

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 hydroid, a monomitic 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, ellipsoid, 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

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Introduction

Wrightoporiopsis YC Dai, Jia J Chen & BK Cui, typified by *W. neotropica* (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.^{2–4} 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 hydroid 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.⁵ 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.⁶ Special color terms follow Anonymous⁷ and Petersen.⁸ 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 negative in 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.^{1,9} The internal transcribed spacer (ITS) regions were amplified with the primers ITS4 and ITS5,¹⁰ 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.¹³ 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 ($\geq 80\%$) 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.^{1,14} 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*.

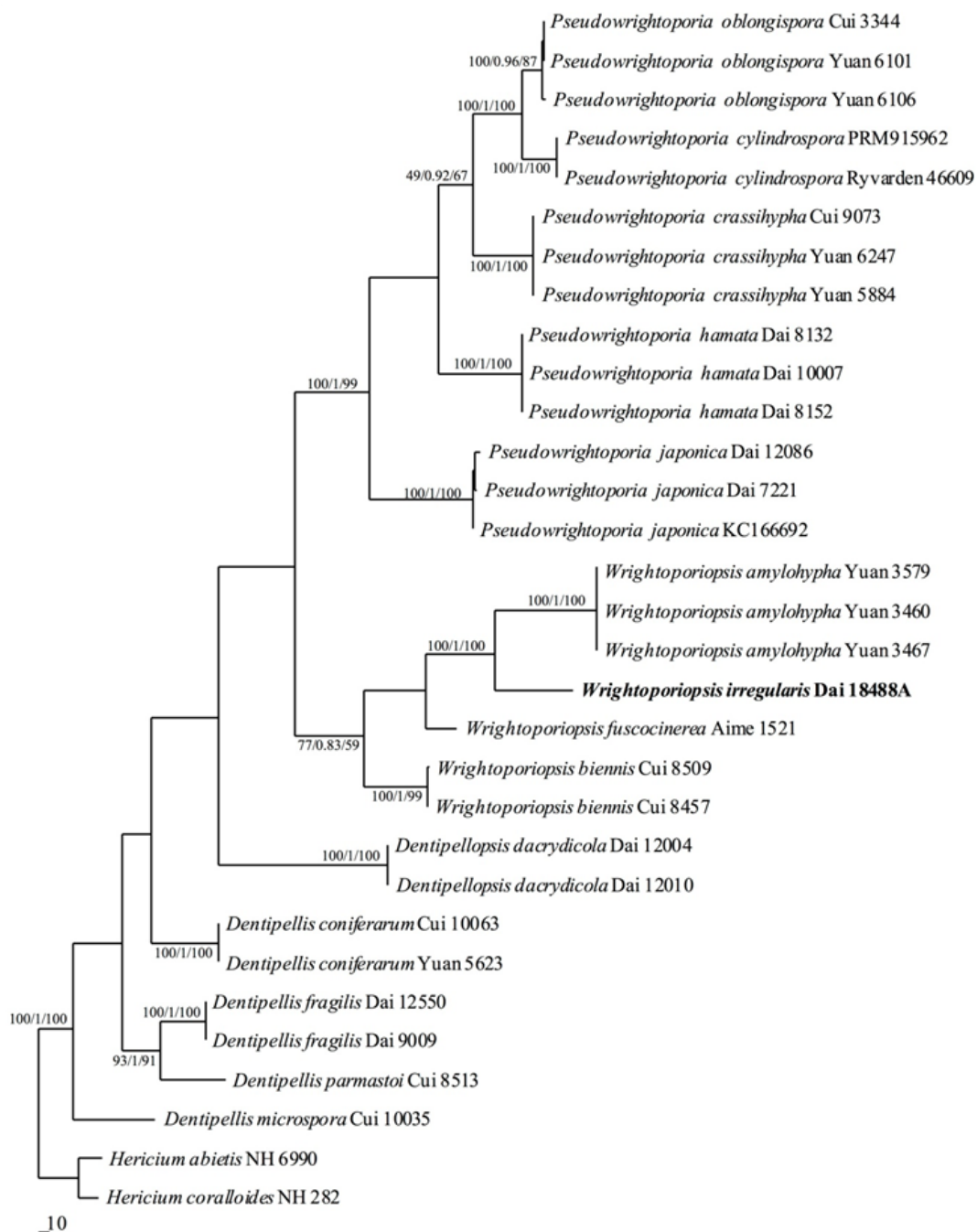


Figure 1 Strict consensus tree illustrating the phylogenetic position of *Wrightoporiopsis irregularis*, generated by maximum parsimony method based on ITS+nLSU sequence data. The topology is from the maximum parsimony analysis along with statistical values from the maximum parsimony, Bayesian inference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

