Lecture Notes in*

- Computer Science(LNBI), vol 5541. Springer, Berlin, Heidelberg.
- https://doi.org/10.1007/978-3-642-02008-7_13
- Pegler DN (1971) *Lentinus* Fr. and related genera from Congo-Kinshasa (Fungi). Bull Jard Bot Natl Belg 41:273–281.
- Pegler DN (1972) Lentineae (Polyporaceae), Schizophyllaceae et especes lentinoides et pleurotoides des Tricholomataceae. Fl Illust Champ Afr Centre Fasc 1:1–26.
- Pegler DN (1983) The genus *Lentinus*: A world monograph. Kew Bull Addit Ser 10: 1–281.
- Pegler DN (1997) The Agarics of São Paulo, Brazil: an account of the agaricoid fungi (Holobasidiomycetes) of São Paulo State, Brazil. Royal Botanic Gardens, UK.
- Psurtseva NV, Zmitrovich IV, Seelan JS, Bulakh EM, Hughes KW, Petersen RH (2021) New data on morphology, physiology, and geographical distribution of *Lignomyces vetlinianus*, its identity with *Lentinus pilososquamulosus*, and sufficient phylogenetic distance from *Le. martianoffianus*. Mycol Progress 20:809–821. <https://doi.org/10.1007/s11557-021-01701-z>
- Putzke J (1994) Lista dos fungos Agaricales (Hymenomycetes, Basidiomycotina) referidos para o Brasil. Cad Pesq Univ Fed Santa Cruz do Sul, Ser Bot 6:3–186.
- Putzke J, Putzke MTL (2002) Os reinos dos fungos v2. Editora da UNISC, Santa Cruz do Sul.
- Raiethelhuber J (1974) Hongos argentinos I. Compañía Impresora Argentina, Buenos Aires.
- Rambaut A, Drummond AJ, Xie D, Baele G, Suchard MA (2018) Posterior summarization in Bayesian phylogenetics using Tracer 1.7. Systematic biology 67(5):901–4.
- Rick J (1907) Fungi austro-americani Fasc. V u. VI. In: Ann Mycol 5:28–31.

- Rick J (1930) Contributio ad Monographiam Polyporacearum et Agaricacearum Brasiliensium IV. *Brotéria, Sér Bot* 24:27–118.
- Ronquist F, Teslenko M, Van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol* 61(3):539–542. <https://doi.org/10.1093/sysbio/sys029>
- Saccardo PA (1887) *Sylloge Fungorum Omnium Hucusque Cognitorum*, vol. V. R. Friedländer & Sohn, Berlin. <https://doi.org/10.5962/bhl.title.5371>
- Salvador-Montoya CA, Popoff OF, Góes-Neto A, Drechsler-Santos ER (2020) Global phylogenetic and morphological reassessment of *Fomitiporella* s.l. (Hymenochaetales, Basidiomycota): taxonomic delimitation of *Fomitiporella* s.s. and segregation of *Rajchenbergia* gen. nov. *Plant Syst Evol* 306(34):1–27. <https://doi.org/10.1007/s00606-020-01648-w>
- Sambrook J, Fritsch EF, Maniatis T (1989) *Molecular Cloning: A Laboratory Manual*, 2nd ed. Cold Spring Harbor Laboratory Press, New York.
- Sanuma OI, Tokimoto K, Sanuma C, Autuori J, Sanuma LR, Martins MS, Junior NM, Ishikawa NK, Apiamö RM (2016) Enciclopédia dos Alimentos Yanomami (Sanöma): Cogumelos. Hutukara Associação Yanomami e Instituto Socioambiental, São Paulo.
- Seynes J de (1897) Recherches pour servir à l'histoire naturelle et à la flore des champignons de Congo Français 1:1-29.
- Soltis PS, Soltis DE (2003) Applying the bootstrap in phylogeny reconstruction. *Statist Sci* 18(2):256–267. <https://doi.org/10.1214/ss/1063994980>
- Sousa-Guimarães DK, Alves-Silva G, Camacho O, Menolli Jr N, Góes-Neto A, Souza JF, Robledo RL, Neves MA, Drechsler-Santos ER (2022) "Data for: Studies on

- Panus* (Panaceae, Polyporales): morphology and phylogeny assist new species descriptions". Harvard Dataverse, V2. <https://doi.org/10.7910/DVN/DZVFKL>.
- Spegazzini C (1889) Fungi Puiggariani: Pugillus I. Bol Acad Nac Ci Cordoba 11: 1–381.
- Stamatakis A (2014) RAxML Version 8: A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies. Bioinformatics 30(9):1312–1312.
<https://doi.org/10.1093/bioinformatics/btu033>
- Stevenson G (1964) The Agaricales of New Zealand V. Kew Bull 19(1):1–59.
- Teixeira AR (1946) Himenomycetos brasileiros III. Bragantia 6:165–188.
- Teixeira AR (1995) Método para estudo das hifas do basidiocarpo de fungos poliporáceos. Manual nº 6. Instituto de Botânica, São Paulo.
- Thiers B [continuously updated] Index Herbariorum: a global directory of public herbaria and associated staff. New York Botanical Garden's Virtual Herbarium.
Home page at: <http://sweetgum.nybg.org/ih/>
- Tibpromma S et al. (2017) Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers 83:1–261.
<https://doi.org/10.1007/s13225-017-0378-0>
- Tibpromma S, Hyde KD, Bhat JD, Mortimer PE, Xu J, Promputtha I, Doilom M, Yang JB, Tang AMC, Karunaratna SC (2018) Identification of endophytic fungi from leaves of Pandanaceae based on their morphotypes and DNA sequence data from southern Thailand. MycoKeys 33:25–67.
<https://doi.org/10.3897%2Fmycokeys.33.23670>
- Turland NJ, Wiersema JH, Barrie FR, Greuter W, Hawksworth DL, Herendeen PS, Knapp S, Kusber WH, Li DZ, Marhold K, May TW, McNeill J, Monro AM, Prado J, Price MJ, Smith GF (2018) International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code) adopted by the Nineteenth International Botanical

