An Acad Bras Cienc (2023) 95(3): e20220779 DOI 10.1590/0001-3765202320220779
Anais da Academia Brasileira de Ciências | *Annals of the Brazilian Academy of Sciences*
Printed ISSN 0001-3765 I Online ISSN 1678-2690
www.scielo.br/aabc | www.fb.com/aabcjournal

ECOSYSTEMS

A new record of *Sulzbacheromyces caatingae* (Basidiomycota, Agaricomycetes) from Mato Grosso do Sul and a worldwide infrageneric identification key

MARCOS J. KITAURA, MAYARA C. SCUR, JEAN-MARC TORRES, ALINE P. LORENZ & EMERSON F. LEITE

Abstract: *Sulzbacheromyces* is a genus of basidiolichen that includes nine species scattered on the African, American, and Asian continents. Sequences of the universal barcode of Fungi, the nuclear internal transcribed spacer – nuITS region, are available to all known species of the genus. Specimens of *Sulzbacheromyces caatingae* were collected during two expeditions in the Morro of Paxixi, Mato Grosso do Sul state, Midwest region of Brazil, in the *Cerrado* biome, where it was reported for the first time to the state. Morphological and anatomical analyses were performed. Specimens from Mato Grosso do Sul have a light green to indistinct thallus, while specimens from Ceará, Paraíba, and Piauí states present a thin green crust on the substrate. The nuITS sequences were also generated, and the distribution of *S. caatingae* was plotted with the haplotypes. Morphological differences were not reflected in the molecular analysis, which confirmed the identification of the species. In addition, an identification key to the known *Sulzbacheromyces* species is provided.

Key words: Aquidauana, *Cerrado***,** clavarioid, distribution, Lepidostromataceae, lichen.

INTRODUCTION

The molecular and morphological approaches have updated the phylogenetic relationships of the lichen-forming fungi, including the ones with clavarioid basidiomes that belong to Lepidostromataceae (Hodkinson et al. 2014, Sulzbacher et al. 2016, Liu et al. 2019, Coca et al. 2018, 2023).

Nowadays, Lepidostromataceae encompasses three genera of lichenized fungi with clavarioid and club-shaped basidiomata: *Sulzbacheromyces* B.P. Hodk. & Lücking, with nine known species, is characterized by a crustose thallus and lacking cortical structures; *Lepidostroma* Mägd. & S. Winkl., with five species, thallus distinctly squamulose and cellular cortex; and the monospecific genus *Ertzia* B.P. Hodk & Lücking, with thallus microsquamulose and jigsaw-puzzle-shaped cortical cells (Robert et al. 2005, Hodkinson et al. 2014).

Sulzbacheromyces species are reported to Africa (1 sp.), South America (4 spp.), and Asia (4 spp.) (Table I). The universal barcode of Fungi (Schoch et al. 2012, Lücking et al. 2020), the nuclear ribosomal internal transcribed spacer region (nuITS), has been generated to all known species, inferring the genus geographical distribution (Sulzbacher et al. 2012, 2016, Hodkinson et al. 2014, Liu et al. 2018, 2019, Coca et al. 2018, 2023). The species are divided into Neotropics, Africa, and Southeast Asia clades (Coca et al. 2023). With more than 50 nuITS

Table I. **The *Sulzbacheromyces* species, including the main morphological and anatomical characteristics.**

Name	Type locality	Thallus and prothallus	Basidiomes	Trama	Color Basidiomes	Basidiospores	Reference
S. bicolor D. Liu, Li S.Wang & Goffinet	China, Yunnan Province	Green to dark green, forming a thin layer on the substrate; prothallus white, grey or sliver	Simple or once or twice branched; 3.0–23.0 × 0.3–1.0 mm;	Densely agglutinated	Almost white but grey or pale yellow at the top and white in the lower portion	(3.5–)4.6–7.3–7.5(–8.5) × (3.5–)4.5–5.2–6(7.5) µm	Liu et al. (2018)
S. caatingae (Sulzbacher & Lücking) B.P. Hodk. & Lücking	Brazil, Piauí, Ceará, Paraíba, Mato Grosso do Sul	Green, forming a thin crust on the substrate; prothallus not mentioned	Simple, unbranched. 18.0–36.0 × 0.5–1.5 mm;	hyaline middle layer leaving large interspace, or with densely agglutinated hyphae	Brownish outer layer, pale yellowish inner layer; or dull orange-pink overall, context dull yellow	5–9 × 2.5–4.5 µm	Sulzbacher et al. (2012, 2016)
S. chocoensis Coca, Lücking & Moncada	Colombia, Chocó	Olive green; prothallus not mentioned	Unbranched at the apex. 4.0–10.0 × 1.0–2.0 mm;	With pseudo-paraplectenchymatous	Reddish orange to yellowish, with white stipe when fresh	6 × 4 µm	Coca et al. (2018)
S. fossicolus (Corner) D. Liu & Li S. Wang	Malaya, China and Thailand	Dark green, forming a thin layer on the substrate; Prothallus absent	Simple, sometimes once or twice branched from the base. 0.3–25.0 × 0.5–1.2 mm;	Densely agglutinated	Pale or cream white when fresh and hydrated, beige when dried	(5)5.5–5.6–6.5(6.6) × (2.5)3.8–4.5 (5) µm	Corner (1950), Liu et al. (2018)
S. leucodontius Coca, Gómez-Gómez, Guzmán-Guillermo & Dal Forno	Colombia, Brazil and Mexico	Like-moss green coloration, forming a thin granulose film; Prothallus absent	Simple, (6)10–20 (25) × 0.4–0.9 mm	Not specifically reported	White to ivory withe	3 × 6 µm	Coca et al. (2023)
S. miomboensis De Kesel & Ertz	Rep. D. of the Congo	Indistinct, forming a thin membranous crust on the substrate; prothallus not reported	Simple, not branched. 20.0–42.0 × 1.5–1.9 mm. Never circled by transverse cracks in mature	Presence of thigmoplect, and central aeroplect tissues	Orange to reddish-orange except for the orange-white base; specimens drying pale orange or orange white often with a pinkish hue	(7.7–) 8–9.6–11.2 (–10.8) × (3.8–) 4.1–4.7–5.4 (–5.5) µm	Liu et al. (2018)

Table I. Continuation.

