Contribution to Neotropical data of *Geastrum* section *Corollina* (Basidiomycota): Two new earth–stars from Caatinga vegetation, Brazil

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Abstract

The Caatinga is a unique phytogeographical domain of semi–arid vegetation in northeastern Brazil. Although, it includes rare and endemic birds and mammals, it is poorly represented in the Brazilian Conservation Area Network. In this paper we describe two new species of the genus *Geastrum* section *Corollina: G. caatingense* and *G. parvistellum*, based on morphological data and molecular analyses of ITS/LSU nrDNA. Species description, images, and taxonomic discussion are provided.

Keywords gasteroid fungi · Geastraceae · phylogeny · systematic · taxonomy ·

Introduction

Caatinga is a unique phytogeographical domain in Brazil, comprising about 10% of the territory of this "continental" country. The vegetation grows under semi–arid conditions, a climate unusual in a tropical region. It is mainly characterized by scarcer and concentrated rains (mean of less than 1 mm per year), mean temperature of 26–28 ºC and a high level of evapotranspiration (Prado 2003, Leal et al. 2005, Moro et al. 2016). The Caatinga includes rare and endemic taxa, but just 2% of its area is protected in conservation units (Castelletti et al. 2003).

Recently, the genus *Geastrum* has been a focus of systematic and taxonomic studies (Kasuya et al. 2012, Jeppson et al. 2013, Zamora et al. 2014). Historically the genus is considered as of subcosmopolitan distribution, and has been investigated more intensively in temperate areas (Paleartic and Neartic regions) than in tropical areas. However, this scenario has changed in the last decade, during which more than ten new species of the genus were discovered from Brazil (Fazolino et al. 2008, Silva et al. 2013, Cabral et al. 2014a, Cabral et al. 2014b, Sousa et al. 2015, Crous et al. 2016, 2017, 2018, Cabral et al. 2017).

One of the 14 sections recently proposed for the genus *Geastrum* is the section *Corollina* J.C. Zamora. It groups species with very heterogeneous morphology, mainly recognized by peristome fibrillose to irregularly plicate, basidioma frequently saccate, but rarely arched, exoperidium hygroscopic or not, mycelial layer normally not encrusting debris, rarely encrusted, endoperidial body sessile (-Zamora et al. 2014). The sect. *Corollina* is divided into three subsections: subsect. *Lageniformia* J.C. Zamora, mainly characterized by strongly delimited, fibrillose peristome, presence of horn–like crystal on rhizomorphs and mycelial layer composed of generative hyphae; *Marginata* P. Ponce de León, mainly characterized by strongly delimited fibrillose peristome, presence of acicular crystals on rhizomorphs and two sub–layers in the mycelial layer, outer layer with skeletal hyphae and inner layer with generative hyphae; and subsect. *Plicostomata* V.J. Staněk, mainly characterized by non–delimited or weakly delimited peristome, irregularly plicate, presence of acicular crystals on rhizomorphs and two sub–layers in the mycelial layer, outer layer with skeletal hyphae and inner layer with generative hyphae.

The sect. *Corollina* has some undetermined species (*Geastrum* sp.) (Zamora et al. 2014). Furthermore, there are few studies with *Corollina*' specimens from Neotropical Region, where exists high potential to found undescribed species for science (Hawksworth, 2001). Thus, the aimed of this study is to enhance the knowledge of the sect. *Corollina*, describing two news species of from Neotropical region, Brazil (Caatinga vegetation), with analyses based on morphological and molecular data.

Materials and Methods

Colletion Site and Morphological Analysis

The specimens were collected during the rainy season of 2015 in an area of Caatinga *sensu stricto* vegetation (6º36'18" S, 38º32'44" W, 273 meters above sea level), localized in the ecoregion of "Depressão Sertaneja Setentrional" (Velloso et al. 2002). Morphological studies were performed according to Sousa et al. (2014a, 2014b) with dried basidiomata at variable stages of development. Color definition was based on Kornerup & Wanscher (1978). For light microscopy (LM), slides containing basidiospores, eucapillitial, and exoperidial hyphaemounted on 5% (w/v) KOH were examined under a Nikon Eclipse Ni light microscope coupled with a Nikon DS–Ri

camera. Thirty basidiospores were measuremed at 1000 × magnification including ornamentation. Scanning Electron Microscopy (SEM) was used to observeultrastructure of basidiospores ornamentation, eucapillitium and endoperidial surfaces. Statistical measurements of basidiospores given in the descriptionfollowed Sousa et al. (2017). All analyzed samples have been deposited in the collection of the Federal University of Rio Grande do Norte, Natal, Brazil (UFRN–Fungos).