- Congress Shenzhen, China, July 2017. *Regnum Vegetabile* 159. Koeltz Botanical Books, Glashütten. <https://doi.org/10.12705/Code.2018>
- Vargas-Isla R, Capelari M, Meloni N, Nagasawa E, Tokimoto K, Ishikawa NK (2015) Relationship between *Panus lecomtei* and *P. strigellus* inferred from their morphological, molecular and biological characteristics. *Mycoscience* 56(6):561–571. <http://dx.doi.org/10.1016/j.myc.2015.05.004>
- Vellinga EC, Noordeloos ME (2001) Glossary. In: Noordeloos ME, Kuyper ThW, Vellinga EC (eds) *Flora agaricina neerlandica*, vol 5. CRC Press, Boca Raton, pp 6–11.
- Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *J Bacteriol* 172:4238–4246. <https://doi.org/10.1128/jb.172.8.4238-4246.1990>
- Vinjusha N, Kumar TA (2022) Validation of *Panus bambusinus* and *P. roseus* (Panaceae, Polyporales). *Phytotaxa* 533(4):235–236. <https://doi.org/10.11646/phytotaxa.533.4.7>
- White TJ, Bruns T, Lee S, Taylor JW (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (eds) *PCR protocols: a guide to methods and applications*. Academic Press Inc, New York, pp 315–322.
- Zmitrovich IV, Kovalenko AE (2016) Lentinoid and polyporoid fungi, two generic conglomerates containing important medicinal mushrooms in molecular perspective. *Int J Med Mushrooms* 18:23–38. <https://doi.org/10.1615/intjmedmushrooms.v18.i1.40>
- Zmitrovich IV, Malysheva VF (2013) Towards a phylogeny of *Trametes* alliance (Basidiomycota, Polyporales). *Mikol Fitopatol* 47(6):358–380.

Table S1. Species, collections, and sequences used in the phylogenetic tree and their Genbank accession numbers. New sequences generated in this study are highlighted in **bold**.

Taxon	Clade in this study	Voucher	Country	ITS	nrLSU	Genbank code
<i>Panus</i> sp.	'bambusinus' 'velutinus' (<i>Panus capelariae</i> sp. nov.)	AK61b	India	MW453097	N/A	
<i>Panus capelariae</i> sp. nov.	'velutinus' (<i>Panus capelariae</i> sp. nov.)	DG11	Brazil	MT669126	MT669146	
<i>Panus capelariae</i> sp. nov.	'velutinus' (<i>Panus capelariae</i> sp. nov.)	MAR1154	Brazil	MT669127	MT669147	
<i>Panus capelariae</i> sp. nov.	'velutinus' (<i>Panus capelariae</i> sp. nov.)	SGE238	Brazil	MT669128	MT669148	
<i>Panus capelariae</i> sp. nov.	'velutinus' (<i>Panus capelariae</i> sp. nov.)	EC072	Brazil	N/A		OR652618
<i>Panus similis</i>	'velutinus' (<i>Panus capelariae</i> sp. nov.)	TENN58995	Argentina	N/A		AY615998
<i>Panus similis</i>	'velutinus' (<i>Panus capelariae</i> sp. nov.)	TENN59829	Argentina	N/A		AY615999
<i>Panus similis</i>	'velutinus' (<i>Panus capelariae</i> sp. nov.)	TENN59008	Argentina	N/A		AY616000
<i>Panus ciliatus</i>	'ciliatus' (<i>Panus ciliatus</i>)	SP446150	Brazil	MT669118	MT669140	
<i>Panus ciliatus</i>	'ciliatus' (<i>Panus ciliatus</i>)	DEH2430A	USA	N/A		AY616008
<i>Panus conchatus</i>	'ciliatus' (<i>Panus ciliatus</i>)	NEHU.MBSR.05	India	KM282285	N/A	
<i>Panus conchatus</i>	'ciliatus' (<i>Panus ciliatus</i>)	UOC SIGWI S24	Sri Lanka	KR818817	N/A	
<i>Panus conchatus</i>	'ciliatus' (<i>Panus ciliatus</i>)	JZ30	India	MG719287	N/A	
<i>Panus conchatus</i>	'ciliatus' (<i>Panus ciliatus</i>)	HFJAU-ND073	China	MN622763	N/A	
<i>Panus conchatus</i>	'ciliatus' (<i>Panus ciliatus</i>)	A52	Philippines	OM102535	N/A	
<i>Panus conchatus</i>	'ciliatus' (<i>Panus ciliatus</i>)	LE-BIN 3343	Viet Nam	OQ023307	N/A	
<i>Panus</i> sp.	'ciliatus' (<i>Panus ciliatus</i>)	SL1818	Singapore	OR527371	N/A	
<i>Panus</i> sp.	'ciliatus' (<i>Panus ciliatus</i>)	SL1878	Singapore	OR527372	N/A	
<i>Panus</i> sp.	'ciliatus' (<i>Panus ciliatus</i>)	FAFU2021-5-19	China	OK643782	OK643606	
<i>Panus</i> sp.	'ciliatus' (<i>Panus ciliatus</i>)	G028	China	KJ195662	N/A	
<i>Panus</i> sp.	'ciliatus' (<i>Panus ciliatus</i>)	LAH37667	Pakistan	OQ302558	N/A	