S. sinensis (R.H. Petersen & M. Zang) D. Liu & Li S. Wang	China, Japan, Korean Peninsula, South Korea and Philippines	Green to dark green, forming a thin layer on the substrate; prothallus white grey or silver, shiny	Simple, rarely 2-3-5 apical branched, up to 55.0 × 1.0–2.5 mm,	Densely agglutinated	Orange to red-orange, turning ochraceous upon drying, with transverse cracks when mature	(5)5.9–9.8–11.5(12) × (2.5)4.5–5.6–7(7.5) µm	Liu et al. (2018, 2019)
S. tutunendo Coca, Lücking & Moncada	Colombia, Chocó	Olive green, terricolous and partially on rotten wood; prothallus not reported	Often branched above the middle. 15.0–30.0 × 0.15–0.2 mm,	With pseudo-paraplectenchymatous tissue	Reddish orange to yellowish orange	6 × 4 µm	Coca et al. (2018)
S. yunnanensis D. Liu, Li S. Wang & Goffinet	China, Yunnan province	Dark green, distinct when growing in the shade and depression or yellow green or light yellow; prothallus absent	Rarely once branched, with two conspicuous, wide, longitudinal depressions or grooves. 3.0–65.0 × 0.5–2.3 mm	Densely agglutinated	Orange in shaded habitat, base dark ochraceous turning ochraceous upon drying, surface pruinose	(8.1)8.8–9.9–11.2(12.5) × (3.6)4–4.8–5.8(5.8) µm	Liu et al. (2018)

sequences analyzed, *S. caatingae* (Sulzbacher & Lücking) B.P. Hodk. & Lücking, *S. chocoensis* Coca, Lücking & Moncada, *S. leucodontius* Coca, Gómez-Gómez, Guzmán-Guillermo & Dal Forno (MB 848881), and *S. tutunendo* Coca, Lücking & Moncada clustered in the Neotropics clade; *S. bicolor* D. Liu, Li S. Wang & Goffinet, *S. fossicolus* (Corner) D. Liu & Li S. Wang, *S. sinensis* (R.H. Petersen & M. Zang) D. Liu & Li S. Wang, and *S. yunnanensis* D. Liu, Li S. Wang & Goffinet in the Southeast Asian clade; and *S. miomboensis* De Kesel & Ertz in a well-supported Africa clade that is nested in the Asian clade (Liu et al. 2019, Coca et al. 2023).

Despite the known phylogeny, considerable morphological variation has been reported to the species of this genus (Sulzbacher et al. 2016, Liu et al. 2019), but the characters with taxonomical importance are not established and the infrageneric key is outdated. Therefore, this manuscript aims to describe specimens of *Sulzbacheromyces caatingae* collected in the *Cerrado* biome of Mato Grosso do Sul (Brazilian Midwest region), comparing them to specimens found in the Brazilian Northeast region (Sulzbacher et al. 2016), using morphological, anatomical, and molecular data. In addition, we plotted the distribution of the species with the known *S. caatingae* haplotypes and provided an infrageneric key to the known *Sulzbacheromyces* species.

MATERIALS AND METHODS

Field trips were realized during 2021/2022 in the Morro do Paxixi, municipality of Aquidauana, state of Mato Grosso do Sul, located in the Brazilian Midwest region, and all specimens collected were deposited in the herbaria of the Fundação Universidade Federal de Mato Grosso do Sul (CGMS). The location and distribution of the *S. caatingae* specimens, reported in previous studies (Sulzbacher et al. 2012, 2016), were used to build a distribution map through QGIS Buenos Aires v. 3.26. (http://www.qgis.org), using the Brazilian biomes shape file. In addition, the climatologic data were obtained in the Instituto Nacional de Pesquisas Espaciais (http://clima1.cptec.inpe.br/) and compared with the collection dates.

For the genetic analyses, DNA extractions of fresh specimens were performed using the Wizard® Genomic DNA Purification Kit (Promega), following the manufacturer's protocol. The nuITS region was amplified using the ITS1F (Gardes & Bruns 1993) and ITS4 (White et al. 1990) primers, according to the thermal cycling parameters reported in Sulzbacher et al. (2012).

The dataset was constituted by sequences of *Sulzbacheromyces* produced by Sulzbacher et al. (2012, 2016), Yanaga et al. (2015), He et al. (2016), Liu et al. (2018, 2019) and Coca et al. (2018, 2023), including the following species: *S. bicolor, S. caatingae, S. chocoensis, S. fossicolus, S. leucodontius*, *S. miomboensis, S. tutunendo, S. sinensis* and *S. yunnanensis* (Supplementary Material - Table SI). Sequences of *Lepidostroma calocerum* (KT354925 and KT354927) were used as outgroups.