Molecular Analyses

Genomic DNA was extracted from approximately 10 mg of gleba from dried basidiomata as described in Sousa et al. (2017). Amplifications were carried out using illustraTM PureTaqTM Ready–To–GoTM PCR Beads (Healthcare, Buckinghamshire, UK) with a final volume of 25 µl. Two regions were amplified by Polymerase Chain Reaction (PCR): Internal Transcribed Spacer (ITS nrDNA), including the 5.8S of the ribosomal RNA, and Large SubUnit (LSU nrDNA), with the primer pairs ITS1F/ITS4B (White et al. 1990, Gardes & Bruns 1993) and LR0R/LR7 (Vilgalys & Herster 1990, Rehner & Samuels 1994), respectively. When amplifications were weak (less than 10 ng/ µl), nested–PCR to ITS and seminested–PCR to LSU was done using 1 µl of amplification product from the first PCR. For the nested–PCR to ITS, the primers ITS5/ITS4 were used (White et al. 1990), and for seminested–PCR to LSU, the primers LR0R/LR5 were used (Vilgalys & Herster 1990, Rehner & Samuels 1994). Before sequencing, 20 µl of the amplification products were purified using Speedtools PCR Clean–up Kit (Biotools, B & M Labs, S.A). Purified PCR products were then sequenced at Macrogen (Seoul, Korea), with the primer pairs used in the amplification.

Editing and consensus assembly of DNA sequences were performed using Sequencher v.4.1.4 (Gene Codes, Ann Arbor, Michigan, USA). Sequences were submitted to GenBank under the accession numbers indicated in Table 1. Both ITS and LSU sequences were compared with homologous *Geastrum* sequences retrieved from GenBank. The multiple alignments were optimized visually in MEGA v. 5.2 (Kumar et al. 2016). Sequences of two specimens of *Geastrum hungaricum* (MJ9317 and MJ8915) were included as outgroup. The concatenated alignment was analyzed by Maximum Parsimony (MP), using PAUP* v.4.0b10 during phylogenetic analysis. A heuristic search was performed, with branch swapping and using the TBR algorithm, with initial trees obtained by stepwise addition of random additional sequences repeated 10 times, and bootstrap (MPbs) of ten thousand replicates. A Maximum Likelihood Analysis (ML) was also carried out using RAxML in the CIPRES portal (CIPRES Science Gateway v.3.3), with GTRGAMMA as the model of evolution (Stamatakis 2014), with bootstrap (MLbs) of one thousand replicates.

Results

Molecular analyses

The concatenated dataset (ITS/LSU) included 38 specimens of *Geastrum* (36 ingroup sequences of Sect. *Corollina*, and two of *G. hungaricum* as outgroup). Seventy–two sequences were retrieved from GenBank and four were newly generated in this study (Table 1, the new sequences are shown in bold.). In MP analysis of 1643 positions, 1262 positions were constant, 140 parsimony–uninformative, and 241 were parsimony–informative. Gaps were treated as "missing data". Parsimony tree scores were identical for the eight most parsimonious trees obtained: Consistency Index (CI) = 0.5457, Retention Index (RI) = 0.7033and Homoplasy Index (HI) = 0.4543. The strict

consensus of these trees is shown in Fig. 1. The three ML consensus trees have similar topology (not shown). Bootstrap percentages (MPbs and MLbs) are indicated in Fig.1.

Morphological and phylogenetic analyses of the specimens represent two species new to science, i.e. *Geastrum caatingense* J.O. Sousa, M.P. Martín & Baseia, and *Geastrum parvistellum* J.O. Sousa, M.P. Martín & Baseia. Both are included in sect. *Corollina*. *Geastrum caatingense* grouped in subsect. *Marginata*, as a sister species of two specimens from Spain (*Geastrum* sp. 1) in Fig. 1; however this relationship is not well supported (less than 50 bootstrapsupport). *Geastrum parvistellum* grouped in subsect. *Plicostomata*, with a sequence of undetermined *Geastrum* (*Geastrum* sp. 2) in Fig. 1 from Australia (MEL 2382911) and this relationship is strongly supported by good bootstrap values (MPbs = 98, MLbs = 100).

Taxonomy

Geastrum caatingense J.O. Sousa, M.P. Martín & Baseia (Fig. 2)

MYCOBANK NO.: MB825153

Diagnosis: This species is mainly recognized by hygroscopic rays, distinctly delimited, fibrillose peristome, ephemeral mycelial layer which expose the coriaceous fibrous layer with longitudinal cracks. *Geastrum caatingense* is close to *Geastrum corollinum*, however *G. caatingense* differs by non–pruinose endoperidium, non–ephemeral mycelial layer with presence of encrustations, and larger basidiospores (5.7–6.5 × 5.2–6.2 μm). *Geastrum saccatum* is also similar to *G. caantingense*, but *G. caatingense* has hygroscopic rays, as well as an encrusted mycelial layer and a fibrous layer with longitudinal cracks.

