



# Fungi *Seifertia sikhotensis* – a new species, and *Synnemapestaloides rhododendri* – a new record for Russia, causing blight disease of *Rhododendron brachycarpum* subsp. *fauriei* in the Central Sikhote-Alin

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Manuscript received: 23.03.2026  
Review completed: 04.05.2026  
Accepted for publication: 06.05.2026  
Published online: 09.05.2026

## ABSTRACT

A new species of the synnematosus fungus, *Seifertia sikhotensis* (Melanommataceae, Dothideomycetes), was described based on morphological data and multilocus sequence analysis (ITS+LSU+tef1- $\alpha$ ). This study also provides the first record of *Synnemapestaloides rhododendri* (Sporocadaceae, Sordariomycetes) in Russia. Both species were found infecting *Rhododendron brachycarpum* subsp. *fauriei* in its native continental populations located in the Sikhote-Alin Mountain Range (Primorsky Krai, Russia). The fungi form black synnemata with capitate apices, causing necrotic brown or greyish lesions on leaves, flower buds and twigs of *R. brachycarpum* subsp. *fauriei*. Detailed morphological descriptions of the studied fungal collections are provided and accompanied by the illustrations of microstructures, phylogenetic tree, and comparisons with related species. The specimens and data generated here are important for future studies into the evolution, the distribution patterns and ecological role of *Seifertia* spp. and other synnematosus fungi on wild rhododendrons in Russia.

**Keywords:** Ascomycota, taxonomy, diversity, phylogeny, Primorsky Krai, Russian Far East

## РЕЗЮМЕ

Мальшева В.Ф., Дудка В.А., Мальшева Е.Ф., Бондарчук С.Н. Грибы *Seifertia sikhotensis* – новый вид, и *Synnemapestaloides rhododendri* – новая находка в России, вызывающие увядание *Rhododendron brachycarpum* subsp. *fauriei* в центральном Сихоте-Алине. В статье описан новый для науки вид *Seifertia sikhotensis* (Melanommataceae, Dothideomycetes), на основании морфологического и филогенетического (ITS+LSU+tef1- $\alpha$ ) анализов. Также приводятся сведения о первой находке *Synnemapestaloides rhododendri* (Sporocadaceae, Sordariomycetes) в России. Оба вида поражают *Rhododendron brachycarpum* subsp. *fauriei* и были обнаружены в его природных континентальных популяциях на территории Сихоте-Алиния (Приморский край, Россия). Грибы образуют черные синнемы с головками на вершине, вызывающие некротические коричневые или сероватые поражения на листьях, цветочных почках и ветвях *R. brachycarpum* subsp. *fauriei*. В статье приведены подробные морфологические описания изученных коллекций грибов, сопровождаемые иллюстрациями микроструктур, филогенетическим деревом и сравнениями с родственными видами. Полученные здесь образцы и данные важны для будущих исследований эволюции, закономерностей распространения и экологической роли видов *Seifertia* и других паразитических грибов на дикорастущих рододендронах в России.

**Ключевые слова:** Аскомицота, таксономия, разнообразие, филогения, Приморский край, Российский Дальний Восток

Over long periods of time, humans have been dramatically altering their habitats, not only by exploiting natural resources but also by transporting and cultivating plant species outside their native range. It is well known that non-native plant species are often used in agricultural and forestry practices. This human-mediated globalization of plant ranges is steadily increasing. This trend has inevitable consequences, including impacts on natural ecosystems (Lovett et al. 2016, Santini et al. 2018). Thus, it has been shown that the number of invasive forest pathogens has increased exponentially over the past four decades. Before

1919, existing invasive forest pathogens were spreading across Europe. Subsequently, new invasive forest pathogens were introduced primarily from North America and, more recently, from Asia (Santini et al. 2013).

Environmental conditions in new and original habitats, as well as ecological characteristics, significantly influence the diffusion rates and pathogenicity of parasitic organisms. Global climate change has been shown to negatively impact plant photosynthesis, making plants more vulnerable to biotic attacks, especially by necrotrophic and root-infecting fungi (Hunjan & Lore 2020). Atmospheric conditions, par-

ticularly temperature and humidity, have a significant impact on fungal pathogenicity (Kumar & Mukhopadhyay 2025).

The genus *Rhododendron* L. is a species-rich genus of the family Ericaceae Juss., comprising more than 1200 species worldwide (Frodin 2004). Thirteen species occur in the Russian Far East (Khokhryakov & Mazurenko 1991). Of particular interest are the species listed in the Red Data Book of the Russian Federation (Geltman 2024), which have a fragmented range and small populations. One of these taxa is *Rhododendron fauriei* Franch. – a rare relict evergreen species found outside of Russia only in Korea and Japan. In Russia, known continental populations of *R. fauriei* (apart from the Kuril Islands) are only located on the Central part of Primorsky Krai, in the Sikhote-Alin Mountain Range, on the territory of the Sikhote-Alin Nature Reserve. It grows in dark-coniferous forests (with *Picea ajanensis* (Lindl. et Gord.) Fisch. ex Carr., *Abies nephrolepis* (Trautv.) Maxim. and *Pinus koraiensis* Siebold et Zucc.), from 650 to 850 m above sea level, mainly on the northern and northeast slopes in the Sikhote-Alin (Bondarchuk 2014, Pimenova 2015). Here, *R. fauriei* is characterized by group accommodation, where larger trees are surrounded by a lot of small undergrowth (Flyagina 1972). Seeds germinate mainly in deadwood, overgrown with moss. Plants develop slowly, reaching a height of 4–6 meters at 80–100 years of age. Recent studies based on phylogenetic analysis of several nuclear and chloroplast markers have shown that *Rhododendron brachycarpum* D. Don ex G. Don and *R. fauriei* should be considered as a single polymorphic species *R. brachycarpum* (Terentieva et al. 2025). In this article we follow the generally accepted international classification and consider this taxon as *Rhododendron brachycarpum* subsp. *fauriei* (Franch.) D.F. Chamb. (POWO 2026).

