Seifertia shangrilaensis sp. nov. (Melanommataceae), a new species from Southwest China

JUNFU LI1,2,3,4, RUNGTIWA PHOOKAMSAK2,3,4,7, AUSANA MAPOOK3,4, SARANYAPHAT BOONMEE3, JARAYAMA D. BHAT5,6, KEVIN D. HYDE1,2,3,4 & SAISAMORN LUMYONG1,*
1Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand.
2World Agroforestry Centre, East and Central Asia, 132 Lanhei Road, Kunming 650201, China.
3Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand.
4School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand.
5Formerly, Department of Botany, Goa University, Goa-403206, India.
6128/1-J, Azad Housing Society, Curca, Goa Velha-403108, India.
7Key Laboratory of Biodiversity and Biogeography, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China.
Correspondence to*: scboi009@gmail.com

Abstract

A new Seifertia species was isolated from hanging rachides of Rhododendron decorum in Yunnan Province, Southwest China. The new taxon was compared with the type species, S. azalea and differs in having wider conidiophores, with hyaline to subhyaline and smaller conidia, while S. azalea has olive-brown to brown, rarely branched conidiophores, and pale brown or olive-brown, very rarely septate conidia. Phylogenetic analyses of combined LSU, SSU and TEF1-α sequence data show that S. shangrilaensis forms a robust clade with S. azalea nested among the species of Melanommataceae in the order Pleosporales. A new species, S. shangrilaensis is introduced in this study, and Seifertia should be placed in Melanommataceae (Pleosporales, Dothideomycetes) based on phylogenetic analysis. Description and illustration of Seifertia shangrilaensis are provided with notes and its introduction is supported by molecular data.

Keywords: Dothideomycetes, hyphomycetous fungi, Melanommataceae, phylogeny, taxonomy

Introduction

Seifertia was introduced as a monotypic genus by Partridge and Morgan-Jones (2002) and is typified by S. azaleae (Peck) Partridge & Morgan-Jones which was originally described as Periconia azaleae Peck. with the names Briosia azaleae (Peck) Dearn, Cephalotrichum azaleae (Peck) Kuntze, Pycnostyssamus azalea (Peck) E.W. and Sporocybe azaleae (Peck) Sacc. treated as synonyms (Partridge & Morgan-Jones 2002, Glawe & Hummel 2006, Index Fungorum 2016).

Seifertia azalea has been reported as a cosmopolitan taxon causing bud blast and twig blight of azaleas and rhododendrons in Japan, Europe and North America (Mason 1941, Ellis 1976, Farr et al. 1996, Partridge & Morgan-Jones 2002, Glawe & Hummel 2006). However, Seifertia species are relatively poorly studied worldwide, and have not been studied in the southwest of China. Based on phylogenetic analysis of LSU sequence data, Seifert et al. (2007) treated Seifertia azalea in Dothideomycetes, as closely related to Mycosphaerella mycopappt A. Funk & Dorworth, but unrelated to Mycosphaerella sensu stricto. Crous et al. (2009, 2013) placed Seifertia in Pleosporales which was shown to be allied to Xenostigmina, a synanamorph of Mycopappus, based on combined ITS and LSU phylogenetic analyses. There is little molecular data to resolve the natural placement of Seifertia in Dothideomycetes.

The aim of this study is to introduce a new species, Seifertia shangrilaensis, collected from Yunnan Province, Southwest China. The species is described and illustrated with phylogenetic support. Seifertia shangrilaensis is the first record of Seifertia for China.
Materials and methods

Isolation and morphology
The specimen was collected from a living branch of *Rhododendron decorum* Franch. (Ericaceae) in Yunnan Province, southwest China and brought to the laboratory for examination and description of fungal morphology. The specimens were observed under a Motic SMZ 168 series dissecting stereo-microscope. The conidial structures were picked up using a surgical needle and a squash mount was prepared in 10% lacto-glycerol for examination under a Nikon Eclipse 80i compound microscope. Photographs were made with a Canon 600D digital camera using DIC microscopy. The macro-morphological structures were photographed with a Discovery V.8 stereo-microscope fitted with a CARL ZEISS Axio Cam ERC5S microscope camera. Tarosoft (R) Image Frame Work program and a Adobe Photoshop version CS5 (Adobe Systems Inc., The United States) were used for measurements and photographic plates.