The alignment was performed in Geneious v9.1.2 (Kearse et al. 2012) using the MAFFT v7.308 algorithm with standard settings (Katoh et al. 2002). GBlocks 0.91b (Talavera & Castresana 2007) was used to exclude the non-reliable aligned sites using the less stringent settings. Geneious v9.1.2 was also used to check the divergence among the *S. caatingae* nuITS sequences. Phylogenetic trees were estimated with the Bayesian inference (BA) and Maximum Likelihood (ML) approaches using the MrBayes 3.2.7a (Huelsenbeck & Ronquist 2001, Ronquist & Huelsenbeck 2003) and RaxML 8.2.12 (Stamatakis 2014), respectively, in the Cipres web portal (https://www.phylo.org/) (Miller et al. 2010).

For the Bayesian analysis (BA), the nucleotide substitution and site heterogeneity model used were TrN+I+G, following the results from the Bayesian Inference Criterion in jModelTest2 (Darriba et al. 2012, Guindon & Gascuel 2003). In MrBayes, a chain length of 10,000,000 generations sampled every 1,000 steps were settled. After discarding 25% of the first trees, the 50% majority rule consensus tree was generated. In the Maximum Likelihood analysis (ML), the GTR+G was used as the substitution model with 1,000 bootstrap replications and default settings.

FigTree v1.4.2 (http://tree.bio.ed.ac.uk/software/figtree/) was used to edit the trees and check for incongruences between the results produced by the BA and ML methods. Support values above 95 (BA) and bootstrap above 70 (ML) were considered significant for the hypotheses of phylogenetic relationships in the branches.

The material was described according to the protocol of Liu et al. (2018), performing the morphological analyses through stereomicroscope Olympus SZ40, and the anatomical study, as the thallus, basidioles, and basidiospores measures, through Zeiss light microscopy. The images were captured with a Cannon camera, model Rebel T3i, coupled to a stereomicroscope. When the characters were not reported in the description, like prothallus and pruina, we considered them absent (Table I).

RESULTS AND DISCUSSION

Five specimens of *Sulzbacheromyces caatingae* from the Morro do Paxixi, Aquidauana municipality, were collected for the first time in the Mato Grosso do Sul state. The specimens were found in exposed soil at the border of a forest fragment, with the eventual presence of cattle (Figure 1a-c); whereas the Northeast specimens were collected in the sandy soil of road banks and on termite nests, generally near the edges of well-conserved forest (Sulzbacher et al. 2012, 2016).

In the Brazilian Northeast region – about 2.000 km apart from Morro do Paxixi – *S. caatingae* was collected in different vegetal formations of the *Caatinga* and Atlantic Forest biomes, which can also include areas of transitional vegetation between savanna (*Cerrado*) and caatinga-savanna, Atlantic Forest remnants isolated within the *Caatinga* ("brejo de altitude", 400-600 m of altitude) and Atlantic Forest fragments (Sulzbacher et al. 2012, 2016); and now has been only found in the *Cerrado* biome of the Brazilian Midwest region. Therefore, the *S. caatingae* distribution overlaps the South American 'dry diagonal', corresponding to arid, dry and sub-humid regions, ranging from the Brazilian Northeast to Argentinean Northeast, including the *Caatinga*, *Cerrado,* and *Chaco* biomes (Figure 2).

The species was monitored monthly for a year in the Morro do Paxixi, remaining sterile and indistinct from the substrate most of the time, which can be an adaptation to the dry season. In

