**Fulvifomes nonggangensis** and *F. tubogeneratus* (Hymenochaetales, Basidiomycota): Two New Species from Southern China Based on Morphological and Molecular Evidences

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**ABSTRACT**

Two new species of *Fulvifomes* are described from specimens collected in rainforests of Nonggang Nature Reserve of southern China, based on morphological characteristics and molecular phylogenetic analysis of the internal transcribed spacer (ITS) and nuclear large subunit ribosomal DNA (nLSU) sequences. *Fulvifomes nonggangensis* sp. nov. is characterized by perennial, sessile and solitary basidiocarps, planulate pileus, small cystidioles of 9.9–15.4 × 2.9–3.5 μm, large pores of 5–6 per mm, a dimitic hyphal system, and broadly ellipsoid basidiospores of 4.3–5.3 × 3.3–4.2 μm. *F. tubogeneratus* sp. nov. is characterized by perennial, sessile, and imbricate basidiocarps, a duplex context, small pores of 7–8 per mm, a dimitic hyphal system, and ovoid to subglobose basidiospores of 5.72 × 5.00 μm.

**1. Introduction**

Most species in the family Hymenochaetaceae were of medicinal value, while some were plant pathogens causing a white rot [1–3]. *Fulvifomes* Murrill was established by Murrill in 1914 and typified with *F. robiniae* Murrill to accommodate species with perennial and sessile basidiocarps, sulcate surface, ungulate or appinate pilei and smooth, ferruginous or fulvous spores in the family Hymenochaetaceae [4]. *Fulvifomes* comprises 28 species according to Index Fungorum (http://www.indexfungorum.org/Names/Names.asp, accessed on 2020/10/27). *Fulvifomes* was considered as a synonym of *Phellinus* Quéhl for several decades by Ryvarden and other mycologists [5–8], until Wagner and Fischer [9] provided evidence to confirm *Fulvifomes* as an independent generic rank within Hymenochaetaceae based on molecular phylogenetic analyses. Furthermore, the genus *Aurificaria*, represented by *Aurificaria lutceoumbrina*, was very close to *Phylloporia* and *Fulvifomes* reflected by the phylogenetic trees. Zhou [10] re-delimited the circumscription of *Fulvifomes* based on phylogenies inferred from nuclear large subunit ribosomal DNA (nLSU) and internal transcribed spacer (ITS) regions. Hattori et al. [11] also provided the key to worldwide species of *Fulvifomes*. Recently, still several new species were included within *Fulvifomes* [12–15].

During the macrofungal diversity survey in southern China, two additional undescribed species of *Fulvifomes* were found and identified as new by morphological characteristics and phylogenetic analysis inferred from the ITS and nLSU regions.

**2. Materials and methods**

**2.1. Morphological studies**

Specimens in this study were deposited in the herbarium of Guangxi University (GXU). The method of microscopic procedure followed Dai [2]. Special color definition followed Ridgway [16]. Sections were studied at magnification up to ×1500 using a Nikon Eclipse 80i microscope (Nikon Corporation, Tokyo, Japan). Abbreviations were used in text: IKI: Melzer’s reagent; IKI−: negative in Melzer’s reagent; KOH: 5% potassium hydroxide; CB: cotton blue; CB+: cyanophilous; CB−: acyanophilous; L: mean spore length (arithmetic average of all spores); W: mean spore width (arithmetic average of all spores); Q: variation in the L/W ratios between the specimens studied; n: number of spores measured from given number of specimens.
2.2. DNA extraction, PCR, and sequencing

DNA extraction followed the protocol of conventional cetyl trimethylammonium bromide (CTAB) method. Nuclear ITS and nLSU regions were amplified with primer pairs ITS5/ITS4 [17] and LR0R/ LR5 [18]. The PCR products were directly purified and sequenced by Beijing Genomics Institute (BGI; Shenzhen, China). PCR procedure was followed as: initial denaturation at 94 °C for 5 min, followed by 30 cycles at 94 °C for 40 s, 56 °C for 40 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min.