Single spore isolation was carried out to obtain a pure culture as described in Chomnunti et al. (2014). Type specimen is deposited in the herbarium of Mae Fah Luang University (MFLU), Chiang Rai, Thailand and duplicated in the Herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (KUN-HKAS), Yunnan, China. Ex-type living cultures are deposited in Mae Fah Luang University Culture Collection (MFLUCC) and Kunming Institute of Botany Culture Collection (KUMCC). Faces of Fungi and Index Fungorum numbers were provided as in Jayasiri et al. (2015) and Index Fungorum (2016).

DNA extraction, PCR amplification and sequencing
The fungal mycelia were scraped by using a sterilized lancet to reduce the contamination and kept in a 1.5 ml microcentrifuge tube for DNA extraction. The genomic DNA was extracted by using the Biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (BioFlux®, P.R. China) following the protocols in the manufacturer’s instructions. The DNA product was maintained at 4 °C for the DNA amplification and duplicated at -20 °C for long term storage.

The DNA amplification was performed by polymerase chain reaction (PCR) using the respective genes (LSU, SSU and TEF1-α). The primers LROR and LR5 (Vilgalys & Hester 1990) were used to amplify the partial ribosomal RNA for the nuclear large subunit (LSU), NS1 and NS4 (White et al. 1990) were used to amplify the partial ribosomal RNA for the nuclear small subunit (SSU) and EF1-983F and EF1-2218R (Rehner 2001) were used to amplify the translation elongation factor 1-alpha gene (TEF1-α). The final volume of the PCR reaction were 25 μl, containing 1 μl of DNA template, 1 μl of each forward and reward primer, 12.5 μl of 2x Master mixture and 9.5 μl of ddH2O. The PCR thermal cycling conditions were processed by initialization at 94 °C for 3 minutes, followed by 35 cycles of denaturation at 94 °C for 30 seconds, annealing at 55 °C for 50 seconds, elongation at 72 °C for 1 minute, and a final extension at 72 °C for 10 minutes, and final kept at 4°C for keeping DNA. The PCR products were checked on 1% agarose gel electrophoresis stained with ethidium bromide. Purification and DNA sequencing were carried out at Shanghai Biological Engineering Technology Co., Ltd, P.R. China.

Sequence alignment and phylogenetic analyses
Phylogenetic analyses were performed by combined LSU, SSU and TEF1-α sequence data. Sequences generated from this study were analyzed with other similar sequences, obtained from the GenBank and those derived from Crous et al. (2013) and Tian et al. (2015) (Table 1). A single gene alignment was performed by using MAFFT v. 7 (Katoh & Standley, 2013: http://mafft.cbrc.jp/alignment/server/) and manual aligned where necessary in MEGA version 6.0 (Tamura et al. 2013). Further analyses were performed by using RAxML GUI v.0.9b2 (Stamatakis 2006, 2014, Stamatakis et al. 2008, Silvestro & Michalak 2010) and Bayesian analysis (BI) (Huelsenbeck & Ronquist 2001, Huelsenbeck et al. 2001) following the methodology as described in Phookamsak et al. (2015).

The phylograms are represented in Treeview (Page 1996) and drawn in Microsoft power point and converted to jpeg file in Adobe Photoshop version CS5 (Adobe Systems Inc., The United States). The new sequences were submitted in GenBank (Table 1).

Results
Phylogenetic analyses
The combined LSU, SSU and TEF1-α sequence data comprised 36 taxa with *Hysterium angustatum* (CBS 123334, CBS 236.34) selected as the outgroup taxon. The best scoring tree from RAxML analysis is chosen to represent
the phylogenetic relationships among a newly generated taxon with other genera in Melanommataceae and Pleomassariaceae in Dothideomycetes (Fig. 1). The phylogenetic analyses obtained from maximum likelihood and Bayesian analyses gave similar topologies of the relationships in Melanommataceae and Pleomassariaceae and were not significantly different. Phylogenetically shows that *Seifertia shangrilaensis* (MFLUCC 16-0238) belongs to the family Melanommataceae (Pleosporales, Dothideomycetes) which forms a robust clade to *S. azalea* (97% ML, 0.99 PP) and formed a sister group with *Xenostigmina zilleri* (A. Funk) Crous (Fig. 1). Therefore, a new species, *Seifertia shangrilaensis* is established.

**TABLE 1.** Taxa used in the phylogenetic analyses and their corresponding GenBank numbers. The newly generated sequences are indicated in red bold and the type strains are in bold.