During the past 7–8 years it has been noted that in three of the five known populations of *R. brachycarpum* subsp. *fauriei* growing in the territory of the Sikhote-Alin Nature Reserve, the plant did not bloom fully, and severe damage was observed. As a result of continuous monitoring and investigations of *R. brachycarpum* subsp. *fauriei*, a fungal disease of leaves and flower buds with conspicuous symptoms was discovered. Some blighted twigs and leaves with numerous synnematos structures were collected on living trees. The synnematos fungus was characterized by black synnema and conidial head, which causes necrotic brown or greyish lesions on leaves and twigs of *R. brachycarpum* subsp. *fauriei*. After a detailed examination of these structures, we assigned the causing fungus to *Synnemapestaloides rhododendri* T. Handa & Y. Harada using morphological characters and sequences of the internal transcribed spacer (ITS), the standard DNA barcoding region of fungi (Handa et al. 2004, Schoch et al. 2012). *Synnemapestaloides rhododendri* was isolated from twig blight of *Rhododendron brachycarpum* and described as a new genus and species in 2004 (Handa et al. 2004). Until now, this species was found only in Japan. This is the first record of not only the species but also the genus *Synnemapestaloides* for Russia.

Interestingly, conidial structures of another fungus, very similar in morphology to *Seifertia azaleae* (Peck) Partr. & Morgan-Jones, were also found on the surface of concen-

tric necrotic spots on leaves that appear from summer to autumn in close proximity to those on which *S. rhododendri* was collected. Its synnemata were also found on the surface of *R. brachycarpum* subsp. *fauriei* flower buds, causing their necrotic lesions. *Seifertia azaleae* is considered a cosmopolitan taxon causing bud blast and twig blight of azaleas and rhododendrons in Japan, Europe and North America (Farr et al. 1996, Partridge & Morgan-Jones 2002, Glawe & Hummel 2006). This dangerous fungal pathogen had previously been detected in Russia (in the Altai and Primorsky Krai) on wild rhododendrons, but parasitizing on other *Rhododendron* species (Melnik 2000, Egorova et al. 2008). However, despite the striking morphological similarity to *S. azaleae*, our fungus was found predominantly on leaves rather than flower buds, which is quite atypical for the mentioned species, and our specimens also differed significantly from *S. azaleae* in ITS and *tef1-α* sequences, as well as in some microscopic characteristics, which raised doubts about their belonging to the same species.

The aim of this study is to present new data on the pathogenic species *Synnemapestaloides rhododendri* and to describe a new species, *Seifertia sikhbotensis*, both of which were discovered for the first time on *R. brachycarpum* subsp. *fauriei* in Russia. The species are described and illustrated, with morphological descriptions supported by phylogenetic data.

## MATERIAL AND METHODS

### Morphological examination

Dried synnemata were used to implement morphological observations with light (LM) and scanning electron microscopy (SEM).

Microscope photographs of affected parts of plants were taken using a Stereo Microscope Axio Zoom.V16 (Zeiss, Germany) to examine in detail the synnemata morphology of *S. rhododendri* and *S. azaleae*.

All microscopic structures were observed from material mounted in 5 % KOH using an Axio Imager.A1 light microscope equipped with AxioCam 807 color camera (Zeiss, Germany).

To prepare samples for surface structure examination using SEM, dried synnemata were attached to aluminium stubs holders by double-adhesive tape, coated with gold and then observed with a JEOL JSM-6390LA Analytical Scanning Electron Microscope (USA).

### DNA extraction, amplification and sequencing

DNA was extracted from dried synnemata. The procedure of DNA extraction completely corresponded to the manufacturer's protocol of the Phytosorb Kit (Syntol, Russia). The following primers were used for amplification and sequencing: ITS1F-ITS4 (White et al. 1990, Gardes & Bruns 1993) for the ITS1-5.8S-ITS2 fragment (ITS); JS1 and LR6 for nuc 28S rDNA D1-D2 domains (LSU) (Landvik 1996, Kauff & Lutzoni 2002); EF1-983F and EF1-1567R for approximately 500 bp of translation elongation factor 1- $\alpha$  gene (*tef1-α*) (Rehner & Buckley 2005). PCR products were checked in 1 % agarose gels and then were purified applying the CleanMag DNA PCR (Evro-

gen, Russia). Sequencing was performed with an ABI model 3500 Genetic Analyzer (Applied Biosystems, CA, USA). Raw data were edited and assembled in MEGA 11 (Tamura et al. 2021). Sequences generated during this study were deposited at GenBank with corresponding accession numbers.

### Dataset assembly

For this study, 7 ITS, 2 LSU and 1 *tef1-α* were newly generated.

The phylogenetic analysis was performed only for Melanommataceae. For this, addition 21 ITS, 19 LSU and 19 *tef1-α* sequences of species from the genera *Seifertia* Partr. & Morgan-Jones, *Petrakia* Syd. & P. Syd., *Alpinaria* Jaklitsch & Voglmayr and *Melanomma* Nitschke ex Fuckel, including sequences of *Pleomassaria siparia* (Berk. & Broome) Sacc. (as an outgroup), were retrieved from the GenBank database based on previous studies (Benkeen et al. 2020) for molecular analyses. Accession numbers, taxonomic identities of these sequences and collection information for taxa are given in the Table 1.

The sequences of all genetic markers (ITS, LSU, and *tef1-α*) were separately aligned using Muscle option incorporated in MEGA11. For the combined dataset the individual alignment files were concatenated in MEGA11. A partition homogeneity test (PHT) between ITS, LSU and *tef1-α* datasets was performed with PAUP 4.0b10\* (Swofford 2002). The PHT resulted in a P value of 0.4, indicating that no incongruence was detected between all datasets analyzed.

### Molecular phylogenetic analyses

Phylogenetic reconstructions were performed with Maximum Likelihood (ML) and Bayesian Inference (BI) analyses. Before the analyses, the best-fit substitution model was estimated for all alignments using FindModel web server (<https://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html>) under the Akaike information criterion. The GTR+G model was selected for all datasets

and then applied to the analysis of the concatenated ITS+LSU+*tef1-α* dataset of Melanommataceae.

Maximum likelihood analysis was run on IQ-Tree web server (<https://www.hiv.lanl.gov/content/sequence/IQTREE/iqtree.html>) with 1000 bootstrap replicates. Branches with bootstrap support (BS) values greater than or equal to 70% were considered significantly supported (Hillis & Bull 1993). BI analysis was performed with MrBayes 3.2.7 software (Ronquist et al. 2012), for two independent runs, each with 5 million generations under described model and four chains with sampling every 100 generations. To check for convergence of MCMC analyses and to get estimates of the posterior distribution of parameter values, Tracer v1.7.1 was used (Rambaut et al. 2018). We accepted the result where the ESS (Effective Sample Size) was above 200 and the PSRF (Potential Scale Reduction Factor) was close to 1. Tree topologies were then edited and visualized in iTOL (Letunic & Bork 2019).