2.3. Phylogenetic analysis

In this study, eight new sequences were generated and additional sequences were obtained from GenBank are listed in Table 1. The ITS datasets and additional sequences were obtained from Fomitiporella inermis with Clustalx version 1.83 (Information Retrieval, London, England) [20], respectively. Sequence alignment was deposited at TreeBASE (Study Accession URL: http://purl.org/phylo/treebase/phylows/study/TB2:S26455) and was executed by paupwin32_4b4a (Sinauer Associates, Sunderland, MA, USA) [21], MrMtgui version 1.0 (http://www.genedrift.org/mtgui.php) and MrModeltest version 3.2.2 (University of Rochester, NY, USA) [22, 23] to find the best-fit model for further analysis: MrBayesian analyses were performed by MrBayes version 3.2.2 (University of Rochester, NY, USA) [24] with 5,000,000 generations. Phylogenetic tree of maximum parsimony analyses which performed in PAUP* version 4.0b4a (Sinauer Associates, Sunderland, MA, USA) was generated using tree-bisection reconnection (TBR) branch-swapping algorithm, clade robustness was assessed using a bootstrap (BT) analysis with 1000 replicates. Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated. Phylogenetic trees were edited by TreeGraph version 2.3.0-425 beta (BioMed Central, London, England) [25].

Algorithms of two phylogenetic analyses generated nearly congruent topologies for each dataset, only the topology from the MP analysis was presented along with statistical values from the MP and BI algorithms (BS not less than 50% and BPP not less than 0.5) at the nodes.

3. Results

3.1. Phylogenetic analysis

The ITS dataset included sequences from 47 fungal specimens representing 27 taxa. The consensus tree is shown in Figure 1 (TL = 1200, CI = 0.6550, RI = 0.8488, RC = 0.5560, and HI = 0.3450). Best model for the ITS dataset estimated and applied in the Bayesian analysis: HKY + I + G, Lset nst = 2 rates = invgamma, Prset statefreqpr = dirichlet (1,1,1,1). The average standard deviation of split frequencies of Bayesian analysis is 0.004929. Tree topology of the maximum parsimony analysis showed almost same as the tree from Bayesian analysis. The phylogeny based on the ITS dataset (Figure 1) showed that the new species Fulvifomes tubogeneratus clustered with a sequence of F. XHJ-2018b Dai 9642 up to a higher support (BS = 100, BPP = 1.00), then they clustered with F. siamensis to form a small group which evidently fell into the core of Fulvifomes clade; new species F. nonggangensis clustered with F. XHJ-2018b Dai 17470 up to a higher support (BS = 100, BPP = 1.00), then they also clustered with Inonotus rigidus up to a higher support (BS = 100, BPP = 1.00) to form another small group but did not fall into the core of Fulvifomes clade.

The ITS + nLSU dataset included sequences from 38 fungal specimens representing 20 taxa. The consensus tree is shown in Figure 2 (TL = 1613, CI = 0.6820, RI = 0.8400, RC = 0.5729, and HI = 0.3180). Best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis: GTR + I + G, Lset nst = 6 rates = invgamma, Prset statefreqpr = dirichlet (1,1,1,1). The average standard deviation of split frequencies of Bayesian analysis is 0.003023. Tree topology of the maximum parsimony analysis showed almost same as the tree from Bayesian analysis.

In the phylogeny inferred from the ITS + nLSU dataset (Figure 2), F. tubogeneratus fell into the core of Fulvifomes clade, similarly to the phylogeny inferred from the ITS dataset, F. tubogeneratus clustered with F. XHJ-2018b Dai 9642 and Dai 10809 up to a higher support (BS = 100, BPP = 0.98), and then clustered with F. siamensis to form a small group; meanwhile, F. nonggangensis clustered with F. XHJ-2018b Dai 17203 and Dai 17470 with a higher support (BS = 100, BPP = 1.00), then they also grouped with F. rhyliphloeus with high support (BS = 99, BPP = 1.00).

3.2. Taxonomy

Fulvifomes nonggangensis F.C. Huang, H.F. Zheng & Bin Liu, sp. nov. (Figures 3 and 4). MycoBank: MB835790
Table 1. Information for sequences used in this study.