Taxon	Clade in this study	Voucher	Genbank code		
			Country	ITS	nrLSU
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	Contig_M28	India	OK165593	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	JMH44	Tanzania	KM267730	KM267737
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	567	Colombia	OM400540	MZ424282
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	570	Colombia	OM400541	MZ424283
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	CLZhao 1535	China	MG231759	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	FLAS-F-60901	USA	MH016880	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	N. Alshammari	USA	MT032480	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	HONDURAS19-F030a	Honduras	MT571526	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus aff. conchatus</i>)	PUL F27044	USA	MW448620	N/A
<i>Panus sp.</i>	'conchatus' (<i>Panus aff. conchatus</i>)	Cesar73	Mexico	MK141047	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	OMC636	Finland	JN710579	JN710579
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	LE265028	Russia	KM411463	KM434323
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	CBS 267.58	Germany	MH857778	MH869312
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	CLZhao 1452	China	MG231758	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	CBS 254.33	United Kingdom	MH855431	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	KUMCC18-0047	China	MK192053	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	HKAS76595	China	MN546049	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	K(M):250360	United Kingdom	MZ159703	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	inat36307978	USA	OM349507	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	HMJAU-F-1080	China	ON683473	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	iNat48885698	USA	OQ701113	N/A
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	Dai 23421	China	ON417176	ON417226
<i>Panus conchatus</i>	'conchatus' (<i>Panus conchatus s.s.</i>)	LE-BIN 1554	Russia	OL840646	N/A
uncultured fungus fungal sp.	'conchatus' (<i>Panus conchatus s.s.</i>)	454_417	Sweden	KM493891	N/A
<i>Lentinus martianoffianus</i>	'neostrigosus'	NM1813	China	MW680830	N/A
<i>Lentinus</i> sp.	'neostrigosus'	K(M) 179349	Russia	MW161263	N/A
<i>Panus lecomtei</i>	'neostrigosus'	VKGJ07	India	JQ428825	N/A
<i>Panus lecomtei</i>	'neostrigosus'	INPACM1466	Brazil	JQ955721	JQ955730
<i>Panus lecomtei</i>	'neostrigosus'	TMIC35103	Japan	JQ955726	JQ955733
<i>Panus lecomtei</i>	'neostrigosus'	HHB-11042-Sp	USA	KP135328	KP135233

Taxon	Clade in this study	Voucher	Country	Genbank code	
				ITS	nrLSU
<i>Panus lecomtei</i>	'neostrigosus'	CC40	Brazil	MK603978	MK605968
<i>Panus lecomtei</i>	'neostrigosus'	OKMCHD-30684	USA	KP135326	N/A
<i>Panus lecomtei</i>	'neostrigosus'	HHB-6616-Sp	USA	KP135327	N/A
<i>Panus lecomtei</i>	'neostrigosus'	HHB-9614	USA	KP135329	N/A
<i>Panus lecomtei</i>	'neostrigosus'	HNC18-48	China	KT959318	N/A
<i>Panus lecomtei</i>	'neostrigosus'	CF17	China	KY038640	N/A
<i>Panus lecomtei</i>	'neostrigosus'	FCG-1949	Japan	LC415543	N/A
<i>Panus lecomtei</i>	'neostrigosus'	GOM-E1F	India	MH801134	N/A
<i>Panus lecomtei</i>	'neostrigosus'	APBN3	India	MK851549	N/A
<i>Panus lecomtei</i>	'neostrigosus'	HFJAU0382	China	MN258671	N/A
<i>Panus lecomtei</i>	'neostrigosus'	DMRO 991	India	MN332200	N/A
<i>Panus lecomtei</i>	'neostrigosus'	BO24428	Indonesia	OL763317	N/A
<i>Panus lecomtei</i>	'neostrigosus'	10966533	USA	ON375988	N/A
<i>Panus lecomtei</i>	'neostrigosus'	PUL00034474	USA	ON561626	N/A
<i>Panus lecomtei</i>	'neostrigosus'	PUL00031402	USA	ON561699	N/A
<i>Panus lecomtei</i>	'neostrigosus'	iNat120411449	USA	OP749356	N/A
<i>Panus lecomtei</i>	'neostrigosus'	EOS5	Philippines	OR062415	N/A
<i>Panus lecomtei</i>	'neostrigosus'	MO502240	USA	OR203584	N/A
<i>Panus lecomtei</i>	'neostrigosus'	LE5834	Russia	MW161262	N/A
<i>Panus lecomtei</i>	'neostrigosus'	LE-BIN 1711	Russia	OL840632	N/A
<i>Panus lecomtei</i>	'neostrigosus'	TENN51805	USA	N/A	AY615994
<i>Panus lecomtei</i>	'neostrigosus'	Ap7	India	KR824079	N/A
<i>Panus lecomtei</i>	'neostrigosus'	WP	China	MK045850	N/A
<i>Panus lecomtei</i>	'neostrigosus'	F5	India	MK168585	N/A
<i>Panus lecomtei</i>	'neostrigosus'	iNat90996372	USA	OM373469	N/A
<i>Panus</i>					
<i>Panus</i>	'neostrigosus'	HSR32-2	USA	EF694648	N/A
<i>Panus</i>	'neostrigosus'	LE5829	Russia	KM411451	KM411468
<i>Panus</i>	'neostrigosus'	LSPQ-NSM-106	Canada	KU761234	KU761114
<i>Panus</i>	'neostrigosus'	LSPQ-NSM-107	Canada	KU761235	KU761115
<i>Panus</i>	'neostrigosus'	LSPQ-NSM-108	Canada	KU761236	KU761116
<i>Panus</i>	'neostrigosus'	ZRL20151738	N/R	LT716077	KY418901
<i>Panus</i>	'neostrigosus'	Ap17	India	KR824089	N/A
<i>Panus</i>	'neostrigosus'	OBCC 5004	Turkey	MF616402	N/A
<i>Panus</i>	'neostrigosus'	MHHNU 8079	China	MK172822	N/A
<i>Panus</i>	'neostrigosus'	ZD17032503	China	MN523273	N/A
<i>Panus</i>	'neostrigosus'	10617HH	Mexico	MZ100062	N/A
<i>Panus</i>	'neostrigosus'	BIL1324	Philippines	OM102529	N/A
<i>Panus</i>	'neostrigosus'	CL-01	Philippines	OM102530	N/A