<table>
<thead>
<tr>
<th>Species</th>
<th>Culture collection</th>
<th>GenBank accession numbers</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Aposphaeria populina</em></td>
<td>CBS 543.70</td>
<td>EU754130 EU754031</td>
</tr>
<tr>
<td><em>Aposphaeria populina</em></td>
<td>CBS 350.82</td>
<td>JF740265 -</td>
</tr>
<tr>
<td><em>Byssosphaeria jamaicana</em></td>
<td>SMH 1403</td>
<td>GU385152 -</td>
</tr>
<tr>
<td><em>Byssosphaeria jamaicana</em></td>
<td>SMH 3085</td>
<td>GU385154 -</td>
</tr>
<tr>
<td><em>Byssosphaeria rhodophala</em></td>
<td>SMH 3086</td>
<td>GU385155 -</td>
</tr>
<tr>
<td><em>Byssosphaeria rhodophala</em></td>
<td>GKM L153N</td>
<td>GU385157 -</td>
</tr>
<tr>
<td><em>Byssosphaeria salerosa</em></td>
<td>SMH 2387</td>
<td>GU385162 -</td>
</tr>
<tr>
<td><em>Byssosphaeria schiedermayeriana</em></td>
<td>SMH 3157</td>
<td>GU385163 -</td>
</tr>
<tr>
<td><em>Byssosphaeria schiedermayeriana</em></td>
<td>GKM 152N</td>
<td>GU385168 -</td>
</tr>
<tr>
<td><em>Byssosphaeria villosa</em></td>
<td>GKM 204N</td>
<td>GU385151 -</td>
</tr>
<tr>
<td><em>Byssosphaeria musae</em></td>
<td>MFLUCC 11-0146</td>
<td>KPI74477 KPI753947 -</td>
</tr>
<tr>
<td><em>Byssosphaeria siamensis</em></td>
<td>MFLUCC 10-0099</td>
<td>KT289895 KT289897 KT962059</td>
</tr>
<tr>
<td><em>Byssosphaeria schiedermayeriana</em></td>
<td>MFLUCC 10-0100</td>
<td>KT289894 KT289896 KT962060</td>
</tr>
<tr>
<td><em>Herpotrichia diffusa</em></td>
<td>CBS 250.62</td>
<td>DQ678071 DQ678019</td>
</tr>
<tr>
<td><em>Herpotrichia juniper</em></td>
<td>CBS 200.31</td>
<td>DQ678080 DQ678029</td>
</tr>
<tr>
<td><em>Herpotrichia juniperi</em></td>
<td>CBS 468.64</td>
<td>DQ384093 DQ384077 -</td>
</tr>
<tr>
<td><em>Herpotrichia macrotricha</em></td>
<td>GKM 196N</td>
<td>GU385176 -</td>
</tr>
<tr>
<td><em>Herpotrichia macrotricha</em></td>
<td>SMH 269</td>
<td>GU385177 -</td>
</tr>
<tr>
<td><em>Hysterium angustatum</em></td>
<td>CBS 123334</td>
<td>FJ161207 FJ161167 FJ161111</td>
</tr>
<tr>
<td><em>Hysterium angustatum</em></td>
<td>CBS 236.34</td>
<td>FJ161180. GU397359 FJ161096</td>
</tr>
<tr>
<td><em>Melanomma pulvis-pyrius</em></td>
<td>CBS 124080</td>
<td>GU456323 GU456302 GU456265</td>
</tr>
<tr>
<td><em>Melanomma pulvis-pyrius</em></td>
<td>CBS 109.77</td>
<td>FJ201986 FJ201987 GU456274</td>
</tr>
<tr>
<td><em>Melanomma pulvis-pyrius</em></td>
<td>CBS 371.75</td>
<td>FJ201988 FJ201989 GU439019</td>
</tr>
<tr>
<td><em>Melanomma rhododendri</em></td>
<td>ANM 73</td>
<td>GU385198 -</td>
</tr>
<tr>
<td><em>Monotosporella tuberculata</em></td>
<td>CBS 256.84</td>
<td>GU301851 -</td>
</tr>
<tr>
<td><em>Mycopappus aceris</em></td>
<td>CBS 124109</td>
<td>FJ98660.</td>
</tr>
<tr>
<td><em>Pleomassaria siparia</em></td>
<td>CBS 279.74</td>
<td>DQ678078 DQ678027 DQ677923</td>
</tr>
<tr>
<td><em>Prosthemium betulinum</em></td>
<td>CBS 127468</td>
<td>AB553754 AB553644 -</td>
</tr>
<tr>
<td><em>Prosthemium canba</em></td>
<td>JCM 16966</td>
<td>AB553760 AB553646 -</td>
</tr>
<tr>
<td><em>Prosthemium orientale</em></td>
<td>JCM 12841</td>
<td>AB553748 AB553641 -</td>
</tr>
<tr>
<td><em>Prosthemium stellar</em></td>
<td>CBS 126064</td>
<td>AB553781 AB553650 -</td>
</tr>
<tr>
<td><em>Seifertia azalea</em></td>
<td>DAOM 239136</td>
<td>EU030276 -</td>
</tr>
<tr>
<td><em>Seifertia shangrilaensis</em></td>
<td>MFLUCC 16-0238</td>
<td>KU954100 KU954102 KU954101</td>
</tr>
<tr>
<td><em>Xenostigmina zilleri</em></td>
<td>CBS 115686</td>
<td>GU253858 -</td>
</tr>
<tr>
<td><em>Xenostigmina zilleri</em></td>
<td>CBS 115685</td>
<td>GU253857 -</td>
</tr>
<tr>
<td><em>Xenostigmina zilleri</em></td>
<td>CBS 124108</td>
<td>FJ839675 -</td>
</tr>
</tbody>
</table>