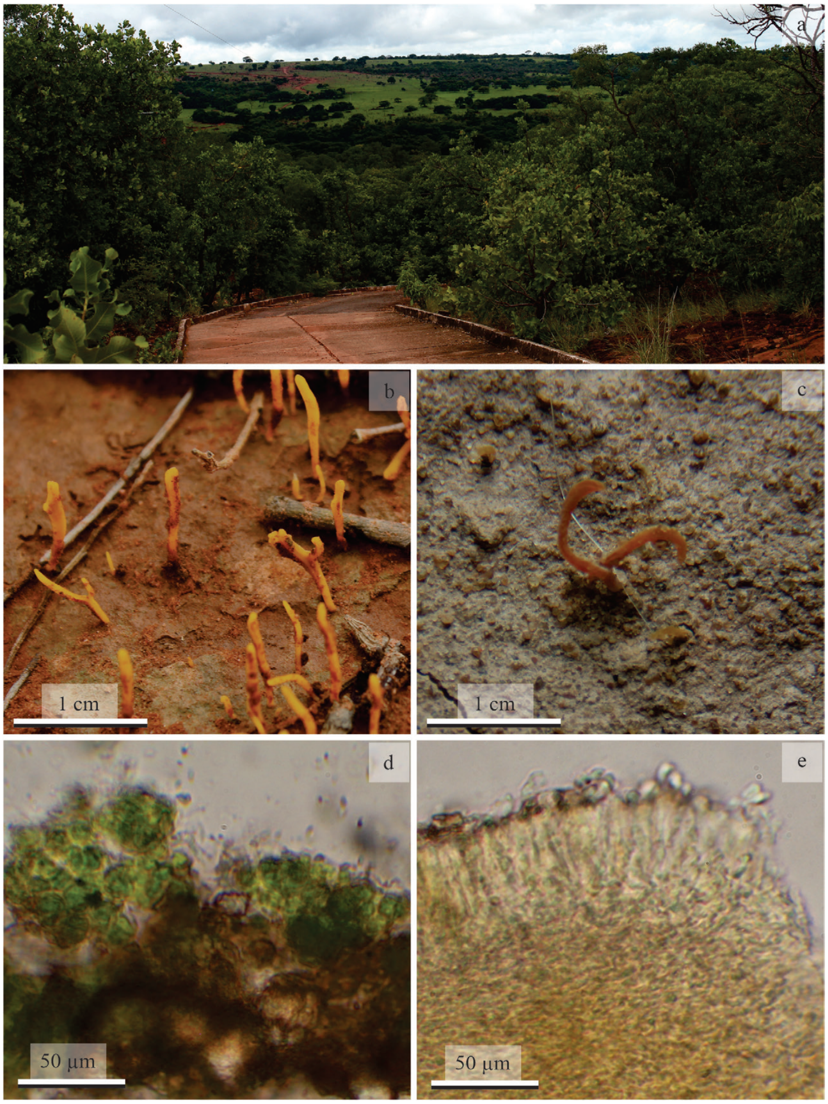

Figure 1. ***Sulzbacheromyces caatingae*** **from Mato Grosso do Sul. a. The species. b. Detail of the fresh material with branched basidioles. c. Detail of the dry material with indistinct thallus. d. Longitudinal section of the basidioles, highlighting the trama tissue. e. Detail of the basidia.**

Mato Grosso do Sul, the basidiomes persisted for one week in January 2021 and March 2022, during the summer (rainy season), after heavy rainfall, dispersing the basidiospores. Sulzbacher et al. (2012, 2016) also mentioned the collection of *S. caatingae* after heavy rainfall in the Northeast region. For instance, the specimen Wartchow 58-2013 was collected in June of 2013 in João Pessoa, with a monthly precipitation mean of 330 mm (Instituto Nacional de Pesquisas Espaciais; http://clima1.cptec.inpe.br/).

Regarding the molecular analyses, three new sequences of the *S. caatingae* nuITS region were generated and analyzed with 67 other sequences (including the outgroup), resulting in a 491 base pairs alignment (Tables SI, II).

The *Sulzbacheromyces* species were clustered with high support values, forming three main groups (Figure 3): the first with the *S. miomboensis* from Africa; the second with *S. yunnanensis*, *S. bicolor*, *S. fossicolus* and *S. sinensis* from Asia; and the third with *S. caatingae, S. chocoensis*, *S. leucodontius*, and *S. tutunendo* species from South America.

Four haplotypes, with divergence up to 1.4%, were defined among the *S. caatingae* nuITS sequences (Figure 2). Three of them were found in specimens collected in the Brazilian Northeast region (marked in blue, yellow and red): (1) GenBank accession number KC170321, (2) KC170320; and (3) KT354933, KT354934, KT354928, KT354929, KT354930, KT354931, KT354932, KT34935, KT354936, and KX431119). Haplotype 4 (marked in green) is exclusive from the Mato Grosso do Sul specimens.

Regarding the morphological and anatomical analyses, variations among the thalli and basidiomes were also found within *S. caatingae*. The thalli from Piauí, Paraíba, and Ceará present a thin green crust on the

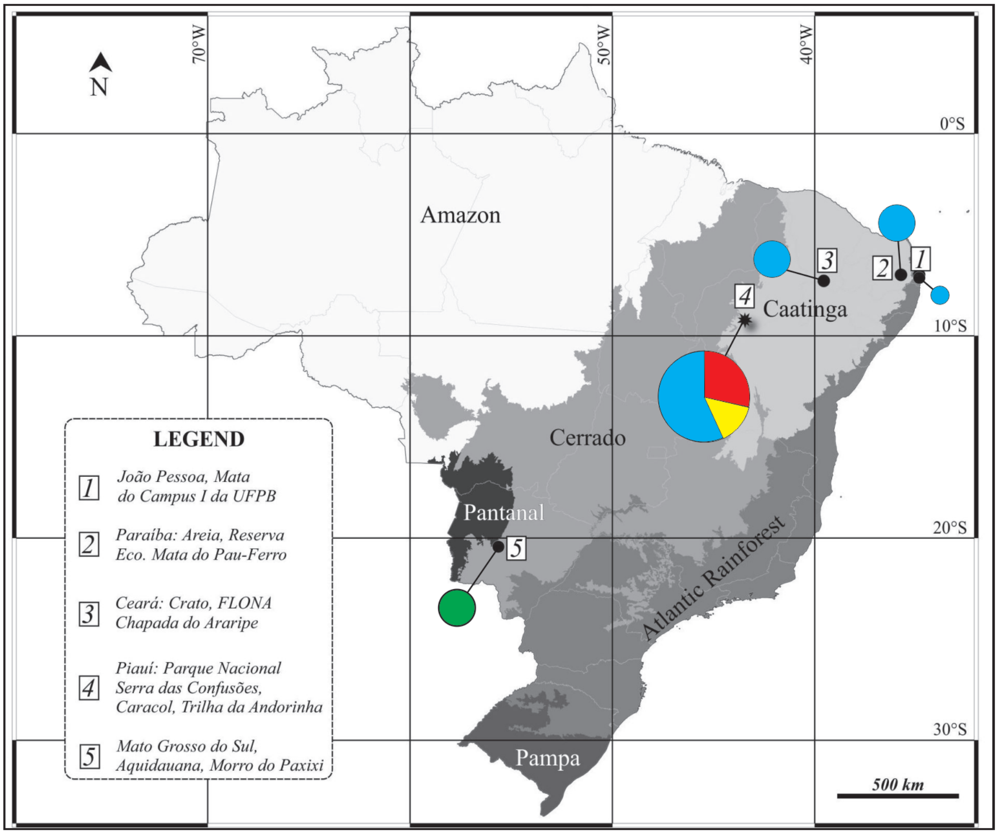

Figure 2. Geographical distribution of the *Sulzbacheromyces caatingae* haplotypes, highlighting the Brazilian biomes.

