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# Addition to Melanommataceae: a new geographical record of *Alpinaria rhododendri* from Shangri La, China

Thiyagaraja V<sup>1,2,3,4,5</sup>, Hyde KD<sup>3,4,5</sup>, Wanasinghe DN<sup>4,5,6</sup>, Worthy FR<sup>4,6</sup> and Karunarathna  $SC^{4,5,6*}$ 

<sup>1</sup>Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Haizhu District, Guangzhou, Guangdong 510225, PR China

<sup>2</sup>Department of Biology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50002, Thailand

<sup>3</sup>Centre of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

<sup>4</sup>Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, People's Republic of China

<sup>5</sup>World Agro Forestry Centre East and Central Asia, Kunming 650201, Yunnan, People's Republic of China

<sup>6</sup>Centre for Mountain Futures, Kunming Institute of Botany, Kunming 650201, Yunnan, People's Republic of China

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#### Abstract

The recently established monotypic genus *Alpinaria* comprises *A. rhododendri*. It occurs on *Rhododendron* species and is distributed across Europe, India and North America. The genus was previously established to epitypify *Cucurbitaria rhododendri* and was assigned to Melanommataceae based on multigene phylogenetic analyses. In this study, a fungal taxon growing on unidentified dicotyledonous wood was collected from Shangri La, Yunnan Province, China. Our taxon clustered with *Alpinaria* in the combined LSU, SSU, ITS and TEF1- $\alpha$  phylogenetic tree based on maximum likelihood and Bayesian analyses. Our collection is characterized by globose, ostiolate ascomata, pseudoparaphyses, cylindrical, bitunicate, fissitunicate asci and 8-spored, ellipsoid and septate ascospores. Morphology and multigene phylogenetic analyses support the identification of our taxon as *A. rhododendri*, a new geographical record for China.

Key words - Dothideomycetes - phylogeny - Pleosporales - Rhododendron - taxonomy

# Introduction

Melanommataceae (Pleosporales) was introduced by Winter (1885) with *Melanomma* as the type genus. The species in this family are mainly saprobic and hyperparasitoid (Zhang et al. 2012, Tian et al. 2015) and have been recorded on the twigs or bark of woody plants in both aquatic and terrestrial habitats. They are distributed across temperate and subtropical regions (Tian et al. 2015, Wanasinghe et al. 2018, Pem et al. 2019). Melanommataceae was previously included in Melanommatales based on its trabeculate pseudoparaphyses (Barr 1983, Liew et al. 2000). However, molecular studies did not support this early classification, leading to the family being transferred to Pleosporales (Liew et al. 2000, Zhang et al. 2012, Hyde et al. 2013, Tian et al. 2015, Pem et al. 2019). Barr (1990) placed *Byssosphaeria, Keissleriella, Melanomma, Ostropella* and *Strickeria* in Melanommataceae. This classification was based on their similar erumpent to superficial ascomata with small, thick-walled cells in the ascomatal wall. Lumbsch & Huhndorf

(2007) accepted 18 genera with six uncertain placements. Kirk et al. (2008) accepted 21 genera in Melanommataceae. However, following the molecular and taxonomic treatment of Mugambi & Huhndorf (2009), further genera were added to this family. Its taxonomy has since been the subject of research by many other authors (Schoch et al. 2009, Wijayawardene et al. 2012, 2014, De Gruyter et al. 2013, Hyde et al. 2013, Tian et al. 2015, Li et al. 2016, Gross et al. 2017, Jaklitsch & Voglmayr 2017, Hongsanan et al. 2020).