Taxon	Clade in this study	Voucher	Genbank code		
			Country	ITS	nrLSU
<i>Panus neostrigosus</i>	'neostrigosus'	FX054	China	OQ450422	N/A
<i>Panus neostrigosus</i>	'neostrigosus'	SR1957-J25	India	OQ623134	N/A
<i>Panus neostrigosus</i>	'neostrigosus'	CL1M	Philippines	OR052689	N/A
<i>Panus neostrigosus</i>	'neostrigosus'	J_25	India	OR138124	N/A
<i>Panus neostrigosus</i>	'neostrigosus'	None	India	KY243930	N/A
<i>Panus neostrigosus</i>	'neostrigosus'	LZ12-14	China	MT898694	N/A
<i>Panus rufus</i>	'neostrigosus'	ZJ1005DKJ01	China	KU863048	N/A
<i>Panus rufus</i>	'neostrigosus'	ZJ1005DKJ02	China	KU863049	N/A
<i>Panus rufus</i>	'neostrigosus'	ZJ1005DKJ03	China	KU863050	N/A
<i>Panus rufus</i>	'neostrigosus'	ZJ1005DKJ04	China	KU863051	N/A
<i>Panus rufus</i>	'neostrigosus'	F1625	China	MW647655	N/A
<i>Panus rufus</i>	'neostrigosus'	F01315	China	ON387630	N/A
<i>Panus rufus</i>	'neostrigosus'	LE-BIN 1566	Russia	OR475685	N/A
<i>Panus rufus</i>	'neostrigosus'	PR-1116 ss-1	N/R	OM337524	OM337524
<i>Panus rufus</i>	'neostrigosus'	DSH-92-139	N/R	N/A	AF287878
<i>Panus</i> sp.	'neostrigosus'	Fun81W3	Brazil	KF496188	N/A
<i>Panus</i> sp.	'neostrigosus'	Fun8D3	Brazil	KF496194	N/A
<i>Panus</i> sp.	'neostrigosus'	M85	Mexico	KP096364	N/A
<i>Panus</i> sp.	'neostrigosus'	GE	N/R	HM245784	N/A
uncultured fungus	'neostrigosus'	LX040884-122-045-D06	N/R	GU053919	N/A
<i>Panus paraibensis</i>	'paraibensis'	JPB 66873	Brazil New	OP963513	N/A
<i>Panus purpuratus</i>	'purpuratus'	PDD:96130	Zealand	MK404671	N/A
<i>Lentinus roseus</i>	'roseus'	HKAS 94715	China	KY490135	KY490137
<i>Lentinus roseus</i>	'roseus'	HKAS 94714	China	KY490136	KY490138
<i>Lentinus roseus</i>	'roseus'	JZ25	India	MG719282	N/A
<i>Panus similis</i>	'velutinus' (<i>Panus similis</i> s.s.)	UOC SIGWI S38	Sri Lanka	KR818820	N/A
<i>Panus similis</i>	'velutinus' (<i>Panus similis</i> s.s.)	LE-BIN 3011	Viet Nam	OL839257	N/A
<i>Panus lecomtei</i>	'asiaticus'	HKAS89836	China South Korea	MN546050	N/A
<i>Panus</i> sp.	'asiaticus'	18107	South Korea	ON053455	N/A
<i>Panus</i> sp.	'asiaticus'	15114	South Korea	ON553390	N/A
<i>Neolentinus kauffmanii</i>	'bambusinus'	VKGJ01	India	JF808173	N/A
<i>Neolentinus kauffmanii</i>	'bambusinus'	VKGJ03	India	JQ428821	N/A
<i>Panus</i> sp.	'bambusinus'	SSM03	India	OQ932792	N/A
<i>Panus</i> sp.	'bambusinus'	DK1	India	JF741922	N/A
<i>Panus</i> sp.	'bambusinus'	MCCT187 SDBR-CMUNK0924	India Thailand	MG279699 OR447474	N/A OR447383

Taxon	Clade in this study	Voucher	Genbank code		
			Country	ITS	nrLSU
<i>Panus</i> sp.	'bambusinus'	SDBR-CMUNK0930	Thailand	OR447475	OR447384
<i>Panus</i> sp.	'bambusinus'	SDBR-CMUNK0931	Thailand	OR447476	OR447385
<i>Panus</i> sp.	'bambusinus'	SDBR-CMUNK0940	Thailand	OR447477	OR447386
<i>Panus</i> sp.	'bambusinus'	CMUNK1100	Thailand	OR447478	OR447387
<i>Panus</i> sp.	'bambusinus'	BAB-4776	India	KP686453	N/A
<i>Panus</i> sp.	'bambusinus'	NHMM-F/0007	India	OL839328	N/A
<i>Panus</i> sp.	'ciliatus'	20170458	Madagascar	MK184520	N/A
<i>Panus</i> sp.	'roseus'	FBD167	Viet Nam	KT965505	N/A
<i>Lentinus</i> cf. <i>velutinus</i>	'velutinus'	Mushroom Observer 243572	Mexico	MF163177	N/A
<i>Lentinus</i> sp.	'velutinus'	WCR1212	Thailand	KT956123	N/A
<i>Lentinus</i> sp.	'velutinus'	WCR1104	Thailand	KT956126	N/A
<i>Lentinus</i> sp.	'velutinus'	20170455	Madagascar	MK184517	N/A
<i>Lentinus</i> sp.	'velutinus'	VDW1055	South Africa	MT304632	N/A
<i>Lentinus</i> sp.	'velutinus'	L17	Thailand	OP522028	N/A
<i>Lentinus velutinus</i>	'velutinus'	VKMK02	India	GQ849478	N/A
<i>Lentinus velutinus</i>	'velutinus'	Prabhu, K.N.	India	KX257370	N/A
<i>Lentinus velutinus</i>	'velutinus'	KM5	India	MK855514	N/A
<i>Panus similis</i>	'velutinus'	LE287548	Viet Nam	KM411466	KM411482
<i>Panus similis</i>	'velutinus'	KWGM 39	India	KY630517	N/A
<i>Panus similis</i>	'velutinus'	LE-BIN 3000	Viet Nam	OL839236	N/A
<i>Panus similis</i>	'velutinus'	DMC 189	Cameroon	N/A	EU908182
<i>Panus</i> sp.	'velutinus'	MEL:2382967	Australia	KP012827	KP012827
<i>Panus</i> sp.	'velutinus'	MEL:2382698	Australia	KP012877	KP012877
<i>Panus</i> sp.	'velutinus'	OTU301	Vietnam	MF942548	N/A
<i>Panus</i> sp.	'velutinus'	AF 516	India	MW462890	N/A
<i>Panus</i> sp.	'velutinus'	J4	Thailand	OL629547	N/A
<i>Panus</i> sp.	'velutinus'	SL1617	Singapore	OR527370	N/A
<i>Panus velutinus</i>	'velutinus'	VKRA1	India	KT722841	KT722841
<i>Panus velutinus</i>	'velutinus'	rxsbn-452	China	MW374215	N/A
<i>Panus velutinus</i>	'velutinus'	SI11	Malaysia	OR178478	N/A
<i>Panus ciliatus</i>	ciliatus' (<i>Panus subfasciatus</i>)	TENN59785	Thailand	N/A	AY616006
<i>Panus conchatus</i>	ciliatus' (<i>Panus subfasciatus</i>)	UOC-MINNP-M13	Sri Lanka	KP776992	N/A
<i>Panus conchatus</i>	ciliatus' (<i>Panus subfasciatus</i>)	fs1 13	China	OP801891	N/A
<i>Panus conchatus</i>	ciliatus' (<i>Panus subfasciatus</i>)	Dai 22458	China	OL477381	OL477382
<i>Panus conchatus</i>	ciliatus' (<i>Panus subfasciatus</i>)	SR1522	India	MT192441	N/A
<i>Panus fasciatus</i>	ciliatus' (<i>Panus subfasciatus</i>)	DMC 184	Cameroon	N/A	EU908180