Abbreviations: ANM: A.N. Miller; CBS: Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands; DAOM: Canadian Collection of Fungal Cultures, Ottawa, Canada; GKM: G.K. Mugambi; IL: I. Lopez; JK: J. Kohlmeyer; KT: K. Tanaka; MAFF: Ministry of Agriculture, Forestry and Fisheries, Japan; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; SMH: S.M. Huhndorf.

**Taxonomy**

*Seifertia shangrilaensis* J.F. Li, Phookamsak & K.D. Hyde, sp. nov. Fig. 2

Index Fungorum number: IF552010; Facesoffungi number: FoF 01885
Etymology:—Refers to the location, where the holotype was collected.

Diagnosis:—Differs from Seifertia azalea in its shorter and hyaline to subhyaline conidia.

**Holotype:** MFLU 16-0267

*Epiphytic* on living rachides of *Rhododendron decorum* Franch. **Sexual morph:** Undetermined. **Asexual morph:** Synnemata 1000–2300 μm high, 120–200 μm wide, erect, simple, unbranched, dark brown to black, with bubble-like, tightly interwoven, branched hyphae, compacted into an elongate bundle. *Mycelium* superficial, partly immersed on the substrate, composed of septate, branched, smooth, thin-walled, pale white to white hyphae. *Conidiophores* (1000–) 1300–2100 (–2150) × (9.5–) 10–11 (–13) μm, (X = 1804.7 × 10.3 μm, n = 40), synnematos, closely packed into a bundle, hyaline to pale brown, thin-walled, smooth, septate, unbranched, straight or flexuous, cylindrical. *Conidiogenous cells* (5–) 7–11 (–12.5) × (4.5–) 5.5–6.5 (–7) μm, (X = 7.9 × 5.8 μm, n = 100), holoblastic, phialidic, integrated, terminal, determinate, subhyaline, cylindrical to subclavate, smooth. *Conidia* (2.5–) 3.5–5 (–6) × 2.5–3.5 μm (X = 4.2 × 3.1 μm, n = 100), phialoconidia, hyaline to subhyaline, fusiform to subglobose, or ellipsoidal, aseptate, borne in basipetally, developing pseudo-chains, clavate, smooth, thin-walled, sometimes aggregated into slimy masses at the apex of the synnema.

**FIGURE 1.** Phylogenetic construction using RAxML tree based analysis of a combined dataset of LSU, SSU and TEF1-α. Bootstrap support values for maximum likelihood (ML, black), equal or greater than 70% and Bayesian posterior probabilities (PP, red) equal to or greater than 0.95 are shown above the nodes. The tree is rooted to *Hysterium angustatum* (CBS 236.34 and CBS 123334). The type strains are in black bold and the newly generated sequences are indicated in red bold.
Cultural characteristics:—Conidia germinating on PDA within 14 hours at 15 ºC, germ tubes produced from apex. Colonies growing on PDA, reaching 5 mm diam. after 4 weeks at 25 ºC, mycelium semi-immersed to superficial, irregular in shape, flat, slightly raised, with undulate edge, slightly rough on surface, cottony to fairy fluffy, colony from above, initially write to cream at the margin, yellowish-brown in the centre, becoming white at the margin, dark brown at the centre after 4 weeks; from below, initially, cream at the margin, orangish-brown to reddish-brown at the centre, becoming dark brown to black after 4 weeks, producing brown pigmentation in agar.