| Species                        | Geographic origin | Strain no. | GenBank accessions |
|-------------------------------|-------------------|------------|--------------------|
| Fulvifomes elaeodendri        | South Africa      | CMW47808   | MH599093, MH599131 |
| Fulvifomes elaeodendri        | South Africa      | CMW47909   | MH599096, MH599132 |
| Fulvifomes fastuosus          | Thailand          | LWZ 20140801-1 | KR905675 |
| Fulvifomes fastuosus          | Viet Nam          | Dai 18292  | MH390411,          |
| Fulvifomes fastuosus          | Philippines       | CBS 213.36 | AY558615, AYO59057 |
| Fulvifomes fastuosus          | Viet Nam          | Dai 18292  | MH390411, MH390381 |
| Fulvifomes grenadensis        | USA                | JV1212 2 J | KX906756,          |
| Fulvifomes grenadensis        | Costa Rica        | 1607 66    | KX906758,          |
| Fulvifomes grenadensis        | Brazil             | JRF74      | MH480907, MH48087  |
| Fulvifomes grenadensis        | Brazil             | PH6        | MH48096, MH48086   |
| Fulvifomes hainanensis        | China              | Dai 11573  | KC879263, JX866779 |
| Fulvifomes imbricatus         | Thailand           | IFP LWZ 20140728-16 | NR_154003, NG_686762 |
| Fulvifomes imbricatus         | Thailand           | LWZ 20140729-26 | KR905679, KR905671 |
| Fulvifomes imbricatus         | Thailand           | MRN6399    | KX76747,           |
| Fulvifomes indicus            | Zimbabwe           | O 25034    | KC87926,           |
| Fulvifomes kawakami           | Brazil             | PPT152     | MH48095,           |
| Fulvifomes krugiodendri       | USA                | JV1008 21  | KX906761, KX906756 |
| Fulvifomes krugiodendri       | USA                | JV9064.1   | MH390411,          |
| Fulvifomes nonggangensis      | Brazil             | 3028       | MH390431,           |
| Fulvifomes nonggangensis      | China              | GXU1127    | MT571504, MT571502 |
| Fulvifomes nonggangensis      | China              | GXU2254    | MT571503,           |
| Fulvifomes nonggangensis      | Thailand           | STRX52     | JX104703, JX104755 |
| Fulvifomes nonggangensis      | Viet Nam           | Dai 18309  | MH390389,           |
| Fulvifomes XHJ-2018b          | China              | Dai 17203  | MH390419, MH390397 |
| Fulvifomes XHJ-2018b          | China              | Dai 17470  | MH390418, MH390395 |
| Fulvifomes XHJ-2018e          | USA                | JV 0904/65 | MH390422,           |
| Fulvifomes XHJ-2018e          | USA                | JV 0312/23.1 | MH390423,          |
| Fulvifomes XHJ-2018e          | USA                | JV 0904/76 | MH390424,           |
| Fulvifomes XHJ-2018h          | China              | Dai 9642   | MH390429, MH390379 |
| Fulvifomes XHJ-2018h          | China              | Dai 10809  | MH390428, MH390378 |
| Fulvifomes XHJ-2018i          | USA                | JV 0904/68 | MH390408,           |
| Fulvifomes XHJ-2018i          | USA                | JV 1109/77 | MH390409,           |
| Fulvifomes XHJ-2018i          | China              | Dai 17911  | MH390405,           |
| Fulvifomes XHJ-2018i          | China              | Dai 17917  | MH390406,           |
| Fulvifomes squamosus          | Peru                | CS385      | MF479268, MF479265 |
| Fulvifomes squamosus          | Peru                | CS456      | MF479267, MF479266 |
| Fulvifomes thailandicus       | Thailand           | IFP LWZ 20140731-1 | NR154002,          |
| Fulvifomes thailandicus       | Thailand           | LWZ 20140731-1 | KR905672, KR905665 |
| Fulvifomes tubogeneratus       | China              | GXU2468    | MTS580805, MTS580800 |
| Fulvifomes tubogeneratus       | China              | GXU2478    | MTS580806, MTS580801 |
| Fulvifomes yorou               | Benin              | OA80097    | MN017126, MN017120 |
| Fomitiporella inermis         | USA                | JV 1109/19 A | KX181304,         |
| Fomitiporella inermis         | USA                | JV 1009/56 | KX181306, KX181347 |
| Fomitiporella inermis         | USA                | JV 0509/57 K | KX181305, KX181346 |
| Fomitiporia tsugina           | USA                | TOL2-1     | KCS51821, KCS51845 |
| Fomitiporia tsugina           | USA                | TOL2-3     | KCS51823, KCS51845 |
| Inonotus porrectus            | CAV-30             | HQ589219   |                    |
| Inonotus porrectus            | CAV-31             | HQ589220   |                    |
| Inonotus rigidus               | China              | Cui 8588   | KX674579, KX674580 |
| Inonotus rigidus               | China              | Cui 8465   | KX674580,          |
| Onnia tomentosa               | Canada             | Bud-551-C1 | JX110072, JX110116 |
| Phellinus merrilli            | USA                | PM950703-1 clone 2 | EU053531 |
| Phellinus merrilli            | USA                | PM950703-1 clone 3 | EU053532 |
| Phellinus robiniae            | USA                | CBS 211.36 | AY558646, AYO59038 |
| Phellinus robiniae            | USA                | CFMR2693   | KX065961, KX065995 |
| Phellinus robiniae            | USA                | CFMR2735   | KX065962, KX065996 |
| Phellinus piptadeniae         | Brazil             | MF008      | KPI42289,          |
| Phellinus piptadeniae         | Brazil             | MF027      | KPI42291,          |
| Phellinus piptadeniae         | Brazil             | MF034      | KPI42295, KPI42276 |
| Phellinus piptadeniae         | Brazil             | MF036      | KPI42297,          |
| Phellinus piptadeniae         | Brazil             | MF038      | KPI42299, KPI42278 |
| Phylloporia ephedrae          | Turkmenistan       | 13690      | MH151184,          |
| Phylloporia gutta             | China              | Cui6945    | MH151184,          |
| Phylloporia gutta             | China              | Cui6945    | MH151184,          |
| Tropicoporus bohmeriae        | Thailand           | LWZ 20140729-10 | KT23640,          |
| Tropicoporus bohmeriae        | Thailand           | LWZ 20140729-13 | KT23641,          |