Taxon	Clade in this study	Voucher	Genbank code		
			Country	ITS	nrLSU
<i>Panus</i> sp.	ciliatus' (<i>Panus subfasciatus</i>)	Mushroom Observer 355306	USA	MN180806	N/A
<i>Panus</i> sp.	ciliatus' (<i>Panus subfasciatus</i>)	MO506033	USA	OR336204	N/A
<i>Panus subfasciatus</i>	ciliatus' (<i>Panus subfasciatus</i>)	MFLU 16-2129	Thailand	LT614958	LT614958
<i>Panus</i> sp.	'speciosus'	SL1683	Singapore	OR354954	N/A
<i>Panus</i> sp.	'speciosus'	SL2082	Singapore	OR354978	N/A
<i>Panus speciosus</i> sp. nov.	'speciosus'	DG25	Brazil	MT669129	MT669149
<i>Panus speciosus</i> sp. nov.	'speciosus'	DS1151	Brazil	MT669130	MT669150
<i>Panus stipitonotatus</i> sp. nov.	'velutinus'	CATO176	Brazil	MT669131	MT669151
<i>Panus stipitonotatus</i> sp. nov.	'velutinus'	GAS850	Brazil	MT669132	MT669152
<i>Panus stipitonotatus</i> sp. nov.	'velutinus'	DG06	Brazil	MT669133	MT669153
<i>Panus stipitonotatus</i> sp. nov.	'velutinus'	MIBF205	Brazil	MT669134	N/A
<i>Panus stipitonotatus</i> sp. nov.	'velutinus' (<i>Panus stipitonotatus</i> sp. nov.)	DS842	Brazil	N/A	OR652617
<i>Panus stipitonotatus</i> sp. nov.	'velutinus' (<i>Panus stipitonotatus</i> sp. nov.)	DS841	Brazil	N/A	OR652616
<i>Panus parvus</i>	'strigellus'	URM80840	Brazil	MT669125	MT669145
<i>Panus</i> sp.	'strigellus'	M2028-7-P30	Panama	JQ922124	JQ922124
<i>Panus</i> sp.	'strigellus'	FK1670	Brazil	OR676910	OR652623
<i>Panus strigellus</i>	'strigellus'	TENN55993	USA	JQ955728	AY616001
<i>Panus strigellus</i>	'strigellus'	TENN56192	USA	JQ955727	AY616002
<i>Panus strigellus</i>	'strigellus'	INPA222827	Brazil	JQ955722	JQ955729
<i>Panus strigellus</i>	'strigellus'	INPA239979	Brazil	JQ955724	JQ955731
<i>Panus strigellus</i>	'strigellus'	INPA243940	Brazil	JQ955725	JQ955732
<i>Panus strigellus</i>	'strigellus'	DG36	Brazil	MT669135	MT669154
<i>Panus strigellus</i>	'strigellus'	U16-7	Brazil	MG211679	N/A
<i>Panus strigellus</i>	'strigellus'	HUCS/MIUCS 2427	Brazil	MN598074	N/A
<i>Panus strigellus</i>	'strigellus'	DS1872	Brazil	MT669136	N/A
<i>Panus strigellus</i>	'strigellus'	MIBF208	Brazil	MT669137	N/A
<i>Panus strigellus</i>	'strigellus'	B6	Paraguay	MW407012	N/A
<i>Panus strigellus</i>	'strigellus'	H9_CM-UDEA	Colombia	OR160301	OR165097
<i>Panus strigellus</i>	'strigellus'	B6MICIFSP28	Brazil	OQ618220	N/A
<i>Panus strigellus</i>	'strigellus'	MIBF207-15	Brazil	OR676907	N/A
<i>Panus strigellus</i>	'strigellus'	CCIBt3399	Brazil	OR676908	N/A
<i>Panus strigellus</i>	'strigellus'	CCIBt3396	Brazil	OR676909	N/A
<i>Panus strigellus</i>	'strigellus'	CCIBt2499	Brazil	OR676906	N/A