Melanommataceae comprises 35 genera namely; Alpinaria, Aposphaeria, Asymmetricospora, Bertiella. Bicrouania, Byssosphaeria, *Calyptronectria*, *Camposporium*, Exosporiella, Mamillisphaeria, Melanocamarosporioides, Fusiconidium, Herpotrichia, Marjia, Melanocucurbitaria, *Melanodiplodia*, Melanocamarosporium, Melanomma, Monoseptella, Muriformistrickeria, Navicella, Neobyssosphaeria, Petrakia, Phragmocephala, Phragmotrichum, Pseudobyssosphaeria, Pseudodidymella, Pseudostrickeria, *Pleotrichocladium, Praetumpfia,* Sarimanas, Seifertia, Tumularia, Uzbekistanica and Xenostigmina (Hongsanan et al. 2020, Wijayawardene et al. 2020). The asexual morph is mostly coelomycetous (occurs with mononematous, synnematous and pycnidial conidiomata) and rarely hyphomycetous (Tian et al. 2015, Hashimoto et al. 2017). The sexual morph possesses the unique features of this family, including globose or depressed perithecial ascomata, bitunicate and fissitunicate asci and pigmented phragmosporous to muriform ascospores (Sivanesan 1984, Barr 1990, Zhang et al. 2012, Hyde et al. 2013, Tian et al. 2015, Wanasinghe et al. 2018, Pem et al. 2019). The asexual morph has been recorded for the genera Alpinaria, Aposphaeria, Exosporiella, Melanocamarosporioides, Melanocamarosporium, Monotosporella, Mycopappus, Nigrolentilocus, Phragmocephala and Xenostigmina (Wijayawardene et al. 2017, Hashimoto et al. 2017, Pem et al. 2019). Most species in this family have only been recorded as asexual morphs. This is problematic for determining the linkages between the sexual and asexual morphs and will require further extended molecular sampling (Tian et al. 2015). Thus, the position of many previously listed genera has yet to be resolved (Lumbsch & Huhndorf 2007).

Alpinaria has recently been introduced in Melanommataceae to accommodate the type species *A. rhododendri* (Jaklitsch & Voglmayr 2017). *Alpinaria* occurs on *Rhododendron* species in the Himalayan regions of India (*R. chrysanthum*; Müller 1959), Europe (*R. ferrugineum* and *R. hirsutum*; Jaklitsch & Voglmayr 2017), and North America (*Rhododendron* sp.; Mugambi & Huhndorf 2009). This study reports a new geographical record of *A. rhododendri* from Shangri La, China. The taxonomic placement of this species is supported by evidence from both morphology and multigene phylogenetic analyses of LSU, SSU, ITS and TEF1- $\alpha$  sequence data.

#### **Materials and Methods**

#### Sample collection, morphological studies and isolation

Woody material with black fruiting bodies was collected from Shangri La, Diqing Prefecture, Yunnan Province, China in September 2018. The material was brought to the laboratory in paper bags. Material was examined using a Motic SMZ 168 series microscope. Hand sections of the ascomata were mounted with water and examined. Micro-morphological characteristics were photographed using a compound microscope (Nikon ECLIPSE 80i, Japan) fitted with an EOS 600D digital camera (Canon, Japan). All microscopic measurements were made with Tarosoft Image Frame Work (v.0.9.0.7) and images were processed with Adobe Photoshop CS6 version 13.0.

The herbarium specimen was deposited at Mae Fah Luang University (MFLU) Herbarium, Chiang Rai, Thailand. We obtained a Faces of Fungi number for our taxon, as described in Jayasiri et al. (2015). We could not obtain a pure culture of this fungus. Therefore, morphological characteristics observation and DNA extraction were performed from the fresh fruiting structures.

### DNA extraction, PCR amplification and gene sequencing

DNA was extracted directly from the fresh fruiting bodies as described by Wanasinghe et al.

(2018). An E.Z.N.A. <sup>®</sup> Forensic DAT (D3591 – 01, Omega Bio – Tek) DNA extraction kit was used to extract DNA, following the manufacturer's instructions. DNA samples that were intended for use as a template for PCR were stored at 4°C. Duplicates were kept at  $-20^{\circ}$ C for long-term storage. DNA sequence data were obtained from partial sequences of ribosomal and protein-coding genes. The large-subunit ribosomal RNA (LSU), small-subunit ribosomal RNA (SSU), internal transcribed spacer (ITS) and translation elongation factor 1-alpha (TEF1- $\alpha$ ) were amplified with the primer pairs LR0R/LR5 (Rehner & Samuels 1994), NS1/NS4 (White et al. 1990), ITS5/ITS4 (Vilgalys & Hester 1990) and EF1-983F/EF1-2218R (Rehner 2001), respectively.