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

Taxa	Sample no.	Locality	GenBank accession no.	
			ITS	nLSU
<i>Dentipellis coniferarum</i>	Cui 10063	China	JQ349106	JQ349092
	Yuan 5623	China	JQ349107	JQ349093
<i>D. fragilis</i>	Dai 12550	China	JQ349110	JQ349096
	Dai 9009	China	JQ349108	JQ349094
<i>D. microspora</i>	Cui 10035	China	JQ349112	JQ349098
<i>D. parmastoi</i>	Cui 8513	China	JQ349113	JQ349099
<i>Dentipellopsis dacrydicola</i>	Dai 12004	China	JQ349104	JQ349089
	Dai 12010	France	–	JQ349090
<i>Hericium abietis</i>	NH 6990	Canada	AF506453	AF506453
<i>H. coralloides</i>	NH 282	Sweden	AF506459	AF506459
<i>Pseudowrightoporia crassihypha</i>	Cui 9073	China	KM107871	KM107890
	Yuan 5884	China	KM107872	KM107891
	Yuan 6247 (holotype)	China	KM107873	KM107892
<i>P. cylindrospora</i>	0810/1a	USA	GU594161	KJ807078
	Ryvarden 46609	USA	KJ513290	KJ807079
	Dai 8132	China	KM107868	KM107887
<i>P. hamata</i>	Dai 8152 (holotype)	China	KM107869	KM107888
	Dai 10007	China	KM107870	KM107889
	Dai 7221	China	FJ644289	KM107882
<i>P. japonica</i>	Dai 12086	China	KJ513293	KM107883
	KUC 20110908	Korea	KC166692	KC166692
	Cui 3344	China	KM107865	KM107884
<i>P. oblongispora</i>	Yuan 6101 (holotype)	China	KM107866	KM107885
	Yuan 6106	China	KM107867	KM107886
	Yuan 3460	China	KM107875	KM107894
<i>Wrightoporiopsis amylohypha</i>	Yuan 3467	China	KM107876	KM107895
	Yuan 3579 (holotype)	China	KM107877	KM107896
<i>W. biennis</i>	Cui 8457	China	KJ807066	KJ807074
	Cui 8506 (holotype)	China	KJ807067	KJ807075
<i>W. fuscocinerea</i>	Aime 1521 (holotype)	Guyana	KM107897	–
<i>W. irregularis</i>	Dai 18488A (holotype)	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 hydroid 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 up to 1cm, 3cm wide and 8mm thick at base. Pileal surface sulphur

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 hydroid, 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.



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

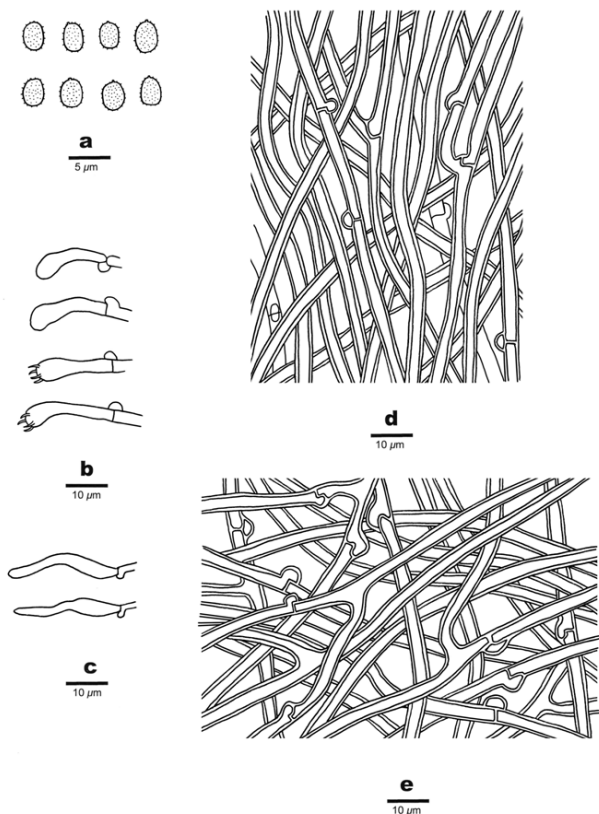


Figure 3 Microscopic structures of *Wrightoporiopsis irregularis* (Holotype). A: Basidiospores. B: Basidia and Basidioles. C: Cystidioles. D: Hyphae from trama. E: Hyphae from context.

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).

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, *W. neotropica* (Ryvarden) YC Dai, Jia J Chen & BK Cui, and *W. roseocontexta* (Ryvarden & Iturr.) YC Dai, Jia J Chen & BK Cui.¹ *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 regular poroid hymenophore with pores 5–6/mm, dextrinoid tramal skeletal and the presence of gloeoplerous hyphae.¹ *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.² *W. fuscocinerea* can be distinguished from *W. irregularis* by its perennial and resupinate basidiocarp, 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.² *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.³ *W. roseocontexta* is similar to *W. irregularis* by sharing indextrinoid 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.⁴

Key to species of *Wrightoporiopsis*

- 1 Skeletal hyphae non-dextrinoid.....2
- Skeletal hyphae dextrinoid3
- 2 Hymenophores poroid, olivaceous brown, pores 8–10/mm; basidiospores globose, 3–4µm in diam
W. roseocontexta
- Hymenophores poroid to hydroid, sulphur yellow to luteous, pores or spines 2–4/mm; 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 inamyloid4
- 4 Basidiocarps annual; basidiospores ellipsoid
W. neotropica

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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