A new species of *Wrightoporiopsis* (Russulales, Basidiomycota) and a key to accepted species in the genus

**Abstract**

A new species of *Wrightoporiopsis*, *W. irregularis* sp. nov., is described and illustrated from southern China. It is characterized by annual, pileate, imbricated and sulphur yellow basidiocarps, irregular hymenophore varying from poroid to hydnoid, a mononitic hyphal structure in context but dimitic in the trama, generative hyphae bearing clamp connections, indextrinoid skeletal hyphae, the absence of gloeocystidia, cystidia and gloeoplerous hyphae, the presence of fusoid cystidioles, ellipsoidal, thin-walled, finely asperulate, strongly amyloid, and acyanophilous basidiospores measuring 2.8–3.3×2.2–2.5μm. Phylogenetic analysis based on the combined ITS (internal transcribed spacer region) and nLSU (the large nuclear ribosomal RNA subunit) dataset demonstrated *W. irregularis* is a new lineage in *Wrightoporiopsis*.

**Keywords:** hericiaceae, taxonomy, wood-inhabiting fungi

**Introduction**

*Wrightoporiopsis* YC Dai, Jia J Chen & BK Cui, typified by *W. neutropica* (Ryvarden) YC Dai, Jia J Chen & BK Cui, was recently established by Chen et al.1 Some of taxa in the genus were previously treated under *Wrightoporia Pouzar.*2 However, Phylogenetic analysis demonstrated that *Wrightoporiopsis* is distant from *Wrightoporia sensu stricto*, and these two genera in fact belong to two families, Hericiaceae and Wrightoporiaceae, respectively.1 *Wrightoporiopsis* is characterized by pileate, yellow to yellowish-brown basidiocarps, a dimitic hyphal system with generative hyphae bearing clamp connections, skeletal hyphae usually dextrinoid, basidiospores ellipsoid to subglobose, hyaline, finely asperulate, strongly amyloid, and causing a white rot.1

During a field trip in Hainan Province of southern China, a yellowish specimen with poroid to hydnoid hymenophore was collected, it has a dimitic hyphal structure with generative hyphae bearing clamp connections, and asperulate, amyloid basidiospores, so it belongs to *Wrightoporia sensu lato* based on these morphological characters, and was not recorded in China.4 After phylogenetic analysis of ITS+nLSU sequences and re-examination morphology in laboratory, it turn out to represent a new species of *Wrightoporiopsis*. In this paper its illustrated description is given and an identification key to accepted species of *Wrightoporiopsis* is provided.

**Materials and methods**

**Morphology**

The studied specimens are deposited in the herbaria of the Institute of Microbiology, Beijing Forestry University (BJFC). Morphological descriptions are based on field notes and herbarium specimens. Microscopic analyses follow Chen et al.,1 and Dai.8 Special color terms follow Anonymous9 and Petersen.4 In the text, the following abbreviations were used: KOH stands for 5% potassium hydroxide, CB stands for Cotton Blue, CB– stands for acyanophilous, IKI stands for Melzer’s reagent, IKI+ stands for amyloid in Melzer’s reagent, L stands for arithmetic average of all spore length, W stands for arithmetic average of all spore width, Q for L/W ratio, n (a/b) stands for measured from given number of spores (a) number of specimens (b).

**Molecular phylogeny**

The genomic DNA were obtained from dried specimens using the CTAB rapid plant genome extraction kit (Aidlab Biotechnologies, Co., Ltd., Beijing) following the manufacturer’s instructions.19 The internal transcribed spacer (ITS) regions were amplified with the primers ITS4 and ITS5,18 and the nuclear large subunit (nLSU) ribosomal RNA gene regions with the primers LR0R and LR7.11 The PCR procedure for ITS and nLSU was follows Chen.1 The amplicon purified and sequenced by the Beijing Genomics Institute, China with the same primers as in amplifications. All newly generated sequence was deposited in GenBank (http://www.ncbi.nlm.nih.gov).

In addition to the newly generated sequences, additional ITS and nLSU sequences of *Wrightoporiopsis* and related species from previous studies1 were obtained from GenBank (Table 1) to explore the phylogenetic position of our specimen. All sequences were aligned using ClustalX v.1.8312 and manually adjusted in BioEdit.15 Before the phylogenetic analysis, ambiguous regions at the beginning and the end of the alignment were deleted and gaps were manually adjusted to optimize the alignment. The edited alignment was deposited at TreeBase (http://purl.org/phylo/treebase; submission ID 23041).