## RESULTS

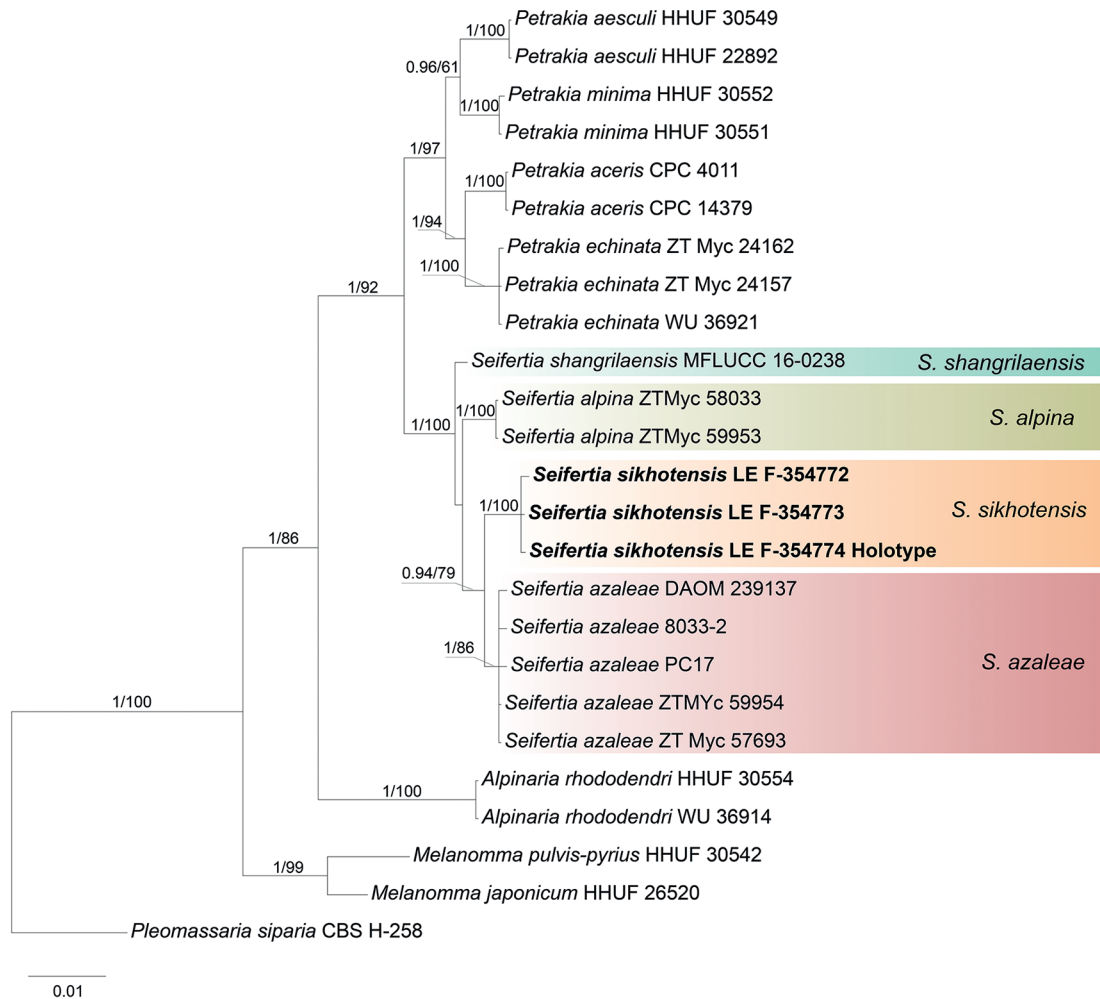
### Phylogeny

The combined DNA sequence dataset (ITS+LSU+*tef1-α*) used to infer delimitation at the genus and species levels for Melanommataceae members contained 2299 characters (ITS: 1–455, *tef1-α*: 456–1341, LSU: 1342–2299), including gaps. It comprised 11 specimens of *Seifertia* and additional 13 specimens of related taxa from the family Melanommataceae, excluding outgroup. Both Bayesian and Maximum likelihood analyses produced the same topology. Therefore, we present only the BI tree with both PP and BS values (Fig. 1).

Phylogenetic analysis using three genetic markers revealed four major clades corresponding to the genera *Seifertia*, *Petrakia*, *Alpinaria* and *Melanomma*, consistent with earlier studies (Benkeen et al. 2020). Species of the genus *Seifertia* form a single monophyletic clade with the highest support (PP = 1, BS = 100 %) in the resulting phylogenetic

**Table 1.** Specimens used in the phylogenetic study of Melanommataceae, including GenBank accession numbers of ITS, LSU and *tef1-α* sequences.