Etymology: *nonggangensis* (Lat.): referring to the locality of the type specimen.

Type: China, Guangxi Autonomous Region, Chongzuo, Longzhou County, Nonggang Nature Reserve, on living trunks of angiosperm tree, September 19 2012, GXU1127 (Holotype in GXU).

rDNA sequences ex holotype: MT571504 (ITS), MT575102 (nLSU).
Description: Basidiocarps perennial, sessile, solitary, occasionally smaller pileus fused along adjacent margins with other, broadly attached on living trunk, and old fruit body also found on dead trunk, without odor or taste, woody hard. Pileus applanate, of old fruit body (4–5 years) projecting up to 11.1 cm, 14.1 cm wide, and 6.4 cm thick at base. Pileal surface capucine orange, orange to amber brown when fresh, capucine yellow to orange at the actively growing part, orange to antique brown, argus brown when dry, densely tomentose, up to 0.1 cm thick, rough, nodulose, separated by a dense black line tissue from context, concentrically sulcate indistinct to distinct, part of tomentum becoming thinner, nodulose less, and sulcate zone more distinct with age, margin capucine yellow to orange when fresh and capucine orange to raw sienna when dry, obtuse. Pilei of old basidiocarps (4–5 years) argus brown, raw umber to almost black, concentrically sulcate zone distinct, margin narrow, and each year re-expanding from the position beneath the margin forming by previous year, making peripheral part usually looked like slowly descending ladders, and the periphery also radially cracked. Context up to 2.8 cm thick, apricot yellow to orange citrine, woody hard, occasionally a few black line tissues randomly distributed in context. Context of old basidiocarps (4–5 years) up to 1.5 cm thick, carob brown to chestnut brown, and its tomentum becoming a thin layer. Tube layers capucine orange, orange to argus brown, woody hard, not

Figure 1. Phylogenetic tree was generated using maximum parsimony analyses based on ITS sequences. Bootstrap values (before the/) higher than 50% and Bayesian posterior probabilities (after the/) more than 0.50 are indicated along the branches.
stratified, or indistinct, up to 4.9 cm thick. Pores surface shining, raw sienna to antique brown when fresh, orange, argus brown to medal bronze when dry, sterile margin absent or narrow. Pores surface of old basidiocarps (4–5 years) orange citrine to medal bronze; sterile margin narrow to 2.8 mm width. Pores circular to angular, 5–6 per mm; dissepiments thin to thick, entire or some lacerate on margin.

Hyphal system dimitic, generative hyphae simple septate, tissue darkening in KOH, unchanged in Melzer’s reagent.

Generative hyphae from tomentum hyaline, thin-walled, frequently branched with simple septate, 1.6–3.8 μm in diam. Skeletal hyphae from tomentum yellow to brown, thick-walled with a wide to narrow lumen, occasionally branched, simple septate often in part of hyphae with wide lumen, 4.6–14.1 μm in diam.