The PCR amplification was performed using a final volume of 25 µl, comprised of 2.0 µl of DNA template, 1 µl of each forward and reverse primers, 12.5 µl of Taq PCR Super Mix (a mixture of Easy Taq TM DNA Polymerase, dNTPs, obtained buffer) (Beijing Trans Gen Biotech Co., Chaoyang District, Beijing, PR China) and 8.5 µl of sterilized water. The PCR amplification was accomplished by an initial denaturation at 94°C for 3 minutes, followed by a further 35 cycles. Each cycle consisted of denaturation at 94°C for 30 seconds, annealing for 50 seconds and elongation at 72°C for 1 minute. A final extension was conducted for 10 minutes at 72°C. The annealing temperatures were 54°C for LSU and ITS, 48°C for SSU and 51°C for TEF1- $\alpha$ . PCR products were observed on 1% agarose electrophoresis gels stained with ethidium bromide. DNA purification and sequencing were performed by Shanghai Sangon Biological Engineering Technology & Services Co. (Shanghai, P.R. China). The nucleotide sequence data acquired were deposited in GenBank (2020). Alignments and phylogenetic trees were submitted to TreeBASE under submission number 26007.

#### Phylogenetic analyses and species recognition

The BLAST search engine of the National Centre for Biotechnology Information (NCBI) was preliminary identification of DNA sequences of the for the new strain used (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Phylogenetic trees were constructed based on LSU, ITS, SSU and TEF1-α sequence data with 54 strains, including our new strain Alpinaria rhododendri (MFLU 20-0278) (Table 1). Sequences of available closely related taxa to A. rhododendri from Melanommataceae were retrieved from GenBank (2020). Pleomassaria siparia (CBS 279.74) and Prosthemium betulinum (VM 20040721) were treated as outgroup taxa based on Liu et al. (2017) whereas Melanommataceae shows sister clade relationship to Pleomassariaceae.

Phylogenetic analyses of both individual and combined data were performed under maximum likelihood (ML) and Bayesian criteria. Multiple alignments were made with MAFFT v. 7 (http://mafft.cbrc.jp/alignment/server), using default settings (Katoh et al. 2017) and further refined manually with BioEdit v. 7.0.5.2. Terminal ends of the sequences and ambiguous regions were trimmed manually where necessary using BioEdit v. 7.0.5.2 (Hall 1999) and excluded from the dataset. The phylogeny web tool "ALTER" (Glez-Peña et al. 2010) was used to convert sequence alignment from FASTA to PHYLIP for RAXML analysis and from FASTA to NEXUS format for Bayesian analysis. The ML phylogenetic tree was generated using the RAxML-HPC2 on XSEDE (8.2.8) (Stamatakis 2014) in the CIPRES Science Gateway platform (Miller et al. 2010) with 1000 separate runs. MrBayes v. 3.1.2 was used to perform Bayesian analysis (Huelsenbeck & Ronqvist 2001). The best evolutionary models for phylogenetic analyses were selected independently for each locus using MrModeltest v. 2.3 (Nylander 2004) under the Akaike Information Criterion (AIC). The GTR+I+G model was selected as the best-fit model for LSU, ITS and TEF1-α while HKY model was selected as the best-fit model for SSU to evaluate Posterior probabilities (PP). Markov Chain Monte Carlo sampling (MCMC) was run for 5,000,000 generations and trees were sampled every 100<sup>th</sup> generation. The first 10% of the trees that represented the burn-in phase were discarded and only the remaining 90% of the trees were used for calculating posterior probabilities (PP) for the majority rule consensus tree. The resulting trees were drawn in FigTree v1.4.0 (Rambaut 2012), then copied to Microsoft PowerPoint 2013 and converted to jpeg files using Adobe Photoshop CS6 version 13.0.