Types: BRAZIL. Paraíba State: Triunfo, 28.II.2015, G.S. Baracho 12.180 (holotype UFRN–Fungos 2843, isotype UFRN–Fungos 2960). GenBank accession ITS = MH253884, LSU = MH253886.

Etymology: "*caatingense*" refers to the vegetation of the type locality.

Expanded basidiomata saccate, 7–14 mm high (including peristome) × 11–29 mm wide. Exoperidium splitting into 6–10 rays, revolute when fresh, involute, rolling up above the endoperidial body or planar when dry, hygroscopic; Mycelial layer pallid orange (5A3), papery, strongly encrusted with debris, peeling away in irregular patches with age; Fibrous layer white to orange white (5A2), coriaceous, with longitudinal cracks; Pseudoparenchymatous layer dark brown (6E4; 7F4), persistent when young or peeling away in irregular patches with age. Endoperidial body orange gray (6B2), brownish gray (6C2) to yellowish white (5A2), depressed globose to subglobose, 5–12 × 9–16 mm, subsessile, surface glabrous, without pruinose material. Apophysis absent or reduced, lighter color than endoperidium. Pedicel inconspicuous (< 0.5 mm high), lighter than endoperidium. Peristome finely fibrillose, distinctly delimited by orange white (5A2) line, strongly conic (up to 3.2 mm high, up to 5.2 mm diam.) lighter than endoperidium. Gleba grayish brown (6F3). Mycelial layer composed of hyaline to yellowish hyphae, 2.5–3.2 μm diam., unbranched, thick–walled (0.5–1.0 μm), surface encrusted, lumen evident. Fibrous layer composed of hyaline hyphae, 4.2–7.9 μm diam., thin–walled (0.7–1.2 μm), surface not encrusted, lumen evident. Pseudoparenchymatous layer composed of hyaline subglobose to elongated hyphal cells, 17.0–46.0 × 17.8–34.1 μm, thick–walled (0.8–1.5 μm). Endoperidium composed of interlaced hyphae. Eucapillitial hyphae yellowish, 3.8–6.7 μm wide, thin walled (0.5–0.8 μm), surface

encrusted, densely verrucose, lumen evident. Basidiospores brownish, subglobose, 5.7–6.5 × 5.2–6.2 µm [x = 6.0 ± 0.2 × 5.8 ± 0.2, Q_m = 1.04, n = 30], with ornamentation less conspicuous under LM; densely verrucose under SEM, with columnar to triangular warts (0.9–1.7 µm high), slight pointed or rounded apex, with some confluent tips; apiculus inconspicuous.

Habitat and distribution: Found in Caatinga vegetation, growing on sandy soil covered by leaf–litter.

Geastrum parvistellum J.O. Sousa, M.P. Martín & Baseia Fig. 3

MycoBank: MB825154

Diagnosis: This species is mainly recognized by small basidiomata (6–12 mm wide), sub–hygroscopic rays, encrusted mycelial layer, irregularly plicate and weakly delimited peristome. *Geastrum parvistellum* is close to *G. morganii*, however *G. parvistellum* has smaller basidiomata (6–12 mm wide), involute rays, ephemeral and encrusted mycelial layer. *Geastrum arenarium* is also a similar species to *G. parvistellum*, but *G. parvistellum* has smaller basidiomata (6–12 mm wide), non–pruinose endoperidial body, weakly delimited peristome, and larger basidiospores (4.8–6.5 × 4.8–6.3 µm).

Type: BRAZIL. Paraíba State: Triunfo, 28.II.2015, G.S. Baracho 12.181 (holotype UFRN–Fungos 2841, isotype UFRN–Fungos 2961). GenBank accession ITS= MH253885, LSU = MH253887).

Etymology: "*parvistellum*" (derived from Latin: *parvo* = small; *stella* = star) refers to the small size of the basidiomata.