Context generative hyphae hyaline to pale yellow, thin- to slightly thick-walled, frequently branched, simple septate 2.6–5.2 μm in diam; context skeletal hyphae dominant, orange to brown, occasionally branched, thick-walled with a wide to narrow lumen, simple septate often in part of hyphae with wide lumen, 3.6–10.6 μm in diam.

Tramal generative hyphae hyaline to pale yellow, thin- to slightly thick-walled, simple septate, frequently branched, 2.4–3.7 μm in diam; tramal

Figure 2. Phylogenetic tree was generated using maximum parsimony analyses based on combined ITS + nLSU sequences. Bootstrap values (before the/) higher than 50% and Bayesian posterior probabilities (after the/) more than 0.50 are indicated along the branches.
Figure 3. Basidiocarps of Fulvifomes nonggangensis. A: pileal surface of a mature basidiocarp; B: tube surface of a mature basidiocarp; C: a young basidiocarp; D: two aged basidiocarps. Scales bar: 1 cm.

Figure 4. Microscopic structures of Fulvifomes nonggangensis. Scales bar: 10 μm. A, B, C: basidia; D: basidioles; E: basidiospores; F: cystidioles (arrow pointed); G: generative hyphae from tomentum (arrow pointed); H: skeletal hyphae from tomentum; I: 1, tramat generative hyphae, 2, tramat skeletal hyphae; J: generative hyphae from context (arrow pointed); K: skeletal hyphae from context (arrow pointed).
skeletal hyphae orange to brown, dominant, rare branched, thick-walled with a wide to narrow lumen, simple septate occasionally in part of hyphae with wide lumen, 3.1–8.2 μm in diam.

Hymenial setae lacking; cystidioles present, fusoid, hyaline, thin-walled, 9.9–15.4 × 2.9–3.5 μm; basidia clavate to barrel-shaped, hyaline, with basal simple septum and four sterigmata, 7.9–17.4 × 2.8–6.8 μm; basidiocarps clavate, barrel to elliptical shape, 8.3–18.8 × 3–6.8 μm.

Basidiospores broadly ellipsoid, brown, slightly thick-walled, smooth, IKI–, CB–, or weak reaction (4.2–)4.3 × 3.3–4.4 μm, L = 4.93 μm, W = 3.73 μm, Q = 1.32 (n = 62).

Habitat: growing on living angiosperm trunks.

Additional specimens examined: China, Guangxi, Chongzuo, Nonggang Nature Reserve, on living angiosperm trunks, June 20 2012, GXU0501, GXU0766, and GXU1102; on dead angiosperm trunks, November 18 2018, GXU2254.

Note: Differs from other species by basidiocarps perennial, sessile, solitary, pileus applanate, the periphery of pilei radially cracked on old fruiting body. Pores circular to angular, 5–6 per mm. Hyphal system dimitic; generative hyphae simple septate; tissue darkening in KOH, unchanged in Melzer’s reagent.

**Fulvifomes tubogeneratus** F.C. Huang, H.F. Zheng & Bin Liu, sp. nov. (Figures 5 and 6).

MycoBank: MB835791

Etymology: *tubogeneratus* (Lat.): referring to new fruit body generated from tube surface.

Type: China, Guangxi Autonomous Region, Chongzuo, Longzhou County, Nonggang Nature Reserve, on dead trunks of angiosperm tree, November 19 2018, GXU2468 (Holotype in GXU).

rDNA sequences ex holotype: MT580805 (ITS), MT580800 (nLSU).

Description: Basidiocarps perennial, sessile, broadly attached on dead drunk, frequently new fruit bodies generated on surface of tubes, occasionally on pileal surface, imbricate. Pileus semicircular to subcircular, applanate, up to 10.2 × 7.4 and 4.1 cm thick, pileus surface distinctly concentrically sulcate, velutinate, brussels brown to medal bronze, margin entire, acute or dull, cadmium yellow to raw sienna, and claret brown when age. Context wood hard, yellow ochre, buckthorn brown to cinnamon brown, duplex, separated by a black line, the upper context up to 0.6 cm, lower context up to 3.1 cm, black lines also frequently distributing in context, tubes, and between context and tube with age. Pore surface shining, rood’s brown to burnt umber, pores not appearing on too young fruit body, but gradually increasing with mature, and some places of surface no pores differentiation and development even fruit body becoming old, and remaining with velutinate, these places capucine yellow, orange to cadmium yellow when young, brussels brown when old, sterile margin with the same color, up to 2.2 cm (no pores differentiation area) even old, pores angular or circular, 7–8 per mm; dissepiments most thin, and parts thick, entire, or some lacerate on margin. Tubes concolorous with pore surface, woody hard, up to 0.8 cm long, not stratified when young, but indistinct stratified with age, rood’s brown to chocolate.