### Results

# **Phylogenetic analyses**

Multiple genes (LSU, SSU, ITS, TEF1- $\alpha$ ) were used for the phylogenetic analyses. The topologies of the obtained trees for each gene were compared manually to verify the topology. The single gene tree topology and the tree topology obtained from the combined alignment were congruent. The alignment comprised of 3184 total characters, including gaps. The best scoring RAxML tree was selected to represent the relationships among the taxa, with the final ML optimization likelihood value of -11562.305313 (Fig. 1). The parameters for the GTR+I+G model of combined LSU, SSU, ITS and TEF1- $\alpha$  were as follows: estimated base frequencies; A = 0.248033, C = 0.239570, G = 0.269928, T = 0.242468, substitution rates AC = 1.925381, AG = 2.852414, AT = 1.658061, CG = 1.082188, CT = 12.456589 and GT = 1.000000. The ML and Bayesian analyses both resulted in trees with similar topologies (data not shown). Bayesian posterior probabilities from MCMC were evaluated with final average standard deviation of split frequencies = 0.009434. In the phylogenetic analyses, our new strain *Alpinaria rhododendri* (MFLU 20-0278) clustered with the extant strains of this species with high statistical support (98%/0.97).

# Alpinaria rhododendri (Niessl) Jaklitsch & Voglmayr, Sydowia 69: 84 (2017) Fig. 2

Index Fungorum number: 819136, Facesoffungi number: FoF07843

Saprobic on dead wood. Sexual morph: Ascomata perithecial, 355–420 µm high × 390–460µm diam., ( $\bar{x} = 387.5 \times 425 \mu$ m, n = 5), superficial, solitary or in groups, globose to subglobose, often fusing laterally, black, ostiolate. Ostiole papillate, filled with brown cells. Peridium coriaceous, composed of two layers, outer layers 20–50 µm, heavily pigmented, thin walled, dark brown cells of textura angularis, inner layers 30–40 µm, light brown, thick walled cells of textura prismatica and textura angularis vary between regions. Hamathecium composing numerous, branched pseudoparaphyses. Asci 95–110 × 8–10 µm ( $\bar{x}$ = 101.5 × 9 µm, n = 20), bitunicate, fissitunicate, cylindrical, apex thick-walled, containing a narrow, inversely funnel-shaped ocular chamber, pedicel short, base knob-like. Ascospores 14–18 × 4–5 µm ( $\bar{x}$  = 16 × 4.5 µm, n = 40), 8-spored, uniseriate, ellipsoid, medium to greyish brown, 1–3 septate, septa appearing thicker than the wall, constricted at the median primary septum, upper part or second cell slightly enlarged, end cells sometimes slightly lighter, obtuse, sometimes with one large guttule per cell, smooth-walled. Asexual morph: undetermined.

Material examined – CHINA, Yunnan Province, Diqing Prefecture, Shangri La, on wood of an unidentified dicotyledonous host, N 27° 55' 05.8", E 099° 36' 33.4", 3234m, 14 September 2018, V. Thiyagaraja (MFLU 20-0278).

# Discussion

Alpinaria was introduced by Niessl (1872) to accommodate Cucurbitaria rhododendri. Petrak (1931) treated this taxon in Gibberidea, with a detailed description. Later, Holm (1968) argued that *M. rhododendri* was a valid name and should be considered as a heterotypic synonym of *C. rhododendri* and transferred Gibberidea rhododendri to Melanomma. Jaklitsch & Voglmayr (2017) initially provided the sequence data for *M. rhododendri* and established the new genus Alpinaria by epitypifying *C. rhododendri*. A subsequent study conducted by Hashimoto et al. (2017) treated Alpinaria under incertae sedis in Pleosporales based on the first morphological observation from the asexual morph that had phylogenetic support. This showed *A. rhododendri* clustered outside of Melanommataceae sensu stricto. Phenotypically, Alpinaria differs from the type genus Melanomma by having thick-walled cells of textura prismatica and textura angularis in the inner layer of peridium and ellipsoid ascospores. In contrast, thin-walled cells of textura angularis with fusoid ascospores were observed in Melanomma (Tian et al. 2015). Nonetheless, Wanasinghe et al. (2018) and Hongsanan et al. (2020) accepted Alpinaria within Melanommataceae based on the results of combined multigene phylogenetic analyses. The taxon which we report from Shangri La, from an unidentified dicotyledonous plant, is the first *Alpinaria* record for China. This finding demonstrates that the geographical range of *Alpinaria* is wider than previously reported. Our study supported taxonomic placement of *A. rhododendri* based on evidence from both morphology and multigene phylogenetic analyses of LSU, SSU, ITS and TEF1- $\alpha$  sequence data.