Phylogenetic analysis was following to previous studies.1,14 Maximum parsimony (MP), Bayesian inference (BI) and Maximum likelihood (ML) methods were used to perform the phylogenetic analysis. The three phylogenetic methods resulted in similar topologies for each dataset. Thus, only the topology from the MP analysis is presented. Branches that received bootstrap support from maximum parsimony (MP), maximum likelihood (BS) and Bayesian posterior probabilities (BPP) greater than or equal to 85% (MP and BS) and 0.95 (BPP) were considered as significantly supported.
Results

Phylogenetic analyses

A total of 60 ITS (30) and nLSU (30) sequences included sequences from 31 fungal collections representing 16 species (Table 1) in this study, were used in the phylogenetic analyses. The alignment, generated by the ITS+nLSU dataset, contained 2147 characters. MP tree yielded four similar topologies (TL=1496, CI=0.606, RI=0.816, RC=0.494, HI=0.394). BI resulted in a similar consensus tree as the MP tree achieving an average standard deviation of split frequencies <0.01 after 2.5 million generations. ML tree also resulted in a topology similar to that with MP tree, and so only show the MP tree. BT values (≥80%) and BPPs (≥0.95) are shown at the nodes (Figure 1). Hericium abietis (Weir ex Hubert) K.A. Harrison and Hericium coralloides (Scop.) Pers. were used as outgroups because they are closely related to Wrightoporiopsis according previous studies.\(^1\)\(^,\)\(^2\) Based on the phylogenetic tree inferred from the combined ITS+nLSU dataset (Figure 1), shows that the newly sequence specimen formed a distinct lineage within Wrightoporiopsis clade, and, so we described a species of the Wrightoporiopsis.

Figure 1: Strict consensus tree illustrating the phylogenetic position of Wrightoporiopsis irregularis, generated by maximum parsimony method based on ITS+nLSU sequence data. The topology is from the maximum parsimony analysis along with statistical values from the maximum parsimony, Bayesian inference analyses and maximum likelihood (bootstrap values and Bayesian posterior probabilities simultaneously not less than 80% and 0.9, respectively) at the nodes.

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Table 1 Specimens and GenBank accession number of sequences used in this study.

| Taxa                             | Sample no. | Locality     | GenBank accession no. |
|----------------------------------|------------|--------------|-----------------------|
|                                  |            |              | ITS                   | nLSU                  |
| Dentipellis coniferarum          | Cui 10063  | China        | JQ349106              | JQ349092              |
|                                   | Yuan 5623  | China        | JQ349107              | JQ349093              |
| D. fragilis                      | Dai 12550  | China        | JQ349110              | JQ349096              |
| D. microspora                    | Cui 10035  | China        | JQ349112              | JQ349098              |
| D. parmastoi                     | Cui 8513   | China        | JQ349113              | JQ349099              |
| Dentipellopsis dacyrdicola       | Dai 12004  | China        | JQ349104              | JQ349089              |
| Hericium abietis                 | NH 6990    | Canada       | AF506453              | AF506453              |
| H. coralloides                   | NH 282     | Sweden       | AF506459              | AF506459              |
|                                  | Cui 9073   | China        | KM107871              | KM107890              |
| Pseudowrightoporia crassihypha   | Yuan 5884  | China        | KM107872              | KM107891              |
|                                  | Yuan 6247  | China        | KM107873              | KM107892              |
|                                  | 0810/1a    | USA          | GU594161              | KJ807078              |
| P. cylindrospora                 | Ryvarden 46609 | USA    | KJ513290              | KJ807079              |
|                                  | Dai 8132   | China        | KM107868              | KM107887              |
| P. hamata                        | Dai 8152   | China        | KM107869              | KM107888              |
|                                  | Dai 10007  | China        | KM107870              | KM107889              |
|                                  | Dai 7221   | China        | FJ644289              | KM107882              |
| P. japonica                      | Dai 12086  | China        | KJ513293              | KM107883              |
|                                  | KUC 20110908 | Korea | KC166692              | KC166692              |
|                                  | Cui 3344   | China        | KM107865              | KM107884              |
| P. oblongispora                  | Yuan 6101  | China        | KM107866              | KM107885              |
|                                  | Yuan 6106  | China        | KM107867              | KM107886              |
|                                  | Yuan 3460  | China        | KM107875              | KM107894              |
| Wrightoporiopsis amylohypha      | Yuan 3467  | China        | KM107876              | KM107895              |
|                                  | Yuan 3579  | China        | KM107877              | KM107896              |
|                                  | Cui 8457   | China        | KJ807066              | KJ807074              |
| W. biennis                       | Cui 8506   | China        | KJ807067              | KJ807075              |
| W. fascocinerea                  | Aime 1521  | Guyana       | KM107897              | –                     |
| W. irregularis                   | Dai 18488A | China        | MH626487              | MH626488              |

New sequences produced by this work are in bold.

**Taxonomy**

**Wrightoporiopsis irregularis**, **YC Dai, Q Chen & XH Ji, sp. nov.** (Figure 2 & Figure 3)

**Mycobank No.:** MB 827087.

**Diagnosis:** Differs from other Wrightoporiopsis species by its sulphur yellow to luteous basidiocarp, poroid to hydnoid hymenophore, a monomitic contextual hyphal structure, indextrinoid skeletal hyphae in trama, the absence of gloeocystidia and gloeoplerous hyphae.

**Type:** China, Hainan Province, Ledong County, Jianfengling Nature Reserve, on dead angiosperm tree, 26 April 2018, **Dai 18488A** (BJFC, holotype).