Taxon	Clade in this study	Voucher	Country	ITS	nrLSU
Genbank code					
<i>Panus strigellus</i>	'strigellus'	DS584	Brazil	N/A	OR652621
<i>Panus strigellus</i>	'strigellus'	DG38	Brazil	N/A	OR652624
<i>Panus strigellus</i>	'strigellus'	DG26	Brazil	N/A	OR652622
<i>Panus strigellus</i>	'strigellus'	DG24	Brazil	N/A	OR652620
uncultured fungus	'strigellus'	LX039935-122-022-E10	N/R	GU053828	N/A
<i>Lentinus badius</i>	'velutinus'	CBS 316.50	Argentina French Guiana	MH856644	MH868154
<i>Lentinus</i> sp.	'velutinus'	RC-GUY-12-024	Brazil	MK546713	N/A
<i>Panus fulvus</i>	'velutinus'	DS1598	Brazil	MT669120	MT669141
<i>Panus fulvus</i>	'velutinus'	DS1684	Brazil	MT669121	MT669142
<i>Panus fulvus</i>	'velutinus'	DS1687	Brazil	MT669122	MT669143
<i>Panus fulvus</i>	'velutinus'	SP446159	Brazil	MT669123	MT669144
<i>Panus fulvus</i>	'velutinus'	DHCR213	Brazil	MT669119	N/A
<i>Panus fulvus</i>	'velutinus'	VOG36	Brazil	MT669124	N/A
<i>Panus fulvus</i>	'velutinus'	TENN58776	USA	N/A	AY615996
<i>Panus</i> sp.	'velutinus'	CMINPA 1713	Brazil	MN602051	N/A
<i>Panus</i> sp.	'velutinus'	FLAS-F-69498	USA	OQ673538	N/A
<i>Panus</i> sp.	'velutinus'	FK1669	Brazil	OR676913	OR652615
<i>Panus</i> sp.	'velutinus'	FK1655	Brazil	OR676912	OR652619
<i>Panus</i> sp.	'velutinus'	VOG51	Brazil	OR676915	N/A
<i>Panus</i> sp.	'velutinus'	VOG48	Brazil	OR676916	N/A
<i>Panus</i> sp.	'velutinus'	VOG38	Brazil	OR676914	N/A
<i>Panus</i> <i>tephroleucus</i>	'velutinus'	CMINPA 1860	Brazil	MN602052	N/A
<i>Panus</i> <i>tephroleucus/fulvus</i>	'velutinus'	CCIBt3398	Brazil	OR676911	N/A
<i>Panus velutinus</i>	'velutinus'	FLAS-F-61663	USA	MH212037	N/A
<i>Panus velutinus</i>	'velutinus'	2C	Mexico	MW605226	N/A
<i>Endopandanicola thailandica</i>	'roseus'	MFLUCC 17-0549	Thailand	MG646963	N/A
<i>Endopandanicola thailandica</i>	'roseus'	MFLUCC 17-0548	Thailand	MG646964	N/A
<i>Endopandanicola thailandica</i>	'roseus'	MFLUCC 17-0572	Thailand	MG646959	N/A
<i>Endopandanicola thailandica</i>	'roseus'	MFLUCC 17-0600	Thailand	MG646960	N/A
<i>Endopandanicola thailandica</i>	'roseus'	MFLUCC 17-0551	Thailand	MG646962	N/A
<i>Panus velutinus</i>	'velutinus'	VOG30	Brazil	MT669139	MT669155
<i>Panus velutinus</i>	'velutinus'	CM10	Brazil	MT669138	N/A
<i>Panus velutinus</i>	'velutinus'	NMJ260	Brazil	OQ626166	N/A
<i>Cerrena unicolor</i>	outgroup	FD-299	USA	KP135304	KP135209
<i>Cerrena unicolor</i>	outgroup	He6082	China	OM100740	OM083972
<i>Cymatoderma caperatum</i>	outgroup	LR37567 (O)	Venezuela	JN649336	JN649336
<i>Cymatoderma elegans</i>	outgroup	Halling9064 (NY)	Australia	JN649341	JN649341

Genbank code					
Taxon	Clade in this study	Voucher	Country	ITS	nrLSU
<i>Panus</i> sp.	outgroup	271-259	Japan	AB509648	N/A

N/A: not available.

N/R: not recovered.

**ANEXO A - AVALIAÇÃO DO ESTADO DE CONSERVAÇÃO DE CYMATODERMA
SCLEROTIOIDES LLOYD**

Avaliação do estado de conservação de *Cymatoderma sclerotioides* Lloyd

Assessment status: Published

Assessment date: 20-08-2020

**Funez, L., Kossmann, T., Guimarães, D.K., Martins da
Cunha, K., Leopoldo, E., Vasco-Palacios, A. &
Drechsler-Santos, E.**



*The IUCN Red List of
Threatened Species™*
ISSN 2307-8235 (online)
IUCN 2021:
T196135502A200624571
Scope(s): Global Language:
English

Cymatoderma sclerotoides

Amendment version

Assessment by: Funez, L., Kossmann, T.,
Guimarães, D.K., Martins da Cunha, K., Leopoldo,
E., Vasco-Palacios, A. & Drechsler-Santos, E.



View on www.iucnredlist.org

Citation: Funez, L., Kossmann, T., Guimarães, D.K., Martins da Cunha, K., Leopoldo, E., Vasco-Palacios, A. & Drechsler-Santos, E. 2021. *Cymatoderma sclerotiooides* (amended version of 2021 assessment). *The IUCN Red List of Threatened Species* 2021: e.T196135502A200624571.

<https://dx.doi.org/10.2305/IUCN.UK.2021-2.RLTS.T196135502A200624571.en>

Copyright: © 2021 International Union for Conservation of Nature and Natural Resources

Reproduction of this publication for educational or other non-commercial purposes is authorized without prior written permission from the copyright holder provided the source is fully acknowledged.

Reproduction of this publication for resale, reposting or other commercial purposes is prohibited without prior written permission from the copyright holder. For further details see [Terms of Use](#).

The IUCN Red List of Threatened Species™ is produced and managed by the [IUCN Global Species Programme](#), the [IUCN Species Survival Commission \(SSC\)](#) and [The IUCN Red List Partnership](#). The IUCN Red List Partners are: [ABQ BioPark](#); [Arizona State University](#); [BirdLife International](#); [Botanic Gardens Conservation International](#); [Conservation International](#); [Missouri Botanical Garden](#); [NatureServe](#); [Re:wild](#); [Royal Botanic Gardens, Kew](#); [Sapienza University of Rome](#); [Texas A&M University](#); and [Zoological Society of London](#).

If you see any errors or have any questions or suggestions on what is shown in this document, please provide us with [feedback](#) so that we can correct or extend the information provided.

THE IUCN RED LIST OF THREATENED SPECIES™

Taxonomy

Kingdom	Phylum	Class	Order	Family
Fungi	Basidiomycota	Agaricomycetes	Polyporales	Panaceae

Scientific Name: *Cymatoderma sclerotiooides* (Lloyd) D.A. Reid

Synonym(s):

- *Stereum sclerotiooides* Lloyd

Taxonomic Source(s):

Index Fungorum Partnership. 2021. Index Fungorum. Available at:
<http://www.indexfungorum.org>.