Expanded basidiomata saccate to arched, 6–8 mm high (including peristome) × 6–12 mm wide. Exoperidium splitting into 5–7 involute rays, rolling up under the endoperidal body, sub–hygroscopic; Mycelial layer grayish orange (5B3), wooly, strongly encrusted with debris, persistent or peeling away in some basidiomata; Fibrous layer white (5A1), coriaceous; Pseudoparenchymatous layer brown (6E5) to dark brown (7F5), persistent, rimose. Endoperidial body orange gray (5B2), brownish orange (5C3) to dark brown (7F4), subglobose, 3–7 × 5–8 mm, sub–sessile, surface furfurcaeous. Apophysis absent. Pedicel absent or inconspicuous (< 1 mm high), lighter than endoperidium. Peristome irregularly plicate, fibrillose with age, weakly delimited, slightly depressed on the endoperidium or mammiform, concolorous or lighter than endoperidium (up to 1 mm high, up to 5.2 mm diam.) Gleba grayish brown (5F3). Mycelial layer composed of hyaline hyphae, 1.2–3.2 µm diam., thin-walled (< 0.5µm) surface encrusted, lumen evident, some clamped hyphae present. Fibrous layer composed of hyaline hyphae, 3.3–4.9 µm diam., thin–walled (0.5–0.9 µm), surface non-encrusted, lumen evident. Pseudoparenchymatous layer composed of subglobose, oval to elongated hyphae, 17.3–36.7 ×14.4–23.9 µm, thick–walled (0.4–1.2 µm). Eucapillitial hyphae brownish, sinuous, umbranched, 3.2–5.3 µm diam., thin-walled (0.5–0.9 µm), surface slight verrucose, encrusted, lumen evident. Basidiospores brownish, globose to subglobose, 4.8–6.5 × 4.8–6.3 µm [x = 5.5 ± 0.5 × 5.4 ± 0.4, Q_m = 1.02, n = 30], ornamentation less conspicuous under LM; verrucose under SEM, formed by triangular to cylindrical warts, slightly truncated, with planar to slightly pointed apex, 0.9–1.2 µm high; apiculus inconspicuous.

Habitat and distribution: Found in Caatinga vegetation, growing on sandy soil covered by leaf–litter.

Discussion

Geastrum caatingense is morphologically very similar to species of subsect. *Marginata*, and our phylogenetic analyses confirm the placement of the species in this subsection. *G. caatingense* is related to *G. corollinum* (Batsch) Hollós and *G. diosiae* J.C. Zamora, both have saccate basidiomata, very well delimited peristome, and hygroscopic rays; however, these two species have smaller basidiospores (4.5–5 µm diam. in *G. corollinum* and 4–5 µm diam. in *G. diosiae*) (Sunhede 1989, Crous et al. 2015). Moreover, *G. corollinum* has a pruinose endoperial body, and ephemeral mycelial layer without encrustations in contrast to *G. caatigense*; and *G. diosiae* has sessile and pruinose endoperial body, and absence of longitudinal cracks on the fibrous layer (Sunhede 1989, Crous et al. 2015).

Geastrum flexuosum (L.S. Domínguez & Castellano) Jeppson & E. Larss. and *Geastrum saccatum* Fr. are phylogenetic close to *G. caatingense*. Nevertheless, the morphology could clearly *G. flexuosum,* because it has hypogeuos sequestrate basidiomata (Jeppson et al. 2013); while G. *saccatum* is distinct to *G. caatingense* by non-hygroscopic rays, absence of longitudinal cracks on the fibrous layer and non-encrusted mycelial layer (Sunhede 1989) (Table 2).

Another species with morphology similar to *G. caatingense* is *G. hungaricum* Hollós. Although these species are phylogenetic distant (*G. hungaricum* is grouped in *Geastrum* section), both have involute rays, distinct delimited peristome, mycelial encrusted and palling away with age. However, *G. hungaricum* has strongly hygroscopic rays, a pseudoparenchymatous layer with thicker walled hyphal cells (> 1.5 µmick vs upto 1.5 µm), and basidiospores with smaller ornamentation (up to 0.7 µm vs up to 1.7 µm) (Sunhede 1989, Zamora et al. 2015).

The phylogenetic analyses showed *Geastrum parvistellum* grouped in subsect. *Plicostomata* with *Geastrum morganii* Lloyd and *Geastrum violaceum* Rick. These three species have irregularly plicate peristome with delimitation weak or absent. On the other hand, *G. violaceum* is easily distinct to *G. parvistellum* by its endoperidium and exoperidium color, purple to violet, and smaller basidiospores (2.7–3.1 µm diam.) (Sousa et al. 2014a); while *G. morganii* is distinct to *G. parvistellum* by mycelial layer persistent, non-encrusted, revolute rays and larger basidiomata (9−28 mm wide) (Sousa et al. 2014b) (Table 2).