Byssosphaeria siamensis MFLUCC 10-0099						
83/0.99 - Byssosphaeria musae MFLUCC 11-0146						
100/1.00 Byssosphaeria salebrosa SMH 2387 Byssosphaeria diffusa CBS 250.62	Byssosphaeria					
Byssosphaeria rhodomphala GKM	L153N					
<sup>69/0.96</sup> Byssosphaeria jamaicana SMH 140	3					
Bertiella macrospora SMH 3953	Bertiella					
Fusiconidium mackenziei MFLUCC 14-0434	Eucioonidium					
<sup>100/0.96</sup> <i>Fusiconidium mackenziei</i> HKAS 95019	Fusiconiaian					
Camposporium antennatum ICMP:15321	Camposporium					
84/- 95/- Phragmocephala garethjonesii MFLUCC 15-0018	Dhraamaaanhala					
Phragmocephala atra MFLUCC 15-0021	Fillagillocephala					
Pseudostrickeria muriformis MFLUCC 13-0764	Pseudostrickeria					
83/0.96 Sarimanas shirakamiense MAFF 244768	0					
100/1.00 Carimanas pseudofluviatile MAFF 239465	Sarimanas					
Pleotrichocladium opacum FMR 12416	Pleotrichocladium					
Monoseptella rosae MFLUCC 17-0815	Monosentella					
100/1.00 <sup>1</sup> Monoseptella rosae TASM 6114	wowoseptena					
99/1.00 100/1.00 Melanomma pulvis pyrius CBS 124080	Melanomma					
Melanomma japonicum MAFF 239634						
Melanocucurbitaria uzbekistanica MFLUCC 17-0829	Melanocucurbitaria					
Alpinaria rhododendri KT 2520						
99/1 00 Alpinaria rhododendri UEMGCB 13867	Alpinaria					
98 <sup>0.97</sup> Alpinaria rhododendri CBS 141994						
98/p.97 Alpinaria rhododendri MFLU 20-0278						
86/0 99 Melanodiplodia tianschanica TASM 6112						
ILI Melanodiplodia tianschanica TASM 6111 99/1.00 Melanodiplodia tianschanica MELUCC 17.0805	Melanodiplodia					
Melandulpidua transchanica MPLOCC 17-0803						
100/1.00 <i>Muriformistrickeria rubi</i> MFLUCC 15-0681	Muriformistrickeria					
Muriformistrickeria rosae MFLU 16-0227						
Seifertia azaleae ZTMYc 59954	Seifertia					
100/1.00 <sup>o</sup> Seifertia shangrilaensis MFLUCC 16-0238	nacamaraanariaidaa					
	nocamarosponoides					
100/1 on Praetumpfia obducens C2						
100/1.00 Praetumpfia obducens CuO	Praetumpfia					
68/0.90 Praetumpfia obducens C54						
Aposphaeria corallinolutea PD 83/367	Aposphaeria					
Aposphaena coralilinolutea MFLO 15-2752						
100/1.00 Uzbekistanica yakutkhanica MFLUCC 17-0842	Uzbekistanica					
<sup>91/1.00</sup> Uzbekistanica rosae hissaricae MFLUCC 17-0819	e Lis on notai nota					
Herpotrichia macrotricha GKM 196N	Herpotrichia					
87/0.991 Marjia tianschanica TASM 6121						
100/1.00 Marija uzbekisanica TASM 6120	Marjia					
100/JI Pleomassaria sibaria CBS 279.74						
Prosthemium betulinum VM 20040721	Outgroup					
0.02						

**Fig. 1** – RAxML tree based on analyses of combined ITS, LSU, SSU and TEF1- $\alpha$  dataset. Bootstrap support values for maximum likelihood greater than or equal to 65% and Bayesian posterior probabilities greater than or equal to 0.95 are given above each branch. The new strain is in blue bold font. The tree is rooted to *Pleomassaria siparia* (CBS 279.74) and *Prosthemium betulinum* (VM 20040721).