Taxonomic Notes:

This species was originally described as *Stereum sclerotiooides* by Lloyd (1922), based on a specimen with no precise geographic data, from the Amazon Forest. In 1959, D.A. Reid placed this species in the genus *Cymatoderma* Reid (1958).

Assessment Information

Red List Category & Criteria: Near Threatened A3c; C1 ver 3.1

Year Published: 2021

Date Assessed: August 18, 2020

Justification:

This is a very rare species, having been recorded from only a limited number of sites since 1922, represented by no more than 25 collections. The species has conspicuous large, colourful basidiomata, thus the small number of collections is probably due to its rarity. Based on the potential area of occurrence, it is conservatively estimated that there are up to 1,000-2,000 sites, each holding 5-10 mature individuals, resulting in a total population size of 10,000-20,000. Although the Amazon Forest domain is the largest and most preserved Tropical Forest in Brazil, the areas where the species occurs are under threat, with the Amazon facing growing deforestation and the possibility of approaching its tipping point (Amigo 2020, INPE 2020). Central American montane forests are under threat throughout much of their range due to land use changes, including timber harvest, conversion to pine and other non-native tree plantations, agriculture, and expansion of towns and cities. Further pressure and population reductions are expected to continue throughout the species range, and as such a population decline of up to 20% is suspected over in the next 20 years. The species is assessed as Near Threatened under criteria A3c; C1.

Previously Published Red List Assessments

2021 – Near Threatened (NT)

<https://dx.doi.org/10.2305/IUCN.UK.2021-1.RLTS.T196135502A196846666.en>

Geographic RangeRange Description:

This species is currently known from the Amazon Forest of Brazil (Mato Grosso and Roraima states), Peru (Loreto Department) and Colombia (Caquetá and Amazonas). It is also known from northern Panama and southern Costa Rica, both in montane tropical forests near Volcán Barú/Cordillera Talamanca. In the Amazon, the known sites are about 1,500-2,000 km away from each other. The species is expected to occur throughout the Amazon and through tropical forests of Colombia into Panama and Costa Rica.

Country Occurrence:

Native, Extant (resident): Brazil; Colombia; Costa Rica; Panama; Peru

Distribution Map



Legend

EXTANT (RESIDENT)

Compiled by:

IUCN 2020



The boundaries and names shown and the designations used on this map do not imply any official endorsement, acceptance or opinion by IUCN.



Population

The species was first recorded in 1922 in the Brazilian Amazon Forest without precise information about its locality. Six other records are known from the Amazon, four in the western Amazon (two from Iquito, Peru in 1984 and one each from two localities in Colombia), one from northern Amazon (Roraima, Brazil in 2008), and one in southern Amazon (Mato Grosso, Brazil in 2018). The species has also been recorded in Central America, in Costa Rica and Panama, where ca. 20 collections have been reported, all in the tropical montane forests in the Cordillera Talamanca. Although this species has a wide distribution, it is likely rare in the Amazon, as there are few records even in well sampled areas. For example, at the Cristalino Particular Reserve, in Mato Grosso state where fungi have been studied and documented intensively in the last decade, just one basidiome of *Cymatoderma sclerotiooides* has been found.

Based on the potential area of occurrence, it is conservatively estimated that there are up to 2,000 sites for the species, each holding 5-10 mature individuals, resulting in a total population size of up to 20,000. However, due to the species' rarity, these numbers could be an overestimate, and the population size may not exceed 10,000 mature individuals.

The Amazon Forest is undergoing rapid deforestation and facing increased fire frequency and intensity, following years of decline (INPE 2020). The forest could be dangerously approaching a tipping point, when the forest can no longer sustain its own water cycles, drastically changing into a savannah, leading to huge biodiversity losses (Amigo 2020).

Central American montane forests are also under threat throughout much of their range due to land use changes, including timber harvest, conversion to pine and other non-native tree plantations, agriculture, and expansion of towns and cities. Further pressures are expected to continue. Deforestation in Colombia has increased in recent years and is anticipated to continue into the near future. Parts of the Talamancas are protected in National parks, but other areas are privately held, and there is limited logging ongoing as well as commercial and housing developments. Additionally, in mountainous areas where this species occurs, the total forest cover has not significantly changed in the last 20 years (MINAE *et al.* 2018).

Overall, the species is suspected to undergo a population decline of up to 20% in the next 20 years.

Current Population Trend: Decreasing

Habitat and Ecology (see Appendix for additional information)

This species likely occurs throughout the Amazon Forest domain to the montane tropical forests of Central America, growing on buried pieces of heartwood.

Systems: Terrestrial

Use and Trade (see Appendix for additional information)

No use/trade is known.

Threats (see Appendix for additional information) The Amazon ecosystem has been facing a rapid increase in deforestation and fire frequency following years of decline (INPE 2020), and the forest could be dangerously approaching a tipping point, when the forest can no longer sustain its own water cycles, drastically changing into a savannah, leading to huge biodiversity losses (Amigo 2020). The Amazon domain in Brazil suffers from continued commercial logging and deforestation for cattle and implementation of soybean plantations as a result of the economy plan for Brazilian Amazonia (Fernside 2008). Even in the Western Amazon (includes parts of Bolivia, western Brazil, Colombia, Ecuador and Peru), which is better preserved than the Eastern Amazon (mostly inside Brazilian territory), there are threats like illegal mining and oil and gas extraction that tend to increase over time (Finer *et al.* 2008). Overall, the suitable area where the species occurs in the Amazon has declined at least 18% in the last 30 years. Central American montane forests are also under threat throughout much of their range due to land use changes, including timber harvest, conversion to pine and other non-native tree plantations, agriculture, and expansion of towns and cities.

Conservation Actions (see Appendix for additional information)

The main action to prevent the decline of the species is preservation of habitat, both known and potential, not yet discovered sites, by creating and appropriately managing conservation areas. More surveys and long term studies are needed to identify other sites and to better estimate the population size. Also, studies on the habitat of the species and its ecological relationships are needed. Currently, there are no available DNA sequences of this species, and its phylogenetic and taxonomic status need to be confirmed.