Material examined:—CHINA, Yunnan Province, Shangrila, on living rachides of Rhododendron decorum (Ericaceae), 20 October 2014, R. Phookamsak, SgL027 (MFLU 16-0267, holotype!, KUN-HKAS 93733, isotype!), ex-type living culture, MFLUCC 16-0238!, KUMCC 16-0002.

Known distribution:—widespread in temperate and boreal regions.

Notes:—Seifertia shangrilaensis is similar to the type species, Seifertia azalea in having narrow and pale conidia, with one or two conidiogenous loci of conidiogenous cells, dark conidiophores and erect, synnemata (Partridge & Morgan-Jones 2002, Glawe et al. 2006, Seifert et al. 2007). However, S. shangrilaensis differs from S. azalea in having hyaline to subhyaline, and wider conidiophores (9.5–12.6 μm vs. 4–7 μm), and smaller conidia (2.5–6 × 2.5–3.6 μm vs. 4–12 × 4–8 μm).

FIGURE. 2. Seifertia shangrilaensis (MFLU 16-0267, holotype). a. Living rachides of Rhododendron decorum. b. Appearance of synnema on rachides. c. A synnema visualized under the compound microscope. d–h. Conidiogenous cells. i–p. Conidia. q–s. Germinating conidia. t–u. Multiple culture colonies from above. v. Single colony on PDA after 4 weeks. Scale bars: t–u = 2 cm, v = 1 cm, a = 0.5 cm, b = 500 μm, c = 200 μm, g–h, j–k, q–s = 10 μm, d–f, i, 1–n = 5 μm.

Discussion

The genus Seifertia is relatively poorly studied and was introduced to accommodate a pathogen species occurring on Rhododendron in the UK. Based on the few sequence data available in GenBank, the placement of Seifertia is uncertain. According to its morphological characters, Seifertia was previously treated in various genera such as Periconia (Peck 1873), Pycnostyssanus (Mason 1941) and also considered a taxonomic synonymy of Sorocybe (Ellis 1976, Carmichael et al. 1980). The type species, Seifertia azalea is characterized by erect, simple, and dark synnemata, unicellular or
Several asexual morphs of melanommataceous genera have been reported. *Seifertia* is known to occur on azaleas and rhododendrons and is a cosmopolitan species causing bud blight or bud blast disease in Japan, Europe and North America (Mason 1941, Ellis 1976, Farr et al. 1996, Partridge & Morgan-Jones 2002, Glawe & Hummel 2006). Insects were thought to play a role of pathogenic distribution (Howell et al. 1962, Pirone 1978, Viennot-Bourgin 1981). Disease symptoms were as initially, infecting dead flower buds, and later, becoming blackened bearing numerous synnemata (Glawe & Hummel 2006). Pirone (1978) reported that 90% death of *Rhododendron* flowers were caused by *S. azalea*, with a perennial infection (Chant & Gbaja 1984, Glawe & Hummel 2006). Farr et al. (2007) listed eight *Rhododendron* species infected by *Seifertia azalea* in the USA viz. *R. arborescens* (Pursh) Torr., *R. catawbiense* Michx., *R. macrophyllum* D. Don ex G. Don, *R. maximum* L., *R. minus* Michx., *R. nudiflorum* (L.) Torr., *R. vaseyi* A. Gray and *R. viscosum* (L.) Torr. Recently, Farr and Rossman (2016) listed only two *Rhododendron* species, *R. hemsleyanum* and *R. ponticum* caused by *S. azalea* in the USA. However, further occurrence, incidence, host and geographical range were relatively poorly known (Glawe & Hummel 2006). Glawe & Hummel (2006) reported a new host, *R. hemsleyanum* infected by *S. azalea* in North America. They mentioned that the disease incidence was limited by a low number of vulnerable genotypes in collection, critical environmental conditions and some other factors.