substrate (Sulzbacher et al. 2012, 2016), whereas the specimens from Mato Grosso do Sul have light green to indistinguishable from the soil. Liu et al. (2018) also reported differences among *S. yunnanensis* thalli according to habitat variation. Dark-green thallus grew in the shade and soil grooves, whereas yellow-green or light-yellow thalli were collected on exposed soil. The basidiomes are unbranched, and the trama tissue has large interspaces in specimens of the Northeast Brazil region, while the basidiomes are unbranched to rarely branched and agglutinated hyphae constitute the trama in specimens of the Midwest Brazil region. Despite the morphological variation, *S. caatingae* from Mato Grosso do Sul showed low genetic variation and the specimens are kept within the species.

Below, we provide a detailed species description and an identification key to the known *Sulzbacheromyces* species.

Taxonomy

Sulzbacheromyces caatingae (Sulzbacher & Lücking) B.P. Hodk. & Lücking, Fung. Divers. 64: 176. 2014. Figure 1a-e.

Type: Brazil, Piauí, Parque Nacional Serra das Confusões, Caracol, Trilha da Andorinha 1; 09°13'S, 43°27'W, 28. Mar. 2011, Sulzbacher 235 (Holotype: UFRS Fungos-1478; isotype: F, and UFRS Fungos-1478?); same locality, 30. Mar. 2011, Sulzbacher 237 (paratype: UFRN Fungos-1479).

Description. *Thallus* crustose, indistinct, forming a thin layer on the substrate, light green, but usually indistinguishable from the soil, slight greenish when observed under a stereomicroscope, constituted by a thin layer of chlorococcoid algae interwoven by hyphae, up to 25 µm (3–5 photobiont cells) thick; without a prothallus. Photobiont spherical, 2.5(–4.0) µm diam., smooth, prostate to the substrate, contiguous. *Basidiomes* are solid, cylindrical to flattened, simple or rarely once branched, 2.0–12.0 × 0.5–1.5 mm, yellow to yellowish orange, smooth, rarely straight, curved or sinuous; apices of basidiomes are acute to slightly flattened, acute or rounded, smooth or with denticles. Tasteless and odorless. *Trama* is composed of parallel, thin-walled hyaline hyphae, ca. 1.0–2.5 µm diam., smooth, densely agglutinated, thin-walled, with oily contents in the hyphae, globose. *Basidia* are clavate when mature, hyaline, 37.5–50.0 ×5.0–7.5 µm, thin-walled, with four fragile sterigmata, ca. 2.5 µm long, guttulate. Basidioles 25.0–40.0 × 5.0 µm, clavate, abundant. *Basidiospores* 5.0–7.5(–8.0) × 3.5–4.5 µm, 6.65 µm mean length (Lm), 3.85 µm mean width (Wm), 1.62 µm average length divided by average width (Q = L/W), 1.42–1.66(–2.28) length/width ratio of individual spores (Q'), n= 30, ellipsoid to bacilliform, thin-walled, hyaline, smooth, guttulate.

Material examined. Brazil, Mato Grosso do Sul state, Aquidauana municipality, Serra de Maracaju, Morro do Paxixi, near to mirante do Paxixi, terricolous, 20°26'32.2"S 55°37'38.1"W, ca. 500 m alt., 22 Jan 2021, leg. M.J. Kitaura & M.C. Scur 5111; Brazil, Mato Grosso do Sul state, Aquidauana municipality, Serra de Maracaju, Morro do Paxixi, near to mirante do Paxixi, terricolous, 20°26'34.7''S, 55°38'13.8''W, ca. 500 m alt., 27. Mar. 2022, Leg. M.J. Kitaura 5476, 5477, 5478 and 5479.

Distribution. Piauí (type locality), Ceará, Paraíba, and Mato Grosso do Sul.

Notes. *Sulzbacheromyces caatingae* is characterized by basidiomes yellowish orange, terete or slightly flattened, simple to rarely once branched, and crustose thallus lacking cortical layer.

An infrageneric identification key to the known *Sulzbacheromyces* species

1a. Thallus with prothallus	2
1b. Thallus without prothallus or prothallus not mentioned	3

Table II. **Information regarding *Sulzbacheromyces caatingae* specimens analyzed in the present study. In bold, the generated sequences.**