In the section *Corollin*a, another species are similar to *G. parvistellum*, as *G. corollinum*. But, *G. corollinum* has a pruinose endoperidium, distinctly delimited peristome, ephemeral mycelial layer without encrustations and smaller basidiospores (4–5 µm) (Sunhede 1989, Kuhar et al. 2012). *Geastrum lageniforme* and *G. saccatum* could also recall *G. parvistellum*, however, these two species differ from *G. parvistellum* due to absence of encrustations on the mycelial layer and distinctly delimited peristome (Sunhede 1989). Additionaly, *Geastrum saccatum* var. *parvulum* Speg. is similar to *G. parvistellum*, mainly due to the small size of the basidiomata (15–20 mm wide). However, *G. saccatum* var. *parvulum* is distinct by having non-hygroscopic rays, sessile endoperidial body and smaller basidiospores (3–5 µm diam.) (Dios et al. 2017).

Although the phylogenetic analyses showed that *G. parvistellum* belongs to subsect. *Plicostomata,* morphologically it is very similar to *Geastrum arenarium* Loyd. (sect.

Geastrum); both have an encrusted mycelial layer, semi–hygroscopic rays and subsessile endoperidial body. Nevertheless, *G. arenarium* has larger basidiomata (15–30 mm wide), a pruinose endoperidial body, distinctly delimited peristome and smaller basidiospores (up to 4 μm diam.) (Bates 2004, Kuhar et al. 2012).

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418 Table 1. *Geastrum* species included in the molecular analyses with their country,
419 collection number and GenBank accession numbers of internal transcribed spacer (ITS)
420 and large subunit (LSU) of nuclear ribosomal DNA. The new sequences in bold.

Species	**Locality**	**Collection number**	**GenBank accession number**	
			ITS	**LSU**
Geastrum caatingense sp. nov**.**	Brazil	UFRN–Fungos 2843	**MH253884**	**MH253886**
Geastrum corollinum	Sweden	MJ2322	KC581972	KC581972
	Spain	MA–Fungi 5746	KF988359	KF988481
	Sweden	Herb. Sunhede 7744	KF988360	KF988482
Geastrum diosiae	Argentina	MA–Fungi 83788	KF988452	KF988587
	Argentina	Ma–Fungi 83789	KF988453	KF988588
Geastrum flexuosum	Sweden	UPS F–119844	KF988371	KF988493
Geastrum lageniforme	Spain	Herb. Zamora 207	KF988388	KF988513
	Spain	Herb. Zamora 316	KF988339	KF988514
	Slovakia	MJ7337	KC581966	KC581966
Geastrum aff. *lageniforme*	Argentina	MA–Fungi 83768	KF988389	KF988516
	Niger	COFC Hama 327	KF988390	KF988517
	Argentina	MA–Fungi 83770	KF988391	KF988518
	Argentina	MA–Fungi 83769	KF988392	KF988519
	Portugal	MA–Fungi 78398	KF988393	KF988520
	Spain	Herb. Ribes 221210–01	KF988394	KF988521
Geastrum morganii	Canada	Herb. Lebeuf HRL0177	KF988406	KF988534
	France	MJ8422	KC581971	KC581971
Geastrum aff. *morganii*	Spain	Herb. Zamora 525	KF988408	KF988536
	Spain	Herb. Zamora 367	KF988407	KF988535
	Argentina	MA–Fungi 83772	KF988409	KF988537
	Argentina	MA–Fungi 83773	KF988410	KF988538
Geasrtum parvistellum sp. nov.	Brasil	UFRN–Fungos 2341	**MH253885**	**MH253887**
Geastrum cf. *saccatum*	Argentina	MA–Fungi 83775	KF988427	KF988555
	Bolivia	MA–Fungi 47185–2	KF988426	KF988554
	Australia	Herb. Sunhede 7749	KF988343	KF988556
	Japan	UPS F–530056	KF988428	KF988558
	Argentina	MA–Fungi 83778	KF988433	KF988563
	Niger	COFC Hama 343	KF988432	KF988562
	Spain	Herb. Zamora 260	KF988430	KF988560
Geastrum sp.1	Spain	MA–Fungi 31143	KF988454	KF988589
	Spain	MA–Fungi 37546	KF988455	KF988590
Geastrum sp.2	Australia	MEL 2382911	KP012780	KP012780
Geastrum sp.3	Australia	TNS KH–AUS10–74	JN845177	JN845301
Geastrum violaceum	Argentina	BAFC 51671	KF988450	KF988585
	Argentina	MA–Fungi 82487	KF988451	KF988586
Outgroup				
Geastrum hungaricum	Hungary	MJ8915	KC581963	KC581963
	Slovakia	MJ9317	KC581964	KC581964