**Etymology:** *Irregularis* (Lat.): referring to the species has irregular hymenophore.

**Description:** Basidiocarp annual, pileate, imbricated, separable from substrate, soft and without odour or taste when fresh, corky when dry. Pilei more or less conchate, laterally fused, projecting up to 1 cm, 3 cm wide and 8 mm thick at base. Pileal surface sulphur

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yellow when fresh, becoming pale luteous when dry, velutinate, azonate; margin blunt. Hymenophores sulphur yellow to buff when fresh, saffron to luteous when dry; margin distinct, concolorous with pileal surface, up to 1mm wide; hymenophore very irregular, poroid to sinuous when juvenile, becoming distinct hydnoid, pores or spines 2–4 per mm. Context concolorous with pileal surface, corky, up to 5mm thick. Tubes or spines concolorous with hymenophore, corky, up to 3mm long.

**Discussion**

Previously five species of *Wrightoporiopsis* were reported: *W. amylohypha* YC Dai, Jia J Chen & BK Cui, *W. biennis* (Jia J Chen & BK Cui) YC Dai, Jia J Chen & BK Cui, *W. fuscocinerea* YC Dai, Jia J Chen & BK Cui, and *W. neotropica* (Ryvarden) YC Dai, Jia J Chen & BK Cui. *W. amylohypha* and *W. biennis* resembles *W. irregularis* by more or less yellowish hymenophore, tissue become red or brown in KOH, and distribution in China. However, *W. amylohypha* has a biennial growth habit, regular poroid hymenophore with pores 5–6/mm, dextrinoid trama skeletal and the presence of gloeoplerous hyphae. *W. biennis* has a biennial growth habit, regular poroid hymenophore with pores 6–9/mm, dextrinoid skeletal hyphae, the presence of gloeoplerous hyphae, and subglobose to broadly ellipsoid, cyanophilous basidiospores measuring 3.3–4×2.6–3.5μm. *W. fuscocinerea* can be distinguished from *W. irregularis* by its perennial and resupinate basidiocarps, regular poroid hymenophore with pores 8–10/mm, dextrinoid skeletal hyphae, the presence of gloeocystidia, and subglobose basidiospores measuring 3–4×2.5–3.5μm. *W. neotropica* is different from *W. irregularis* by resupinate basidiocarps, regular poroid hymenophore with pores 6–8/mm, dextrinoid skeletal hyphae, the absence of cystidioles and distribution in tropical America. *W. roseocontexta* is similar to *W. irregularis* by sharing interdinoid skeletal hyphae, but differs in having resupinate basidiocarps, regular poroid hymenophore with pores 8–10/mm, the absence of cystidioles, globose basidiospores measuring 3–4μm in diam, and distribution in tropical America.

**Key to species of Wrightoporiopsis**

1 Skeletal hyphae non-dextrinoid.........................................2
Skeletal hyphae dextrinoid .................................................3

2 Hymenophores poroid, olivaceous brown, pores 8–10/mm; basidiospores globose, 3–4μm in diam ........................................ W. roseocontexta

Hymenophores poroid to hydnoid, sulphur yellow to luteous, pores or spines 2–4μm; basidiospores ellipsoid, 2.8–3.3×2.2–2.5μm .......... *W. irregularis*

3 Basidiocarps pileate; contextual hyphae amyloid ........................................ W. amylohypha
Basidiocarps resupinate to effused-reflexed; contextual hyphae inamyloid .................................................................4

4 Basidiocarps annual; basidiospores ellipsoid ........................................ W. neotropica

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**Figure 2** A fresh basidiocarp of *Wrightoporiopsis irregularis* (Holotype). Scale bar=1.0cm.

**Figure 3** Microscopic structures of *Wrightoporiopsis irregularis* (Holotype). A: Basidiospores. B: Basidia and Basidioles. C: Cystidioles. D: Hyphae from trama. E: Hyphae from context.

Hyphal system monomitic in the context, dimitic in the trama; generative hyphae bearing clamp connections; all hyphae IKI–, CB–, frequently encrusted by yellowish crystals; tissues becoming bloody red in KOH. Generative hyphae in context hyaline, thin- to thick-walled with a wide lumen, moderately branched, frequent bearing clamp connections, loosely interwoven, 2.5–4μm in diam. Generative hyphae in tubes hyaline, thin- to thick-walled, moderately branched and frequently bearing clamp connections 2.5–4μm in diam; skeletal hyphae frequent, hyaline, thick-walled with a wide lumen, rarely branched, flexuous, interwoven, 3–4.5μm in diam. Fusoid cystidioles present, hyaline, thin-walled, 22–28×4–6μm; basidia clavate, bearing four sterigmata and a basal clamp connection, 22–27×4–5μm; basidioles in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, hyaline, thin-walled, finely asperulate, strongly IKI+, CB–, (2.6–)2.8–3.3(~3.5)×(2–)2.2–2.5(~2.9)μm, L=3.09μm, W=2.33μm, Q=1.34 (n=30/1).
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Basidiocarps biennial to perennial; basidiospores subglobose to globose..........................5

5 Gloeocystidia present, gloeoplerous hyphae absent................. 
*W. fuscocinerea*

Gloeocystidia absent, gloeoplerous hyphae present................... 
*W. biennis*

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**Conflicts of interest**

Authors declare that there is no conflict of interest.

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