GenBank accession nº	Voucher (reference)	Location	Coordinates	Collection date
KC170320	Sulzbacher 237, UFRN-Fungos 1479, paratype, (Sulzbacher et al. 2012)	Piauí: Parque Nacional Serra das Confusões, Caracol, Trilha da Andorinha	09°13’S, 43°27’W	March 30, 2011
KC170321	Sulzbacher 235 UFRN-Fungos 1478, holotype, (Sulzbacher et al. 2012)	Piauí: Parque Nacional Serra das Confusões, Caracol, Trilha da Andorinha	09°13’S, 43°27’W	March 28, 2011
KT354928	Ovrebo 5034, UFRN-Fungos 2502, (Sulzbacher et al. 2016)	Paraíba: Areia, Reserva Ecológica Mata do Pau-Ferro,	06°59’02’’S, 35°44’64’’W	Unknown
KT354929	Sulzbacher s.n.,UFRN-Fungos 2050, (Sulzbacher et al. 2016)	Ceará: Crato, FLONA Chapada do Araripe	07°17’23.14’’S, 39°33’40.19’’W	March 03, 2013
KT354930	Sulzbacher s.n. UFRN-Fungos 2049, (Sulzbacher et al. 2016)	Ceará: Crato, FLONA Chapada do Araripe	07°17’23.14’’S, 39°33’40.19’’W	March 03, 2013
KT354931	Sousa 65, UFRN-Fungos 2051, (Sulzbacher et al. 2016)	Paraíba: Areia, Reserva Ecológica Mata do Pau-Ferro	06°59’02’’S, 35°44’64’’W,	July 17, 2013
KT354932	Wartchow 58-2013, UFRN-Fungos 2105, (Sulzbacher et al. 2016)	João Pessoa, Mata do Campus I da UFPB	07°08’37’’S, 34°50’73’’W	June 18, 2013
KT354933	Sulzbacher 235, UFRN-Fungos 1478, “isotype”, (Sulzbacher et al. 2016)	Piauí: Parque Nacional Serra das Confusões, Caracol, Trilha da Andorinha	09°13’S, 43°27’W	March 28, 2013
KT354934	Sulzbacher 235, UFRN-Fungos 1478, “isotype”, (Sulzbacher et al. 2016)	Piauí: Parque Nacional Serra das Confusões, Caracol, Trilha da Andorinha	09°13’S, 43°27’W	March 28, 2013
KT354935	Sulzbacher 237, UFRN-Fungos 1479, (Sulzbacher et al. 2016)	Piauí: Parque Nacional Serra das Confusões, Caracol, Trilha da Andorinha	09°13’S, 43°27’W	March 30, 2011
KT354936	Sulzbacher 237, UFRN-Fungos 1479, (Sulzbacher et al. 2016)	Piauí: Parque Nacional Serra das Confusões, Caracol, Trilha da Andorinha	09°13’S, 43°27’W	March 30, 2011
KX431119	Ovrebo 1881, (Sulzbacher et al. 2016)	Brazil	Unknown	Unknown
OR083399	**Marcos J. Kitaura 5476 (CGMS)**	**Mato Grosso do Sul, Aquidauana, Morro do Paxixi**	**20°26’34.7”S, 55°38’13.8”W**	**March 27, 2022**
OR083400	**Marcos J. Kitaura 5477 (CGMS)**	**Mato Grosso do Sul, Aquidauana, Morro do Paxixi**	**20°26’34.7”S, 55°38’13.8”W**	**March 27, 2022**
OR083401	**Marcos J. Kitaura 5478 (CGMS)**	**Mato Grosso do Sul, Aquidauana, Morro do Paxixi**	**20°26’34.7”S, 55°38’13.8”W**	**March 27, 2022**
NR120240	Sulzbacher 235, UFRN-Fungos 1478, “type”, (Sulzbacker et al. 2016)	Piauí: Parque Nacional Serra das Confusões, Caracol, Trilha da Andorinha	09°13’S, 43°27’W	Unknown