421 Table 2

422 Comparative table with morphologic characteristics from species of section *Corollina.*

	Section Corollina								
	Subsec. *Plicostomata*			**Subsec. *Marginata***					**Subsec. *Lageniformia***
	G. morganii	***G. parvistellum***	***G. violaceum***	***G. caatingense***	***G. corollinum***	***G. diosiae***	***G. saccatum***	***G. flexuosum***	***G. lageniforme***
Basidiomata wide (mm)	9−28	6–12	9–26	11–29	11–30	5–14	8–44	20–40	15–44
Exoperidium	non-hygroscopic	sub- hygroscopic	non-hygroscopic	hygroscopic	strongly hygroscopic	strongly hygroscopic	non-hygroscopic	non-hygroscopic	non-hygroscopic
Mycelial layer	non-encrusted, pesistent	encrusted, rarely non-peristent	non-encrusted, pesistent	encrusted, rarely non-peristent	non-encrusted, ephemeral	encrusted, normally non-peristent	non-encrusted, persistent, rarely with with longitunidal cracks	encrusted, peristent	non-encrusted, persistent, with longitunidal cracks
Endoperidium suface	with protruding hyphae	furfuraeous	glabrous	glaborus	pruinose	glabrous or incospicuous pruinose	glabrous	reduced or lacking	glabrous
Pedicel	absent	inconspicuous (< 0.5 mm high)	absent	absent or inconspicuous (< 1 mm high)	absent or inconspicuous	absent	absent	absent	absent
Peristome	irregularly plicate	irregularly plicate	irregularly plicate	fibrillose	fibrillose	fibrillose	fibrillose	absent	fibrillose
Peristome delimitation	absent	absent or weak	absent	distinct	distinct	distinct	distinct	absent	distinct
Basidiopores size (-μm diam.)	4.5–6	4.8–6.5	2.7–3.1	5.2–6.5	4.5–5	4–5	4.5–6	4–5	4.5–5

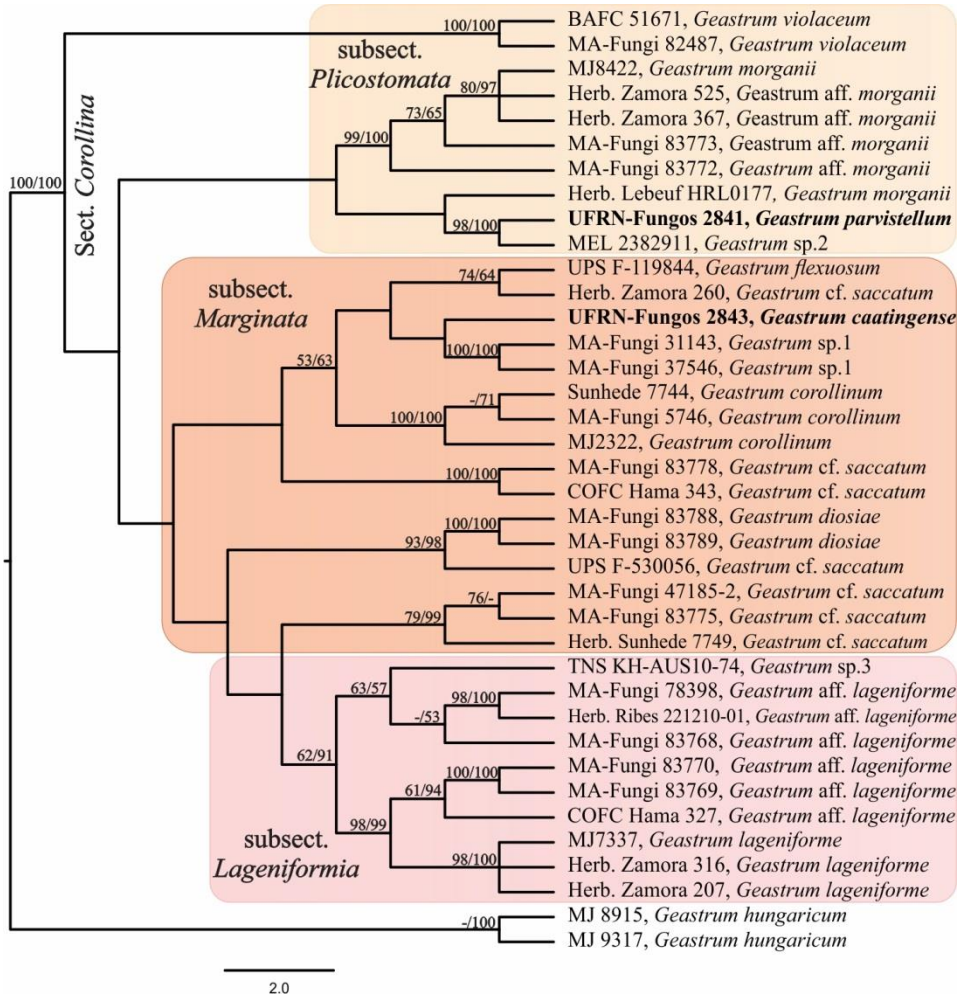

Fig. 1. Strict consensus tree of the eight most parsimonious trees of concatenated ITS and LSU nrDNA sequences of *Geastrum* indicated in Table 1. Numbers over branches are parsimony bootstrap (MPbs) and maximum likelihood bootstrap (MLbs) values. Holotypes of the new species here described are indicated in bold. Locality, collection numbers, and GenBank codes are indicated in Table 1.