Species	Voucher	Host	Country	GenBank accession no.		
				ITS	LSU	<i>tef1-α</i>
<i>Alpinaria rhododendri</i>	HHUF 30554	<i>Rhododendron brachycarpum</i>	Japan	LC203335	LC203360	LC203388
<i>Alpinaria rhododendri</i>	WU 36914 Epitype	<i>Rhododendron ferrugineum</i>	Austria	KY189973	KY189973	KY190009
<i>Melanomma pulvis-pyrus</i>	HHUF 30542	<i>Acer mono var. mayrii</i>	Japan	LC203322	LC203340	LC203368
<i>Melanomma japonicum</i>	HHUF 26520 Holotype	—	Japan	LC203321	LC203339	LC203367
<i>Petrakia aceris</i>	CPC 4011	<i>Acer</i> sp.	Canada	FJ839638	LC203362	LC203390
<i>Petrakia aceris</i>	CPC 14379	<i>Acer macrophyllum</i>	Canada	FJ839625	LC203361	LC203389
<i>Petrakia aesculi</i>	HHUF 30549	<i>Aesculus turbinata</i>	Japan	LC203329	LC203347	LC203375
<i>Petrakia aesculi</i>	HHUF 22892	<i>Aesculus turbinata</i>	Japan	LC194192	LC203348	LC203376
<i>Petrakia echinata</i>	ZT Myc 24162	<i>Acer pseudoplatanus</i>	Switzerland	JQ691629	MK502023	MK502080
<i>Petrakia echinata</i>	ZT Myc 24157	<i>Acer pseudoplatanus</i>	Germany	JQ655727	LC203351	LC203379
<i>Petrakia echinata</i>	WU 36921	<i>Acer pseudoplatanus</i>	Austria	KY189981	KY189981	KY190016
<i>Petrakia minima</i>	HHUF 30552	<i>Fagus japonica</i>	Japan	LC203334	LC203359	LC203387
<i>Petrakia minima</i>	HHUF 30551 Holotype	<i>Fagus japonica</i>	Japan	LC203333	LC203358	LC203386
<i>Pleomassaria siparia</i>	CBS H-258	<i>Betula verrucosa</i>	Netherlands	AB554089	DQ678078	DQ677923
<i>Seifertia alpina</i>	ZT Myc 58033	<i>Rhododendron ferrugineum</i>	Switzerland	MK542906	MK502025	MK502082
<i>Seifertia alpina</i>	ZT Myc 59953 Epitype	<i>Rhododendron ferrugineum</i>	Switzerland	MK502003	MK502026	MK502083
<i>Seifertia azaleae</i>	DAOM 239137	<i>Rhododendron</i> sp.	Canada	EU030274	—	—
<i>Seifertia azaleae</i>	8033-2	<i>Rhododendron</i> sp.	Belgium	PP053424	—	PP100147
<i>Seifertia azaleae</i>	PC17	<i>Rhododendron catawbiense</i>	Germany	PQ772264	—	—
<i>Seifertia azaleae</i>	ZT Myc 59954	<i>Rhododendron</i> sp.	Switzerland	MK502004	MK502028	MK502085
<i>Seifertia azaleae</i>	ZT Myc 57693	<i>Rhododendron</i> sp.	Switzerland	KY231242	MK502027	MK502084
<i>Seifertia shangrilaensis</i>	MFLUCC 16-0238 Holotype	<i>Rhododendron decorum</i>	China	—	KU954100	KU954102
<i>Seifertia sikhotensis</i>	LE F-354774 Holotype	<i>Rhododendron brachycarpum</i> ssp. <i>fauriei</i>	Russia	PZ198034	PZ198030	PZ175071
<i>Seifertia sikhotensis</i>	LE F-354773	<i>Rhododendron brachycarpum</i> ssp. <i>fauriei</i>	Russia	PZ198033	PZ198031	—
<i>Seifertia sikhotensis</i>	LE F-354772	<i>Rhododendron brachycarpum</i> ssp. <i>fauriei</i>	Russia	PZ198032	—	—



**Figure 1** The phylogenetic placement of *Seifertia* species in the Melanommataceae based on Bayesian Inference analysis recovered from three-locus dataset (ITS+LSU+tef1- $\alpha$ ). Posterior probability and Bootstrap support values (PP/BS) are indicated on the branches. All sequences are labeled with taxon name and voucher/isolate number. Sequences newly generated in this study are in bold

tree (Fig. 1). According to the phylogenetic analysis, three studied *Seifertia* specimens from Sikhote-Alin form independent and robust clade (BS = 100 % and PP = 1), which is sister to *S. azaleae*. Both species together are phylogenetically close and nested in the same clade with *S. alpina* (Höhn.) Beenken and *S. shangrilaensis* J.F. Li, Phookamsak & K.D. Hyde. Based on phylogenetic and morphological evidence, we consider these three specimens to represent a new species, described hereby as *Seifertia sikhotensis*.

## Taxonomy

***Seifertia sikhotensis*** Malysheva, V.A. Dudka, E.F. Malysheva & S.N. Bondarchuk, sp. nov. (Figs 2, 3)

**Mycobank** MB863346

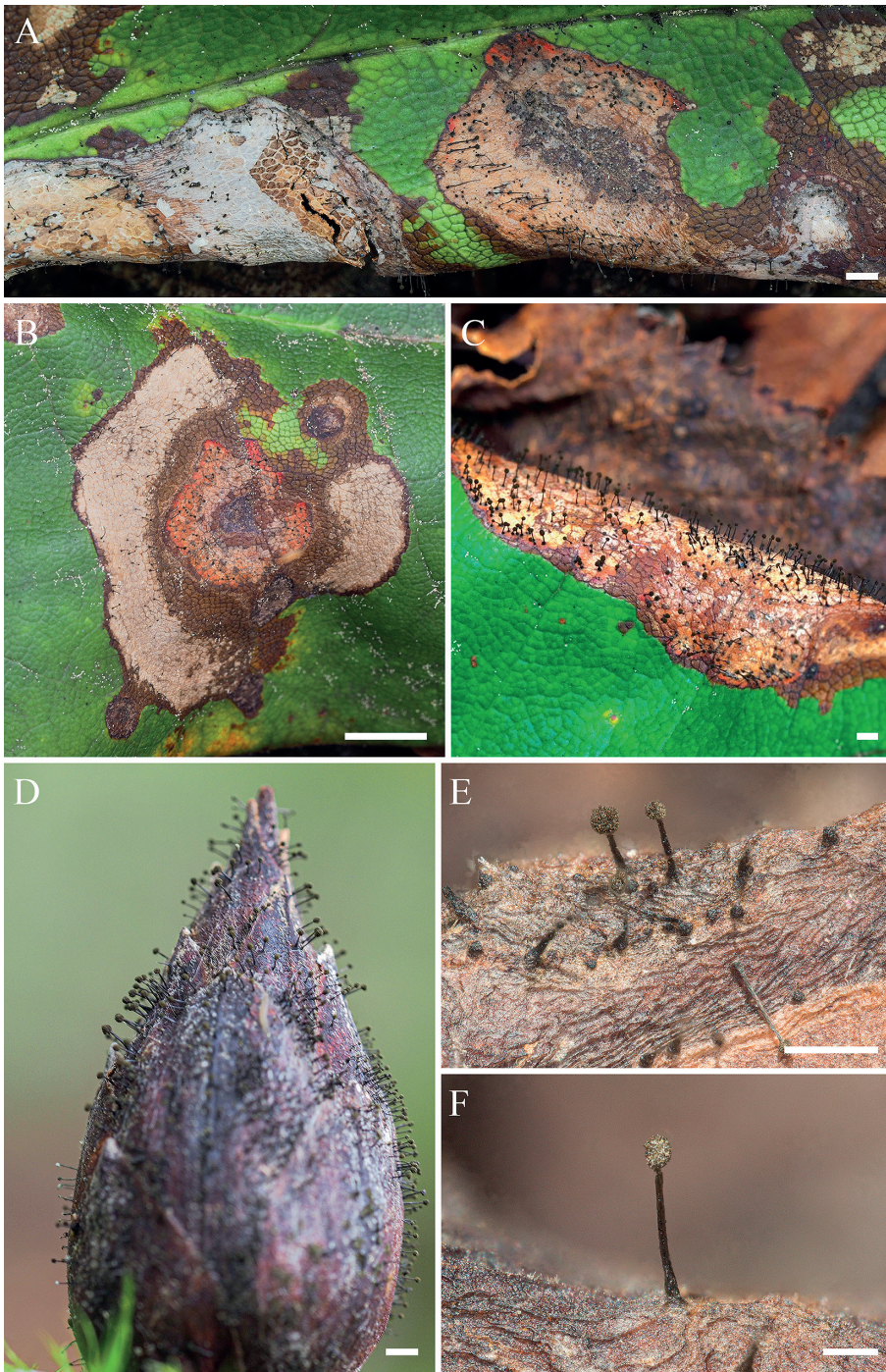
**Holotype.** RUSSIA: Primorsky Krai, Sikhote-Alin Nature Reserve, “Kabaniy” field station, permanent plot “Fori 3”, 45°08'18.4"N 135°53'13.7"E, 927 m a.s.l., forest site dominated by *Rhododendron brachycarpum* subsp. *fauriei*, with *Pinus koraiensis*, *Abies nephrolepis*, *Picea ajanensis* and other trees, on leaves of *Rhododendron brachycarpum* subsp. *fauriei*, 19 Aug. 2025, S.N. Bondarchuk (LE F-354774, GenBank ITS – PZ198034, LSU – PZ198030 and tef1- $\alpha$  – PZ175071).