In our multigene phylogenetic analyses, the new strain MFLU 20-0278 clustered with the strains of *A. rhododendri* (KT 2520, MP4, UFMGCB 13867 and UFMGCB 13863). Our strain shares similar morphological features to other *A. rhododendri* records such as the size of ascomata  $(355-420 \ \mu m \ vs. (270)325-505(630) \ \mu m \ diam)$ , asci  $(95-110 \times 8-10 \ \mu m \ vs. (94)98-114(123) \times (8)8.5-10(10.5))$  and ascospores  $(14-18 \times 4-5 \ \mu m \ vs. (12.5)14.3-17.0(18.5) \times (5)5.5-6.6(7.5) \ \mu m)$ . They also share similarities in their shape of ascomata (globose), asci (cylindrical) and ascospores (ellipsoid to fusoid), papillate ostiole, inversely funnel-shaped ocular chamber, fissitunicate, bitunicate asci, ellipsoid to fusoid ascospores and occasionally present guttules in the ascospores (Jaklitsch & Voglmayr 2017).



**Fig. 2** – *Alpinaria rhododendri* (MFLU 20-0278). a-c Ascomata on substrate. d Vertical-section of an ascoma. e Peridium. f Psuedoparaphyses. g Ostiole. h Ascus apex. i-m Asci. n-q Ascospores. Scale bars:  $a = 500 \mu m$ ,  $b-d = 200 \mu m$ ,  $e = 30 \mu m$ ,  $f= 10 \mu m$ , g, i-m = 50  $\mu m$ , h, n-q = 10  $\mu m$ .

In contrast, our *A. rhododendri* strain differs from other *A. rhododendri* strains in its superficial ascomata. However, erumpent ascomata became superficial in the later stage of *A. rhododendri* (Jaklitsch & Voglmayr 2017). Based on its base pairs, our new strain is not significantly different to other reported strains of *A. rhododendri*. Our *A. rhododendri* strain formed a well-supported clade (98%) with other *A. rhododendri* strains. Some strains of *A. rhododendri* (UFMGCB 13867 and UFMGCB 13863) do not have their complete gene sequences in the GenBank. *Alpinaria rhododendri* has previously been recorded in several other geographical areas, including the European Alps, Europe, the Indian Himalayas and North America (Jaklitsch & Voglmayr 2017).

**Table 1** Taxa used in the phylogenetic analyses with their GenBank accession numbers. The extype sequences are in black bold type and the newly generated sequence from this study is written in blue bold type