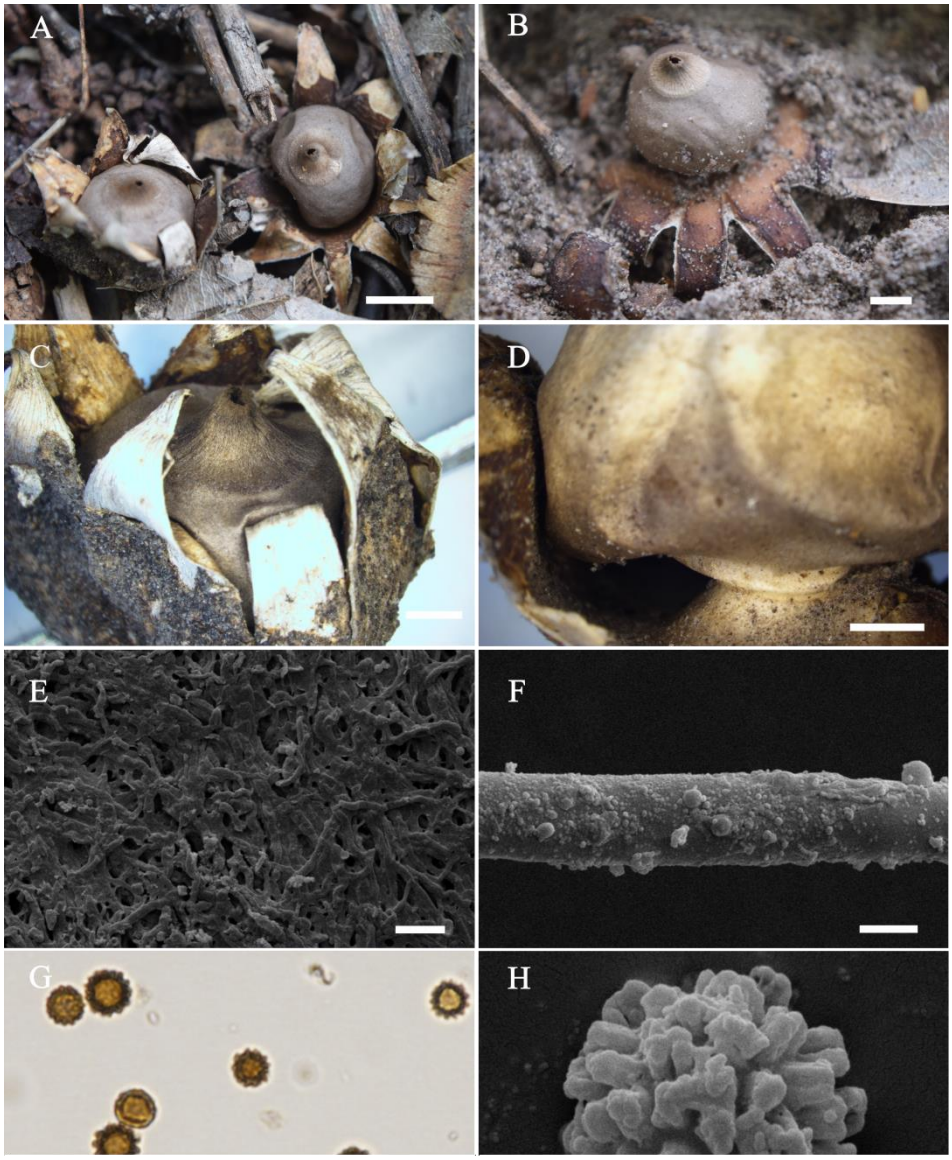

Fig. 2. *Geastrum caatingense* sp. nov. A. Fresh basidiomata *in situ* (UFRN–Fungos 2843, holotype). B. Fresh basidioma *in situ*. C (UFRN–Fungos 2960, isotype). Peristome detail. D. Endoperidial body detail. E. Endoperidium surface under SEM. F. Eucapillitialy hypha under SEM. G. Basidiospores under LM. H. basidiospore under SEM. Scale bars: A–B = 5 mm, C–D = 2 mm, E = 20 µm, F = 2 µm, G = 10 µm, H = 1 µm.