**Diagnosis.** Differs from *Seifertia azaleae* in its shorter synnemata stalk, smaller conidia and occurrence predominantly

on *Rhododendron* leaves, as well as the ITS and tef1- $\alpha$  sequence data.

**Etymology.** The species epithet refers to the location (Sikhote-Alin Mountains) where the type material was collected.

**Description.** Ascomata are unknown. Anamorph structures occur on living flower buds, twigs and especially on leaves of *Rhododendron brachycarpum* subsp. *fauriei*, causes tissue necrosis, darkening and mummification of flower buds, and the formation of brown spots and holes on leaves. Synnemata erect, simple, unbranched, stalk 500–1000  $\times$  50–100  $\mu$ m (up to 215  $\mu$ m at base), tapering upwards, with a capitate powdery apex, dark brown to black. Mycelium superficial, forming whitish membrane layer on the leaf surface, partly immersed on the substrate, composed of septate, smooth, thin-walled, pale brown hyphae. Conidiophores synnematos, straight or flexuous, tightly packed into a bundle, olive-brown, thick-walled (wall 1.0–1.2  $\mu$ m wide), septate, cylindrical, unbranched, 3.5–5.5  $\mu$ m wide. At the tip, hyphae spreading brush-like and turning into conidiogenous hyphae, 4.0–5.5  $\mu$ m wide, septate, slightly thick-walled, olive-brown. Conidia in short chains, separated by narrow isthmi, one-celled or rare two-celled, smooth in LM (the surface of the conidia is clearly tuberculate under a SEM), oblong, subglobose, broadly ellipsoid or broadly amygdaloid, often slightly apiculate on both ends, with single hyaline papilla, pale to dark olivaceous-brown, 5.5–8.0  $\times$  4.5–6.5  $\mu$ m (from 70 measured), slightly



**Figure 2** *Seifertia sikhotensis* sp. nov. on *Rhododendron brachycarpum* subsp. *fauriei* (Franch.) D.F. Chamb. A–C – synnemata on leaf (LE F-354774, holotype); D – synnemata on flower bud (LE F-354772); E, F – synnemata on twigs (LE F-354772). Scale bar: A, C, D – 1 mm; B – 1 cm; E – 500  $\mu$ m; F – 200  $\mu$ m

thick-walled. Two-celled conidia 9.5–11.0  $\times$  4.5–5.0  $\mu$ m, cylindrical or broadly fusiform, slightly constricted at septa.

**Additional specimens examined.** RUSSIA: Primorsky Krai, Sikhote-Alin Nature Reserve, “Kabaniy” field station, permanent plot “Fori 2”, 45°08'28.8"N 135°52'40.1"E, 889 m a.s.l., forest site dominated by *Rhododendron brachycarpum* subsp. *fauriei*, with *Pinus koraiensis*, *Abies nephrolepis*, *Picea ajanensis* and other trees, on leaves of *Rhododendron brachycarpum* subsp. *fauriei*, 19 Aug. 2025, S.N. Bondarchuk (LE F-354773, GenBank ITS – PZ198033, LSU – PZ198031); ibid., “Fori 2”, 45°07'37.9"N 135°51'56.3"E, 652 m a.s.l., forest site dominated by *Rhododendron brachycarpum* subsp. *fauriei*, with *Pinus koraiensis*, *Abies nephrolepis*, *Picea ajanensis*

and other trees, on leaves, twigs and flower buds of *Rhododendron brachycarpum* subsp. *fauriei*, 13 Aug. 2024, V.A. Dudka (LE F-354772, GenBank ITS – PZ198032).

**Habitat and distribution.** On living leaves, flower buds and twigs of *Rhododendron brachycarpum* subsp. *fauriei*; so far known only from the type locality in the Russian Far East.