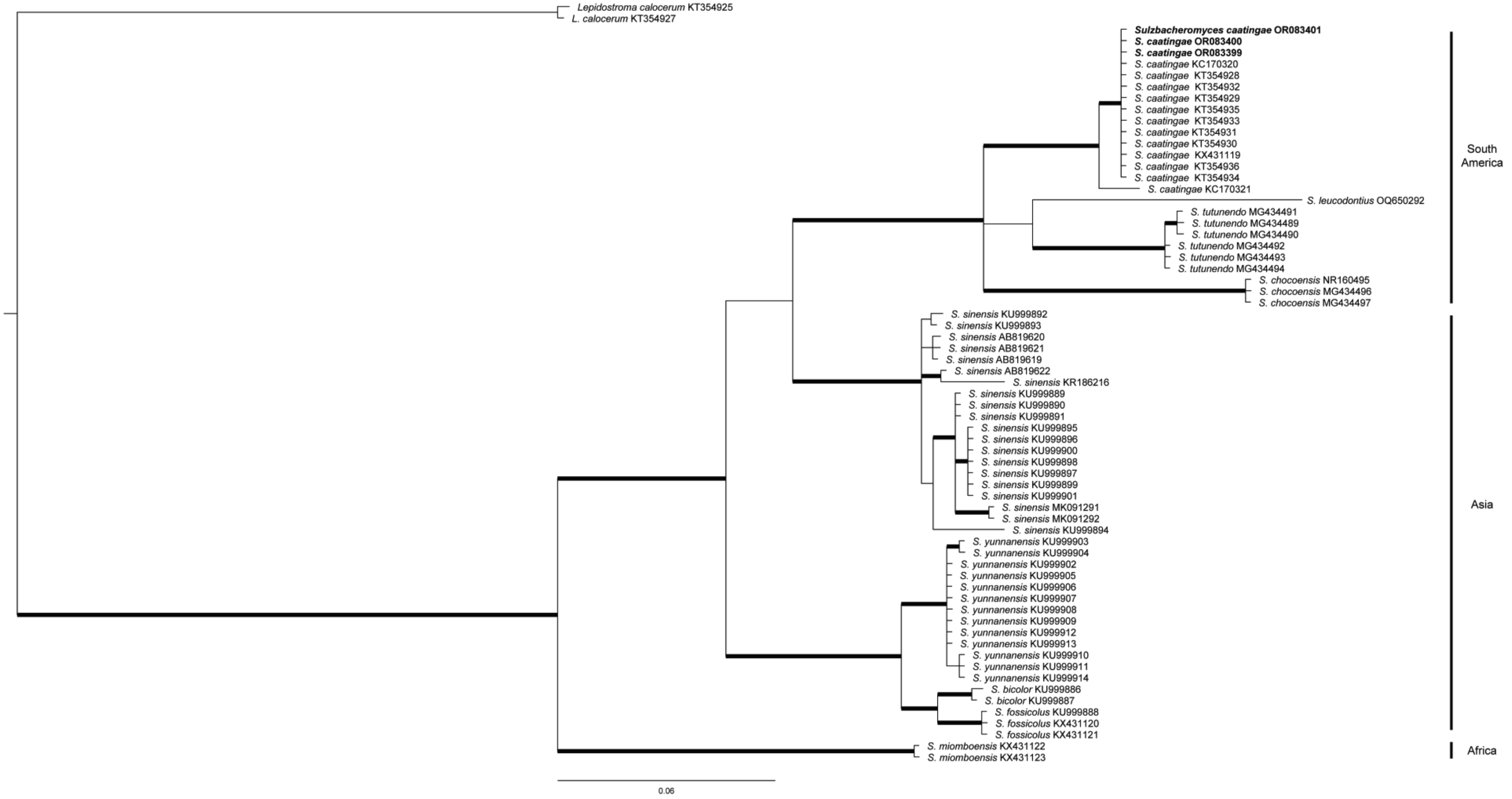

Figure 3. Phylogenetic tree of the *Sulzbacheromyces* nuITS region based on the Bayesian and Maximum Likelihood approaches. Branches in bold correspond to support values above 95 to posterior probabilities and 70 to bootstrap values and are considered significant to the phylogenetic hypothesis. *S. caatingae* in bold correspond to sequences generated in the present study.

2a. Basidiomes almost white, but grey to pale yellow at the top and white in lower portion. Type locality China, Asia. ***S. bicolor***

2b. Basidiomes orange to red-orange, turning ochraceous upon drying. Type locality China, Asia ***S. sinensis***

3a. Basidiomes pale or cream white when fresh and hydrated, beige when dried. 4

3b. Basidiomes yellowish, reddish, brownish or orangish 5

4a. Basidiomes usually twice branched at the base. Chlorococcoid algae. Type locality Singapore or Malaya, Asia ***S. fossicolus***

4b. Basidiomes unbranched. Trebouxioid algae. Type locality Colombia, South America ***S. leucodontius***

5a. Trama constituted by thigmoplect and central aeroplect tissues. Type locality Democratic Republic of the Congo, Africa ***S. miomboensis***

5b. Trama pseudoparaplectenchymatous or constituted by densely agglutinated hyphae 6

6a. Basidiomes with two longitudinal depression or grooves. Type locality China, Asia. ***S. yunnanensis***

6b. Basidiomes lacking longitudinal depression or grooves 7

7a. Basidiomes often branched above the middle. Type locality Colombia, South America ***S. tutunendo***

7b. Basidiomes simple or rarely once branched 8

8a. Crustose thallus green to indistinct to the substrate, basidiomes terete or slightly flattened, with stipe concolorous with the apex. Type locality Brazil, South America ***S. caatingae***

8b. Crustose thallus olive green, basidiomes fusiform to clavarioid, with stipe often white and apex reddish orange to yellowish when fresh. Type locality Colombia, South America ***S. chocoensis***

Acknowledgments

All the authors thank the Fundação Universidade Federal de Mato Grosso do Sul – UFMS/MEC – Brazil, where all manuscript was developed. Marcos J. Kitaura was supported in part by the Fundação Universidade Federal de Mato Grosso do Sul, Brazil (Edital UFMS/PROPP/PROGEP nº 135, de 30 de dezembro de 2021), by the Fundação de Apoio ao Desenvolvimento do Ensino, Ciência e Tecnologia do Estado de Mato Grosso do Sul (FUNDECT – Chamada 04/2019), and the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); and Jean-Marc Torres by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brazil (CAPES) - Finance Code 001".

SUPPLEMENTARY MATERIAL

Table SI.

REFERENCES

COCA LF, GÓMEZ SG, GILLERMO JG, TRUJILLO ET, CLAVIJO L, ZULUAGA A, FORNO MA & LUMBSCH HT. 2023. *Sulzbacheromyces leucodontium* (Basidiomycota, Lepidostromataceae), a new species of basidiolichen widely distributed in the Neotropics. Phytotaxa 597(2): 153-164. https://doi.org/10.11646/phytotaxa.597.2.5.

COCA LF, LÜCKING R & MONCADA B. 2018. Two new, sympatric and semi-cryptic species of *Sulzbacheromyces* (Lichenized Basidiomycota, Lepidostromatales) from the Chocó Biogeographic Region in Colombia. Bryologist 121(3): 297-306.

CORNER EJH. 1950. A monograph of *Clavaria* and allied genera. Ann Bot Mem 1: 1-740.

DARRIBA D, TABOADA GL, DOALLO R & POSADA D. 2012. jModelTest 2: more models, new heuristics and parallel computing. Nat Methods 9: 772.

GARDES M & BRUNS TD. 1993. ITS primers with enhanced specificity for basidiomycetes—Application to the identification of mycorrhizae and rusts. Mol Ecol 2: 113-118.