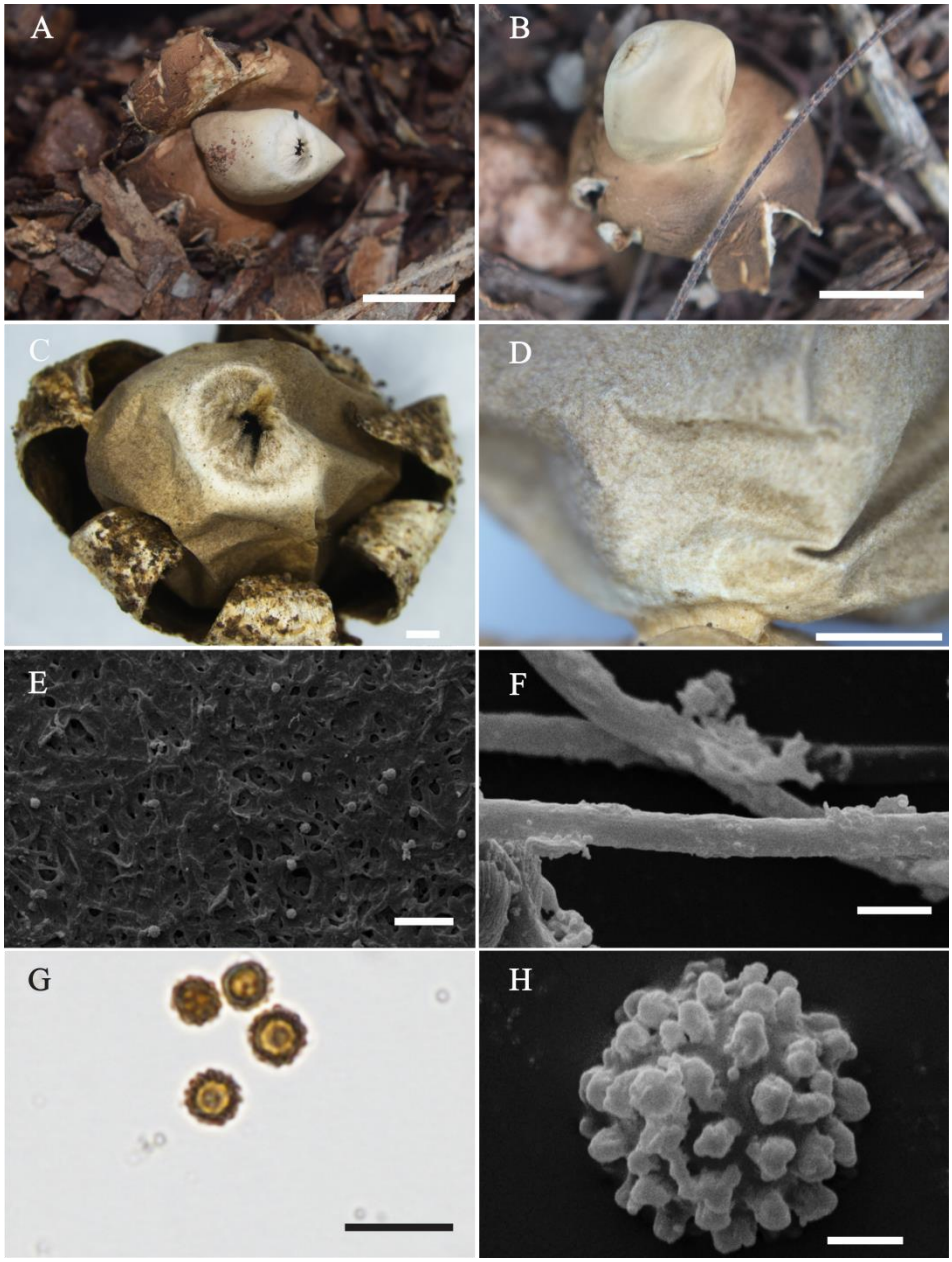

Fig. 3. *Geastrum parvistellum* sp. nov. A. Fresh basidioma *in situ* (UFRN–Fungos 2841, holotype). B. Fresh basidioma *in situ* (UFRN–Fungos 2961, isotype). C. Peristome detail. D. Pedicel detail. E. Endoperidium surface under SEM. F. Eucapillitial hyphae under SEM. G. Basidiospores under LM. H. Basidiospore under SEM. Scale bars: A–B = 5 mm, C–D = 1 mm, E = 20 µm, F = 2 µm, G = 10 µm, H = 1 µm.