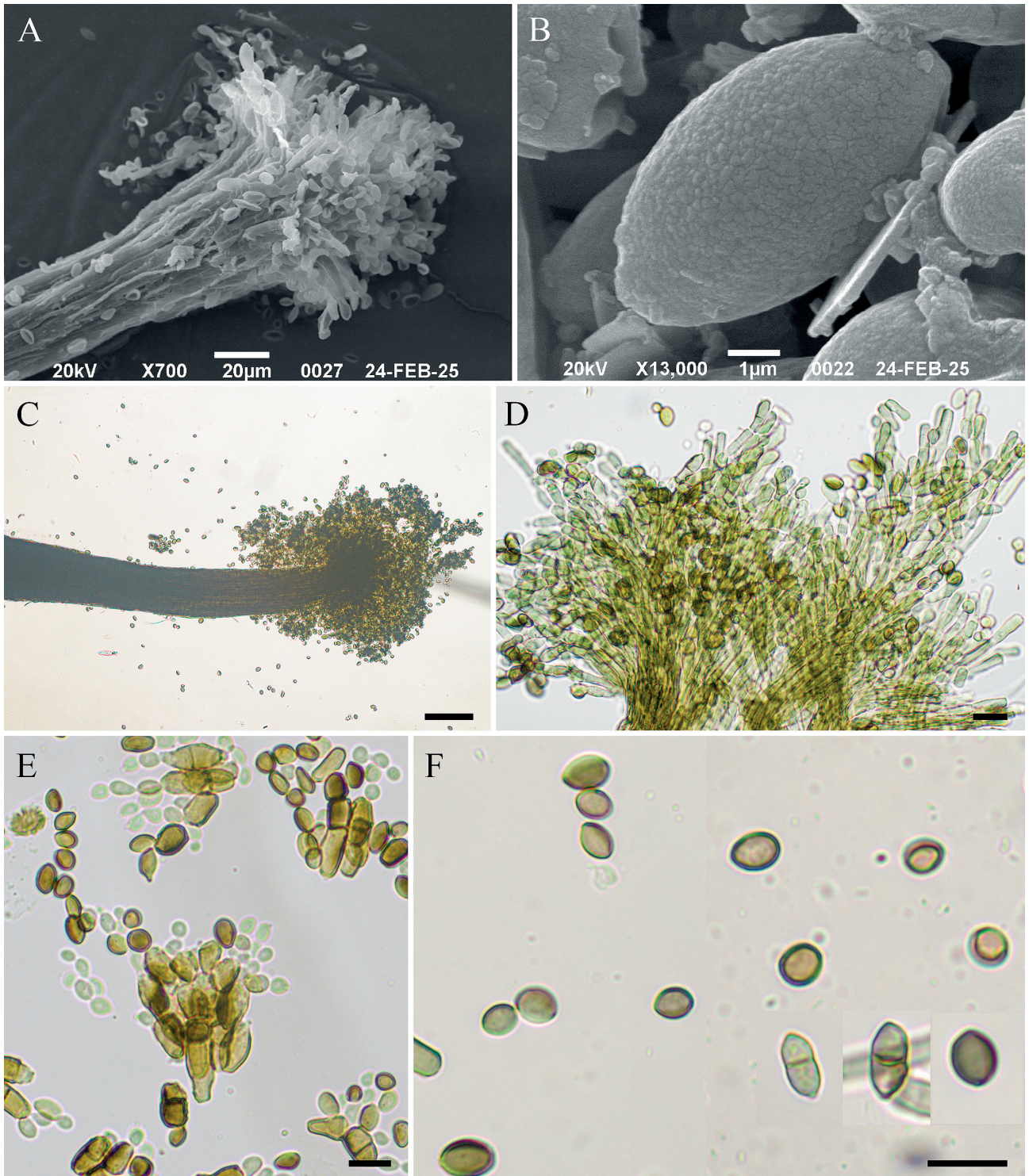
**Notes.** *Seifertia sikhotensis* is morphologically very similar to *S. azaleae*, but differs in shorter synnemata stalk, the length of which does not exceed 1 mm, while the length of the latter species can reach 2.5 mm, and smaller conidia measuring 5.5–8.0  $\times$  4.5–6.5  $\mu$ m (vs. 4–12  $\times$  4–8  $\mu$ m in *S. azaleae*) (Benkeen et al. 2020). Moreover, *S. sikhotensis* blights not only the flower buds and twigs of *Rhododendron brachycarpum* subsp. *fauriei*, but predominantly the leaves, whereas *S. azaleae* is found almost exclusively on the buds and twigs of rhododendrons and only very rarely on the leaves (Kaneko et al. 1988).

*Seifertia alpina* (Höhn.) Beenken, Andr. Gross & Queloz, originally described and distributed in Alps, is distinguished from *S. sikhotensis* in very short synnemata stalk (80–800  $\mu$ m), significantly longer conidia, 4.0–13.3  $\times$  3.0–5.5  $\mu$ m, and occurring as saprotroph on dry fruit umbels and especially on pedicels of *Rhododendron ferrugineum* L. (Benkeen et al. 2020).

Recently described species, *S. shangrilaensis* J.F. Li, Phookamsak & K.D. Hyde, isolated from *Rhododendron decorum* in Yunnan Province of Southwest China, can be separated from *S. sikhotensis* by having hyaline to subhyaline and smaller conidia (2.5–6.0  $\times$  2.5–3.5  $\mu$ m), long synnemata stalk up to 2.3 mm, wider conidiogenous hyphae, 9.5–12.6  $\mu$ m, and occurrence only on *Rhododendron* twigs (Li et al. 2016).

***Synnemapestaloides rhododendri* T. Handa & Y. Harada**, in Handa, Fujita & Harada, Mycoscience 45(2):138 (2004) (Fig. 4)