GUINDON S & GASCUEL O. 2003. A simple, fast and accurate method to estimate large phylogenies by maximum-likelihood. Syst Biol 52: 696-704.

HE G, WANG PR, CHEN SL & YAN SZ. 2016. An unexpected discovery of clavarioid fungi: first record of *Lepidostroma asianum* in China. Mycoscience 57: 150-155.

HODKINSON BP, MONCADA B & LÜCKING R. 2014. Lepidostromatales, a new order of lichenized fungi (Basidiomycota, Agaricomycetes), with two new genera, *Ertzia* and *Sulzbacheromyces*, and one new species, *Lepidostroma winklerianum*. Fungi Diversity 64: 165-179.

HUELSENBECK JP & RONQUIST F. 2001. MRBAYES: Bayesian inference of phylogeny. Bioinformatics 17: 754-755.

KATOH K, MISAWA K, KUMA K & MIYATA T. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucl Acids Res 30: 3059-3066.

KEARSE M ET AL. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28: 1647-1649.

LIU D, GOFFINET B, ERTZ D, DE KESEL A, WANG XY, HUR J-S, SHI HX, ZHANG YY, YANG MX & WANG LS. 2018. Circumscription and phylogeny of the Lepidostromatales (lichenized Basidiomycota) following discovery of new species from China and Africa. Mycologia 109(5): 730-748.

LIU D, WANG XY, WANG LS, MAEKAWA N & HUR JS. 2019. *Sulzbacheromyces sinensis*, an unexpected basidiolichen, was newly discovered from Korean Peninsula and Philippines, with a phylogenetic reconstruction of genus *Sulzbacheromyces*. Mycobiology 47(2): 191-199.

LÜCKING R ET AL.. 2020. Unambiguous identification of fungi: where do we stand and how accurate and precise is fungal DNA barcoding? IMA Fungus 11: 1-32.

MILLER MA, PFEIFFER W & SCHWARTZ T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: Proceedings Of The Gateway Computing Environments Workshop. New Orleans: GCE, p. 1-8.

ROBERT V, STEGEHUIS G & STALPERS J. 2005. The MycoBank engine and related databases. https://www.MycoBank.org/.

RONQUIST F & HUELSENBECK JP. 2003. MRBAYES 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572-1574.

SCHOCH CL, SEIFERT KA, HUHNDORF S, ROBERT V, SPOUGE JL, LEVESQUE CA & CHEN W. 2012. Fungal Barcoding Consortium. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. PNAS 109: 6241-6246.

STAMATAKIS A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30(9): 1312-1313.

SULZBACHER MA, BASEIA IG, LÜCKING R, PARNMEN S & MONCADA B. 2012. Unexpected discovery of a novel basidiolichen in the threatened Caatinga biome of northeastern Brazil. The Bryologist 115(4): 601-609.

SULZBACHER M, WARTCHOW F, OVREBO C, SOUSA J, BASEIA I, MONCADA B & LÜCKING R. 2016. *Sulzbacheromyces caatingae*: Notes on its systematics, morphology and distribution based on ITS barcoding sequences. The Lichenologist 48(1): 61-70.

TALAVERA G & CASTRESANA J. 2007. Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. Syst Biol 56: 564-577.

WHITE TJ, BRUNS T, LEE SB & TAYLOR JW. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In PCR Protocols (INNIS MA, GELFAND DH, SNINSKY JJ & WHITE TJ (Eds..). San Diego: Academic Press, p. 315-322.

YANAGA K, SOTOME K, SUHARA H & MAEKAWA N. 2015. A new species of *Lepidostroma* (Agaricomycetes, Lepidostromataceae) from Japan. Mycosci 56: 1-9.

How to cite

KITAURA MJ, SCUR MC, TORRES JM, LORENZ AP & LEITE EF. 2023. A new record of *Sulzbacheromyces caatingae* (Basidiomycota, Agaricomycetes) from Mato Grosso do Sul and a worldwide infrageneric identification key. An Acad Bras Cienc 95: e20220779. DOI 10.1590/0001-3765202320220779.

Manuscript received on January 12, 2022;
accepted for publication on August 23, 2023

MARCOS J. KITAURA[1]
https://orcid.org/0000-0002-2175-3533

MAYARA C. SCUR[2]
https://orcid.org/0000-0001-9425-0884

JEAN-MARC TORRES[2]
https://orcid.org/0000-0002-6703-338X

ALINE P. LORENZ[2]
https://orcid.org/0000-0002-2810-2282

MERSON F. LEITE[1]
https://orcid.org/0000-0003-2672-187X

[1]Universidade Federal de Mato Grosso do Sul,
Rua Oscar Trindade de Barros, 740, Serraria,
79200-000 Aquidauana, MS, Brazil

[2]Universidade Federal de Mato Grosso do Sul, INBIO, Av. Costa
e Silva, s/n, Universitário, 79070-900 Campo Grande, MS, Brazil

Correspondece to: **Marcos Junji Kitaura**
E-mail: junjimjk@gmail.com

Author contributions

Marcos J. Kitaura and Mayara C. Scur went on field expeditions and made the specimens collections. Marcos J. Kitaura performed the morphological and anatomical analyses and the DNA extractions. Jean-Marc Torres performed the DNA amplifications and revised the morphological analyses. Emerson Figueiredo Leite produced the map. Mayara C. Scur performed the phylogenetic analyses. Aline Pedroso Lorenz analyzed the data and provided financial support. All the authors were involved with the manuscript writing, revision, and data interpretation.