*Seifertia* species has so far not been reported to occur on *Rhododendron decorum*. *Seifertia shangrialaensis* was collected from living rachides of *R. decorum* in South-west China. The species occurs on both living rachides and dead hanging rachides of *R. decorum*. *Seifertia shangrialaensis* appears to be a pathogen causing death of flower buds of *R. decorum*. The development of disease infection might be initially limited where the synnemata occurred, and later, infected widely in other host cells. However, pathogenicity test is not done in this study.

Seifert et al. (2007) treated *Seifertia* in Dothideomycetes based on the large subunit LSU gene sequence data and it clustered with *Mycosphaerella mycoperii*, but was unrelated to *Mycosphaerella sensu stricto*. Crous et al. (2009) re-examined *Xenostigmina* and confirmed that *Xenostigmina* is a synanamorph of *Mycopappus* and showed to be allied with *Seifertia* in Pleosporales. Furthermore, Crous et al. (2013) revealed that *Xenostigmina* and *Mycopappus* clustered in the Phaeosphaeriaceae. Phookamsak et al. (2014), however, they excluded *Mycopappus* and *Xenostigmina* from Phaeosphaeriaceae due to these genera forming a single clade close to Melanommataceae. Tian et al. (2015) accepted *Xenostigmina* and *Mycopappus* in Melanommataceae based on multiple gene phylogenetic analyses. Hyde et al. (2013) and Wijayawardene et al. (2014) did not treat *Seifertia*, while Tian et al. (2015) discussed its relationship with *Xenostigmina* and *Mycopappus*, but did not place it in Melanommataceae.

Several asexual morphs of melanommataceous genera have been reported. *Pyrenochaeta* is the asexual morph of *Herpotrichia* (Sivanesan 1984). *Aposphaeria* and *Phoma*-like asexual morphs have been reported for *Melanomma* species (Sivanesan 1984, Tian et al. 2015). These links however, need to be confirmed in the light of modern taxonomic treatments and molecular data (Tian et al. 2015). In this study, phylogenetic analyses of combined LSU, SSU and TEF1-α sequence data provide a support that *Seifertia* belongs in the family Melanommataceae, Dothideomycetes (*sensu* Hyde et al. 2013, Wijayawardene et al. 2014) and is distinct from *Mycopappus* and *Xenostigmina*.

**Acknowledgements**

We are grateful to the Mushroom Research Foundation and Thailand Research Fund (TRF: BRG5280002) for supporting this research. MFLU grant number 567110754 is thanked for supporting Hyphomycetes studies. Kevin D. Hyde thanks the Chinese Academy of Sciences, project number 2013T2S0030, for the award of Visiting Professorship for Senior International Scientists at Kunming Institute of Botany. Rungtiwa Phookamsak expresses sincere appreciations to The Royal Golden Jubilee Ph. D. Program (PHD/0090/2551) under the Thailand Research Fund for financial support. Ausana Mapook is grateful to Research and Researchers for Industries (RRI) PHD5710012 under the Thailand Research Fund for providing financial support. The author thanks to Eric H.C. McKenzie, Jian-Kui Liu, Dong-Qing Dai, Dhanushka Wanasinghe, Chonticha Singtripop, Qing Tian, Mingkwan Doilom, Ishani D. Goonasekara, Sirinapaonta and Jinzu Sun for their available suggestions and help. Kevin D. Hyde is Visiting Professor at King Saud University.

---

**SEIFERTIA SHANGRILAENSIS SP. NOV.**

Phytotaxa 273 (1) © 2016 Magnolia Press • 39
References


http://dx.doi.org/10.1007/s13225-015-0351-8


http://dx.doi.org/10.1093/molbev/mst010


http://dx.doi.org/10.1093/bioinformatics/12.4.357


http://dx.doi.org/10.5962/bhl.title.58612


http://dx.doi.org/10.1007/s13225-014-0308-3


http://dx.doi.org/10.1007/s13225-015-0352-7


http://dx.doi.org/10.3114/sim.2007.58.09


http://dx.doi.org/10.1093/bioinformatics/btl446


http://dx.doi.org/10.1093/bioinformatics/btu033


http://dx.doi.org/10.1080/10635150802429642


http://dx.doi.org/10.1093/molbev/mst197


http://dx.doi.org/10.1007/s13225-015-0350-9


http://dx.doi.org/10.1051/agro:19810204


http://dx.doi.org/10.1007/s13225-014-0309-2

http://dx.doi.org/10.1016/B978-0-12-372180-8.50042-1