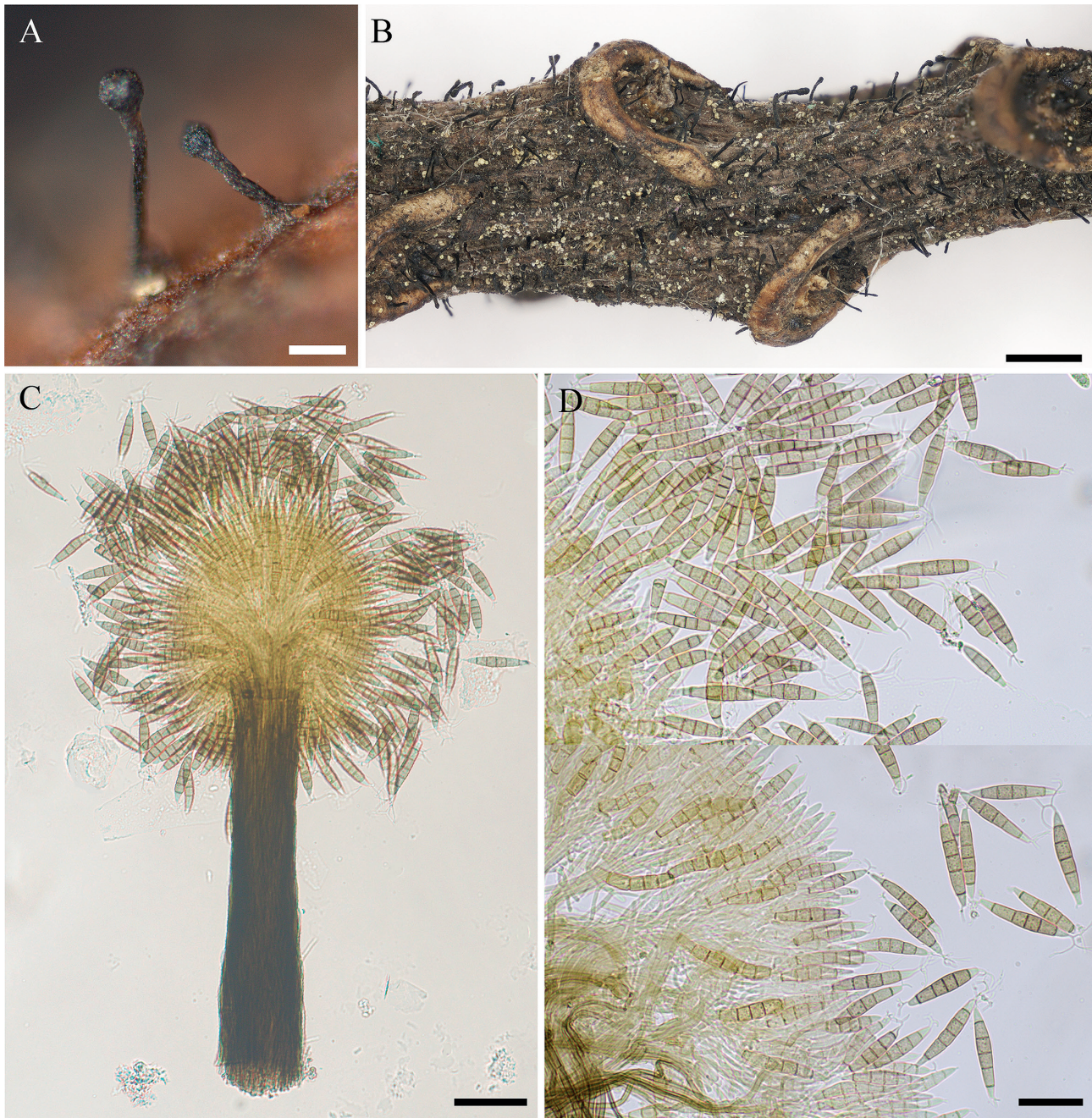
**Description.** Ascomata are unknown. Anamorph structures occur on living leaves and twigs of *Rhododendron brachycarpum* subsp. *fauriei*, mostly epiphyllous, rarely hypophyllous on leaves. Synnemata erect, simple, unbranched, stalk 250–450  $\times$  30–60  $\mu$ m, tapering upwards, with a cylindrical-capitate, black apex. Conidial mass, black, globose to subglobose, subgelatinous. Conidiophores synnematomatous, straight or flexuous, branched, brown, smooth, thin-walled. Conidiogenous cells cylindrical to subcylindrical with annel-



**Figure 3** Microscopic structures of *Seifertia sikhotensis* sp. nov. (all from holotype, LE F-354774). A – head of synnema under SEM; B – conidium under SEM; C – head of synnema; D – part of the synnema head showing conidiogenous cells producing conidia; E – conidiogenous cells and one-celled conidia in chains; F – one-celled and two-celled conidia. Scale bar: C – 50  $\mu$ m; D–F – 10  $\mu$ m

lations, hyaline, smooth. Conidia fusoid, ellipsoidal, straight, brown, 5-septate, slightly constricted at the septa, smooth walled,  $30\text{--}43 \times 5\text{--}7 \mu\text{m}$ , bearing appendages at both ends, basal cell conical with a truncate base, brown or hyaline; four median cells  $22\text{--}28 \mu\text{m}$  long, brown. Apical appendage single, filiform, unbranched or often dichotomously branched, flexuous, centric, up to  $16 \mu\text{m}$  long; basal appendage single or absent, when present, unbranched or irregularly branched, excentric, up to  $7 \mu\text{m}$  long.

**Specimens examined:** RUSSIA: Primorsky Krai, Sikhote-Alin Nature Reserve, “Kabaniy” field station, permanent plot “Fori 2”,  $45^{\circ}08'28.8''\text{N}$   $135^{\circ}52'40.1''\text{E}$ , 889 m a.s.l., forest site dominated by *Rhododendron brachycarpum* subsp. *fauriei*, with *Pinus koraiensis*, *Abies nephrolepis*, *Picea ajanensis* and other trees, on leaves of *Rhododendron brachycarpum* subsp. *fauriei*, 19 Aug. 2025, S.N. Bondarchuk (LE F-354775); *ibid.*, permanent plot “Fori 3”,  $45^{\circ}08'18.4''\text{N}$   $135^{\circ}53'13.7''\text{E}$ , 927 m a.s.l., 13 Aug. 2024, V.A. Dudka



**Figure 4** *Synnemapestaloides rhododendri* T. Handa & Y. Harada on *Rhododendron brachycarpum* subsp. *fauriei* (Franch.) D.F. Chamb. A – synnemata on leaf (LE F-354775); B – synnemata on twig (LE F-353906); C – single synnema (LE F-354775); D – conidia (LE F-354775). Scale bar: A – 100  $\mu$ m; B – 1 mm; C – 50  $\mu$ m; D – 10  $\mu$ m

(LE F-353906, GenBank ITS – PZ198035); *ibid.*, (LE F-353907, GenBank ITS – PZ198037); *ibid.*, permanent plot “Fori 2”, 45°08'28.8"N 135°52'40.1"E, 889 m a.s.l., 13 Aug. 2024, V.A. Dudka (LE F-353905, GenBank ITS – PZ198036); *ibid.*, permanent plot “Fori 1”, 45°07'37.9"N 135°51'56.3"E, 652 m a.s.l., 14 Aug. 2024, V.A. Dudka (LE F-353908, GenBank ITS – PZ198038).