Hyphal system dimitic; generative hyphae simple septate; tissue darkening in KOH, unchanged in Melzer’s reagent.

Upper context generative hyphae frequently branched, simple septate, hyaline to pale yellow, thin to slightly thick-walled with a wide lumen, 1.7–3.3 μm in diam; skeletal hyphae dominant, unbranched, capucine orange to orange, mostly thick-walled with a narrow to wide lumen and septate, and some still with a part of solid, 3–6 μm in diam. Lower context generative hyphae hyaline to pale yellow, frequently branched, thin to slightly thick-walled with a wide lumen, simple septate,
1.9–6.1 μm in diam; skeletal hyphae frequent, occasionally branched, capucine orange to orange, thick-walled with a narrow to wide lumen, a few septate, 3.6–7.2 μm in diam.

Tramal generative hyphae frequent, hyaline to pale yellow, thin to slightly thick-walled, frequently branched, septate, 1.7–3.8 μm in diam; skeletal hyphae frequent, thick-walled with wide to narrow lumen, or solid, occasionally branched, rare septate, pale yellow to orange, 2.5–4.7 μm in diam.

Hymenial setae absent; hyphoid setae pale yellow to orange, frequent, swollen at apex, and subglobose to fusiform, thick-walled, 7–19.8 × 4–7.2 μm; basidia clavate to barrel-shaped, flask-shaped, with four sterigmata, and a simple septum at the base, 9.9–31.4 × 3.1–7.6 μm; basidioles clavate to barrel-shaped, subglobose, 7.5–27.5 × 2.8–8 μm; cystidia and cystidioles absent.

Basidiospores ovoid to subglobose, capucine yellow to mars yellow, slightly thick-walled, smooth, IKI−, CB−, (5−)5.2–6.2(−6.4) × (4.1−)4.5–5.7(−5.8) μm, $L = 5.72 \mu m$, $W = 5.00 \mu m$, $Q = 1.14 \ (n = 60)$.

Habitat: growing on dead trunks of angiosperm trees.

Additional specimens examined: China, Guangxi, Chongzuo, Nonggang Nature Reserve, on dead angiosperm trunks, November 2018, GXU2478.

Note: Differs from other species by basidiocarps perennial, sessile, imbricate, new fruit bodies frequently generated from surface of tubes, context duplex, pores angular or circular, 7–8 per mm. Hyphal system dimitic, hyphoid setae present, basidiospores ovoid to subglobose, 5.72 × 5.00 μm on average.

4. Discussion

Morphology and DNA sequence analysis confirmed that the unique of the two new species *F. nonggangensis* and *F. tubogeneratus*. Species in the genus *Fulvifomes* are somewhat heterogeneous in certain characters, such as the presence or absence of setae and spores being cyanophilous (CB+) or acyanophilous (CB−) [2]. However, the basidiospores of two...
new species in this investigation were both CB–, and hymenial setae absent as well.

Compared with other species, especially querying keys built by Dai [2] and Hattori et al. [11], *F. indicus* (Massee) L.W. Zhou, *F. merrillii* (Murrill) Baltazar & Gibertoni, and *F. squamosus* Salvador-Montoya & Drechsler-Santos are similar to *F. nonggangensis* and *F. tubogeneratus* in morphology, all of their basidiocarps pileate, apllanate, or ungluate to apllanate, tube layers not stratified to indistinct, hymenial setae absent. Nevertheless, each of them has some specific characteristics different from two new species.

*F. indicus* is distinguished from two new species by basidiocarps annual [10], sessile or subcapitate with a contracted base, hyphal system monomitic, pores the largest (4–5 per mm). Furthermore, basidiospores are larger (5.4–6.5 × 4.7–5.5 μm) than that of *F. nonggangensis*.