Credits

Assessor(s): Funez, L., Kossmann, T., Guimaraes, D.K., Martins da Cunha, K., Leopoldo, E., Vasco-Palacios, A. & Drechsler-Santos, E.

Reviewer(s): Mueller, G.M.

Bibliography

- Amigo, I. 2020. When will the Amazon hit a tipping point? *Nature* 578: 505-507.
- Dahlberg, A. and Mueller, G. 2011. Applying IUCN red-listing criteria for assessing and reporting on the conservation status of fungal species. *Fungal Ecology* 4: 1-16.
- Fearnside, P.M. 2008. Amazon Forest maintenance as a source of environmental services. *Anais Da Academia Brasileira de Ciências* 80(1): 101–114.
- Finer, M., Jenkins, C.N., Pimm, S.L., Keane, B. and Ross, C. 2008. Oil and Gas Projects in the Western Amazon: Threats to Wilderness, Biodiversity, and Indigenous Peoples. *PLoS One*.
- INPE - National Institute for Space Research. 2020. Earth Observation General Coordination. Monitoring Program of the Amazon and Other Biomes. Deforestation – Legal Amazon. Available at: <http://terrabrasilis.dpi.inpe.br/downloads/>. (Accessed: 20 March 2020).
- IUCN. 2021. The IUCN Red List of Threatened Species. Version 2021-1. Available at: www.iucnredlist.org. (Accessed: 25 March 2021).
- IUCN. 2021. The IUCN Red List of Threatened Species. Version 2021-2. Available at: www.iucnredlist.org. (Accessed: 04 September 2021).
- Lloyd, C.G. 1922. Letter 66 no.1. In: Lloyd, C.G. (ed.), *Mycological Writtings*, pp. 1106–1136. Lloyd, C.G., Cincinnati, Ohio.
- MINAE, SINAC, CONAGEBIO and FONAFIFO. 2018. Resumen del Sexto Informe Nacional de Costa Rica ante el Convenio de Diversidad Biológica. . Programa de Naciones Unidas para el Desarrollo - Apoyo técnico para que las Partes Elegibles desarrollen el Sexto Informe Nacional para el CDB (6NR-LAC) Costa Rica.
- Reid, D.A. 1958. The genus *Cymatoderma* Jungh. (Cladoderris). *Kew Bulletin* 13(3): 518–530.
- Rivers, M.C., Bachman, S., Meagher, T.R., Nic Lughadha, E. and Brummitt, N.A. 2010. Subpopulations, locations and fragmentation: applying IUCN Red List Criteria to herbarium specimen data. *Biodiversity and Conservation* 19: 2071-2085.
- Welden, A.L. 1960. The genus *Cymatoderma* (Thelephoraceae) in the Americas. *Mycologia* 52(6): 856- 876.

Citation

Funez, L., Kossmann, T., Guimarães, D.K., Martins da Cunha, K., Leopoldo, E., Vasco-Palacios, A. & Drechsler-Santos, E. 2021. *Cymatoderma sclerotoides* (amended version of 2021 assessment). *The IUCN Red List of Threatened Species* 2021: e.T196135502A200624571. <https://dx.doi.org/10.2305/IUCN.UK.2021-2.RLTS.T196135502A200624571.en>

Disclaimer

To make use of this information, please check the [Terms of Use](#).

External Resources

For [Supplementary Material](#), and for [Images and External Links to Additional Information](#), please see the Red List website.

4 CONSIDERAÇÕES FINAIS

Esta tese envolveu extenso trabalho de campo em regiões pouco exploradas do país, combinado com uma revisão minuciosa de espécimes de fungários, incluindo diversos materiais tipo. Como resultado, apresentamos as mais abrangentes filogenias para Panaceae, propomos cinco novas espécies em *Panus*, e quatro novas combinações. Discutimos questões nomenclaturais envolvendo o complexo de espécies de *Lentinus velutinus*, elucidando o basiônimo, seu *sensu stricto*, e propomos a epitificação de *Panus velutinus* e *Cymatoderma sclerotiooides*, com base em novos espécimes sequenciados da localidade tipo.

Adicionalmente, contribuímos para a estabilidade taxonômica de *Panus*, ao propormos a sinonimização do gênero *Endopandanicola* em *Panus*, assim como *P. parvus* em *P. strigellus*. Nossa pesquisa, fundamentada em diversas evidências morfológicas e filogenéticas, rejeita a ocorrência no Brasil de espécies como *P. conchatus*, *P. convivalis*, *P. fulvus*, *P. similis* e *P. tephroleucus*. Após uma análise crítica desses resultados, elaboramos uma chave de identificação para as espécies presentes no Brasil, proporcionando uma ferramenta valiosa para auxiliar na identificação precisa das mesmas. Para *P. conchatus* e *P. similis*, apresentamos bases para o reconhecimento de seu status *sensu stricto*.

A partir dos dados apresentados, notamos que ainda há uma necessidade premente de revisão taxonômica para *Cymatoderma* e *Panus*. Ambos os gêneros apresentam complexidades morfológicas e históricos taxonômicos problemáticos, desafiando a clara delimitação das espécies e suas relações filogenéticas. Enquanto a inclusão de dados moleculares revelou pistas cruciais sobre a relação entre esses táxons, a amostragem insuficiente de espécies de *Cymatoderma* limitou uma compreensão mais completa sobre este gênero. A ausência de estudos moleculares abrangentes para muitas espécies, destaca a necessidade de uma abordagem holística, integrando dados morfológicos e moleculares para uma revisão precisa de *Cymatoderma*.

Para *Panus*, apesar de sua ampla distribuição e importância econômica e biotecnológica, uma falta de consenso sobre o número real de espécies e os múltiplos sinônimos ressalta a urgência de uma revisão taxonômica integrativa.

Esta revisão taxonômica, aliada a abordagens moleculares mais abrangentes, é crucial para esclarecer as relações filogenéticas, delimitar espécies de forma mais precisa e promover uma compreensão mais clara da diversidade e evolução desses gêneros dentro da linhagem de Polyporales. Essa revisão mais completa não apenas contribuirá para uma taxonomia mais sólida, mas também terá implicações significativas em estudos biotecnológicos, conservacionistas e ecológicos relacionados a esses grupos de fungos.