Species	Strain	GenBank Accession Numbers			
		ITS	LSU	SSU	TEF1-α
Alpinaria rhododendri	MFLU 20-0278	MT229210	MT229208	MT229209	MT254066
Alpinaria rhododendri	KT 2520	LC203335	LC203360	LC203314	LC203388
Alpinaria rhododendri	MP4	KY189973	KY189973	KY190004	KY190009
Alpinaria rhododendri	UFMGCB 13867	MK638847	_	_	-
Alpinaria rhododendri	UFMGCB 13863	MK638855	-	-	-
Aposphaeria corallinolutea	MFLU 15-2752	KY554202	KY554197	-	KY554205
Aposphaeria corallinolutea	PD 83/367	_	JF740329	-	_
Bertiella macrospora	SMH 3953	-	_	_	GU327744
Byssosphaeria diffusa	CBS 250.62	-	DQ678071	DQ678019	DQ677915
Byssosphaeria jamaicana	SMH 1403	_	GU385152	_	GU327746
Byssosphaeria musae	MFLUCC 11- 0146	KP744435	KP744477	KP753947	-
Byssosphaeria rhodomphala	GKM L153N	_	GU385157	_	GU327747
Byssosphaeria salebrosa	SMH 2387	_	GU385162	_	GU327748
Byssosphaeria siamensis	MFLUCC 10- 0099	_	KT289895	KT289897	-
Camposporium antennatum	ICMP:15321	EF029221	-	_	_
Camposporium ramosum	CBS 132483	MH866030	_	_	_
Fusiconidium mackenziei	MFLUCC 14- 0434	-	KX611112	KX611114	KX611118
Fusiconidium mackenziei	HKAS 95019	-	KX611113	KX611115	KX611119
Herpotrichia macrotricha	GKM 196N	_	GU385176	_	GU327755
Marjia tianschanica	<b>TASM 6120</b>	MG828909	MG829019	MG829126	MG829206
Marjia tianschanica	TASM 6121	MG828910	MG829020	MG829127	MG829207
Marjia uzbekisanica	<b>TASM 6122</b>	MG828911	MG829021	MG829128	MG829208
Melanocamarosporioides	MFLUCC 17-	MH000192	MH000190	MH000191	MH006610
ugamica	2314				
Melanocucurbitaria	MFLUCC 17-	MG828912	MG829022	MG829129	MG829209
uzbekistanica Melanodiplodia tianschanica	0829 MFLUCC 17- 0805	MG828913	MG829023	MG829130	MG829210
Melanodiplodia tianschanica	TASM 6111	MG828914	MG829024	MG829131	MG829211
Melanodiplodia tianschanica	TASM 6112	MG828915	MG829025	MG829132	MG829212
Melanomma japonicum	MAFF 239634	LC203321	LC203339	NG_065122	LC203367
Melanomma pulvis-pyrius	MPP	KY189979	KY189979	_	KY190014
Melanomma pulvis-pyrius	CBS 124080	_	GU456323	GU456302	GU456265

# Table 1 Continued.

Species	Strain	GenBank Accession Numbers			
_		ITS	LSU	SSU	TEF1-α
Monoseptella rosae	MFLUCC 17- 0815	MG828916	MG829026	MG829133	MG829213
Monoseptella rosae	TASM 6114	MG828917	MG829027	MG829134	MG829214
Muriformistrickeria rosae	MFLU 17-2550	MG828919	MG829029	MG829136	MG829216
Muriformistrickeria rosae	MFLU 16-0227	MG828918	MG829028	MG829135	-
Muriformistrickeria rubi	MFLUCC 15- 0681	-	КТ934253	KT934257	KT934261
Phragmocephala atra	MFLUCC 15-0021	KP698721	KP698725	KP698729	
Phragmocephala garethjonesii	MFLUCC 15- 0018	NR_147636	NG_059548	NG_063567	-
Pleomassaria siparia	CBS 279.74	AB554089	DQ678078	DQ678027	DQ677923
Pleotrichocladium opacum	CBS 142288	HF678530	HF678540	-	-
Pleotrichocladium opacum	FMR 12416	KY853462	KY853523	-	-
Praetumpfia obducens	C2	KY189982	KY189982	-	KY190017
Praetumpfia obducens	C54	KY189984	KY189984	KY190008	KY190019
Praetumpfia obducens	C56	KY189985	KY189985	-	KY190020
Praetumpfia obducens	CuO	KY189987	KY189987	-	KY190021
Prosthemium betulinum	VM 20040721	AB554085	AB553754	AB553644	_
Pseudostrickeria muriformis	MFLUCC 13- 0764	-	KT934254	KT934258	KT934262
Pseudostrickeria ononidis	MFLUCC 14- 0949	-	KT934255	KT934259	KT934263
Sarimanas pseudofluviatile	MAFF 239465	LC001717	LC001714	LC001711	-
Sarimanas shirakamiense	MAFF 244768	LC001718	LC001715	LC001712	-
Seifertia azaleae	ZTMYc 59954	MK502004	MK502028	MK502038	MK502085
Seifertia shangrilaensis	MFLUCC 16- 0238	-	KU954100	KU954101	KU954102
Uzbekistanica rosae-	MFLUCC 17-	MG828975	MG829087	MG829187	MG829242
hissaricae	0819		MCOADOO	MC020100	MCOOOAA
Uzbekistanica yakutkhanica	MFLUCC 17- 0809	MG828977	MG829089	MG829189	MG829244
Uzbekistanica yakutkhanica	MFLUCC 17- 0842	MG828978	MG829090	MG829190	MG829245

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