According to the data of Dai [2], *F. merrillii* differs from *F. nonggangensis* by pilei subungulate to apllanate, pores smaller (7–8 per mm), tube layers indistinct, cystidioles larger (18–22 × 4.5–6 μm), basidiospores subglobose; and differs from *F. tubogeneratus* by basidiocarps subungulate to apllanate, solitary, cystidioles present, and hyphoid setae absent and basidiospores smaller (4.4–5.4 × 3.7–4.7 μm).

*F. squamosus* [13] is distinguishable from two new species by having squamose pilear surface with long scales, hyphal system monomitic in the context, basidiospores with the ventral side flattened, and without cystidioles and hyphoid setae.

Similar to previous phylogenetic studies on *Fulvifomes* [12,14,15], the core of *Fulvifomes* in phylogenetic trees was mainly divided into two clades, one including *F. fastuosus*, *F. imbricatus*, *F. siamensis* et al., another including *F. elaeodendri*, *F. krugiodendri*, *F. squamosus*, *F. thailandicus*, and *F. yoroui* et al.

*F. nonggangensis* is closely related to *F. XHJ-2018b*, *F. rhytiphoeus* (Mont.) Camp.-Sant. & Robledo, and *I. rigidus* B.K. Cui & Y.C. Dai, meanwhile, *F. tubogeneratus* closely related to *F. XHJ-2018h* and *F. siamensis* T. Hatt., Sakay, & E.B.G. Jones (Figures 1 and 2), isolates of *F. XHJ-2018b* and *F. XHJ-2018h* both came from China but were not formally described yet.

*F. rhytiphoeus* was proposed by Campos-Santana et al. [26] as a new complex species, and it resembles *F. nonggangensis* by basidiocarps pileate, apllanate, solitary, with a distinct black line below pileus surface, setae absent. But its tubes were mostly distinctly stratified, pores smaller, 7–9 per mm, context fibrous and easily fragmented, cystidioles absent, and spores subglobose.

*I. rigidus* [27] differed from *F. nonggangensis* in its basidiocarps annual, resupinate, pores smaller, 8–9 per mm, hyphal system monomitic, cystidioles absent, and slightly smaller basidiospores (3.9–4.5 × 2.9–3.7 μm). But it also fitted in *Fulvifomes* with hymenial setae absent, ellipsoid, yellowish brown and thick-walled basidiospores, whether it is necessary to transferred *I. rigidus* to *Fulvifomes* which still needed more evidences.

*F. siamensis* was proposed by Hattori et al. [11], and resembled *F. tubogeneratus* by basidiocarps perennial, context woody hard, pores 7–8 per mm, setae absent. But it differed from the latter by without a distinct black line, and hyphal system monomitic in context, hyphoid setae absent. Moreover, basidiocarps of *F. tubogeneratus* imbricate, and new fruit bodies often generated from tube surface.

Key to species of *Fulvifomes* from China [2,10,28]

1. Hymenial setae absent.................................2
2. Hymenial setae present.................................11
3. Basidiocarps resupinate.................................3
4. Basidiocarps pileate, effused-reflexed....................4
5. Basidiocarps pileate........................................6
6. Basidiocarps perennal, hyphal system dimitic ....7
7. Tube layer distinct..........................................8
8. Tube layer not stratified to indistinct....................9
9. Pores 3–4 per mm, spores ellipsoid, chlamydo-spores absent..................................................F. hainanensis
10. Pores 6–7 per mm, spores subglobose, chlamydo-spores present........................................F. durissimus
11. Hyphoid setae present, cystidioles absent*F. tubogeneratus*
12. Hyphoid setae absent, cystidioles present............10
13. Pores 5–6 per mm, spores broadly ellipsoid, 4.3–5.3 × 3.3–4.2 μm..............*F. nonggangensis*
14. Pores 8–11 per mm, spores subglobose, 4.4–5.4 × 3.7–4.7 μm.........................*F. merrillii*
15. Basidiocarps effused-reflexed to pileate, pores 6–7 per mm .......................*F. johnsonianus*
16. Basidiocarps resupinate, pores 8–11 per mm...12
17. Basidiocarps 2–2.5 μm long, tube layers stratified.....................................................*F. minisporus*
18. Basidiocarps 2.3–4.1 μm long, tube layers not stratified to indistinct.........................13
13. Basidiocarps annual, pore surface cracked when dry, spores CB(−)..............................F. glaucescens
13. Basidiocarps perennial, pore surface not cracked when dry, spores CB(+)..............................F. cesatii

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