**Notes.** A BLAST tool of GenBank (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) was used to search for similar ITS sequences for the studied *S. rhododendri* specimens. All newly generated ITS sequences were completely identical (Per. Ident = 100.00 %) to the sequence obtained from the type material (GenBank ITS – NR175066). However, we observed some minor differences in the morphology of our specimens compared to the original description of

*S. rhododendri* (Handa et al. 2004). Conidia in studied specimens were slightly longer (30–43  $\times$  5–7  $\mu$ m vs. 25–32.8  $\times$  4–6  $\mu$ m in the protologue). Also, the length of the four median cells was 22–28  $\mu$ m in our specimens (vs. 18–23.5  $\mu$ m). The original description indicated that *S. rhododendri* was found on buds, but we did not find synnemata on buds in our specimens.

## DISCUSSION

The genus *Seifertia* was introduced by Partridge and Morgan-Jones in 2002 (Partridge & Morgan-Jones 2003) to accommodate *Periconia azaleae* Peck, which became *Seifertia azaleae*, the type species of the described and originally monotypic genus. The authors of the genus noted a very

close morphological similarity between *Seifertia azaleae* and *Sorocybe resiniae* (Fr.) Fr., but emphasized that these taxa are most likely not related phylogenetically. They established a new genus for the fungus occurring on rhododendrons, while *S. resiniae* is confined to conifers. Subsequent studies confirmed the genetic differences between these two synnematosus species and their belonging to different families and orders of *Pezizomycotina* (Seifert et al. 2007, Benkeen et al. 2020). In recent studies, another species, originally described as *Antromycopsis alpina* Höhn., was transferred to the genus *Seifertia* (*Seifertia alpina*) based on both morphological and phylogenetic data (Benkeen et al. 2020); and one species, *S. shangrilaensis*, was described from China (Li et al. 2016). Thus, before our research, the genus *Seifertia* included only three species.

All species of *Seifertia* seem to be always associated with the genus *Rhododendron* (Ericaceae) and are characterized by either a saprotrophic or necrotrophic lifestyle. The species have erect, predominantly simple, dark-colored, capitate synnemata, unicellular or rarely one-septate thick-walled conidia in chains, macronematous and synnematosus conidiophores and mono- or polyblastic, integrated, terminal and determinate conidiogenous cells (Partridge & Morgan-Jones 2002).

The symptoms of disease caused by *S. sikbotensis* on *R. brachycarpum* subsp. *fauriei* included necrosis of the flower buds, as well as expanding necrotic brown spots on the leaves followed by leaf curling. The entire flower bud turned brown or black, and the leaves became perforated at the center of the spots and gradually died off by winter. Throughout spring to autumn, black hair-like synnemata of a fungus appeared on the blighted flower buds, twigs and leaves (Fig. 2). The blighted flower buds did not bloom and became mummified. Similar symptoms of plant disease are also characteristic of *S. azaleae*. Some authors have suggested that *S. azaleae* may represent a complex of species that can be distinguished with certainty only by molecular data (Endrestøl 2017). The morphology-based species identification in *Seifertia* mainly relies on the characters of synnemata, conidiogenous hyphae and conidia. Based on the combination of these characters, our new species differs from *S. azaleae*, but molecular data provide additional evidence to support the correct distinction between these species. Within the large *S. azaleae* clade, all specimens from different geographic regions of the world (Europe and North America) involved in the analysis (Table 1) demonstrate complete identity of their nucleotide sequences, which may indicate the invasive nature of the species' distribution. The specimens we studied from the Russian Far East fall outside of this clade. In light of these results, we can hypothesize that our new species *S. sikbotensis* does not have an anthropogenic nature of dispersal, and that species of *Seifertia* tend to be more host specific than previously considered. The species could have been overlooked for several years due to minor phytopathological signs on the host plant and insufficient attention from mycologists, or because it has infected another species of *Rhododendron* growing in similar habitats in the same area. However, climate change in recent years, as well as a complex of other

fungal pathogens (such as *Synnemapestaloides rhododendri*), could have weakened *R. brachycarpum* subsp. *fauriei* and increased disease symptoms, or *S. sikbotensis* could have jumped from another species to a severely weakened plant.

The role of insects in the spread of parasitic fungal species has been emphasized by many authors (Endrestøl 2017). The way of dissemination of *S. sikbotensis* among rhododendron populations may have followed a pattern similar to that of *Synnemapestaloides rhododendri*.

In our study, *S. rhododendri* was found on its type host, but for the first time outside its type locality, in a continental, relict population of *Rhododendron brachycarpum* subsp. *fauriei*. It is important to note that *S. sikbotensis* and *S. rhododendri* occur on the same host and cause similar symptoms: necrosis spots of leaves, and dieback of twigs and buds in *Rhododendron brachycarpum*. The synnemata of *S. sikbotensis* and *S. rhododendri* are also very similar in appearance. Among our specimens, we observed that *S. sikbotensis* and *S. rhododendri* might occur on the same leaf. Therefore, to distinguish these species in nature, it is necessary to carry out morphological observations with particular care. At the microscopic level, these two species are very clearly distinguished by the characteristics of their conidia. *Seifertia sikbotensis* conidia are unicellular, small (5.5–8.0 µm long), without appendages, while *S. rhododendri* conidia are six-celled, significantly larger (30–40 µm long) and have distinct appendages at the ends.

The ecological role of *Seifertia* spp. and other synnematosus fungi on wild rhododendrons in Russia is an area of research that is deserve to receive the attention. Detection, description, and genetic characterization of these pathogens is necessary for future research into their control and prevention.

## ACKNOWLEDGEMENTS

All microscopic and molecular studies of specimens were carried out using equipment of the Core Facilities Center “Cell and Molecular Technologies in Plant Science” at the Komarov Botanical Institute RAS (St. Petersburg, Russia). The study was conducted with the financial support of the project No. 124020100148-3 of the Komarov Botanical Institute of the Russian Academy of Sciences.

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