Persoonia 49, 2022: 201–260
www.ingentaconnect.com/content/nhn/pimj

RESEARCH ARTICLE

ISSN (Online) 1878-9080
https://doi.org/10.3767/persoonia.2022.49.07

Diversity of *Sporocadaceae* (pestalotioid fungi) from *Rosa* in China

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Key words

Amphisphaeriales
Ascomycota
new taxa
phylogeny
taxonomy

Abstract *Rosa* (*Rosaceae*) is an important ornamental and medicinal plant genus worldwide, with several species being cultivated in China. Members of *Sporocadaceae* (pestalotioid fungi) are globally distributed and include endophytes, saprobes but also plant pathogens, infecting a broad range of host plants on which they can cause important plant diseases. Although several *Sporocadaceae* species were recorded to inhabit *Rosa* spp., the taxa occurring on *Rosa* remain largely unresolved. In this study, a total of 295 diseased samples were collected from branches, fruits, leaves and spines of eight *Rosa* species (*R. chinensis*, *R. helenae*, *R. laevigata*, *R. multiflora*, *R. omeiensis, R. rugosa*, *R. spinosissima* and *R. xanthina*) in Gansu, Henan, Hunan, Qinghai, Shaanxi Provinces and the Ningxia Autonomous Region of China. Subsequently 126 strains were obtained and identified based on comparisons of DNA sequence data. Based on these results 15 species residing in six genera of *Sporocadaceae* were delineated, including four known species (*Pestalotiopsis chamaeropis*, *Pes. rhodomyrtus*, *Sporocadus sorbi* and *Spo. trimorphus*) and 11 new species described here as *Monochaetia rosarum*, *Neopestalotiopsis concentrica*, *N. subepidermalis*, *Pestalotiopsis tumida*, *Seimatosporium centrale*, *Seim. gracile*, *Seim. nonappendiculatum*, *Seim. parvum*, *Seiridium rosae*, *Sporocadus brevis*, and *Spo. spiniger*. This study also represents the first report of *Pes. chamaeropis*, *Pes. rhodomyrtus* and *Spo. sorbi* on *Rosa*. The overall data revealed that *Pestalotiopsis* was the most prevalent genus, followed by *Seimatosporium*, while *Pes. chamaeropis* and *Pes. rhodomyrtus* were the two most prevalent species. Analysis of *Sporocadaceae* abundance on *Rosa* species and plant organs revealed that spines of *R. chinensis* had the highest species diversity.

Citation: Peng C, Crous PW, Jiang N, et al. 2022. Diversity of Sporocadaceae (pestalotioid fungi) from Rosa in China. Persoonia 49: 201–260. https://doi.org/10.3767/persoonia.2022.49.07.
Effectively published online: 12 December 2022 [Received: 8 May 2022; Accepted: 18 September 2022].

INTRODUCTION

Sporocadaceae (*Xylariales*, *Sordariomycetes*) is a well-known fungal family containing pestalotioid fungi. Traditionally, pestalotioid fungi are circumscribed as a group of coelomycetous fungi having fusoid or nearly fusoid, multi-septate conidia, with appendages at one or both ends (Nag Raj 1993, Maharachchikumbura et al. 2014, Liu et al. 2019).

Pestalotioid fungi were previously classified in *Amphisphaeriaceae*, *Amphisphaeriales* (Eriksson 1986, Samuels et al. 1987). Subsequently, several studies suggested that *Amphisphaeriales* should not be accepted due to the lack of stable phylogenetic support, and hence it was treated as synonym of *Xylariales* (Eriksson 1987, Kang et al. 1999, Smith et al. 2003). Later, Senanayake et al. (2015) revised *Xylariomycetidae* and transferred several important genera of pestalotioid fungi from *Amphisphaeriaceae* to three new families, *Bartaliniaceae*, *Discosiaceae* and *Pestalotiopsidaceae*. Genera such as *Bartalinia* and *Broomella* were transferred to *Bartaliniaceae*, *Discosia* and *Seimatosporium* to *Discosiaceae*, and *Neopestalotiopsis*, *Pestalotiopsis*, *Pseudopestalotiopsis*, *Monochaetia* and *Seiridium* to *Pestalotiopsidaceae*. Crous et al. (2015a) introduced a new family *Robillardaceae* to accommodate *Robillarda*. Subsequently, Jaklitsch et al. (2016) grouped the pestalotioid fungi into a single family and revived the older family name *Sporocadaceae*. Therefore, *Bartaliniaceae*, *Discosiaceae*, *Pestalotiopsidaceae* and *Robillardaceae* became synonyms of *Sporocadaceae*. These families were classified in *Amphisphaeriales* which was resurrected instead of *Xylariales* (Senanayake et al. 2015). Recently, several studies treated *Amphisphaeriales* as a distinct order (Senanayake et al. 2015, Samarakoon 2016, Hongsanan et al. 2017, Wijayawardene et al. 2020). Based on multi-locus phylogenetic analyses with morphological characters, Liu et al. (2019) confirmed the natural taxonomic status of *Sporocadaceae*, which currently contains 33 genera (Liu et al. 2019, Wijayawardene et al. 2020).

Sporocadaceae contains many important plant pathogens associated with diseases on a wide range of plant hosts worldwide (Maharachchikumbura et al. 2014, Liu et al. 2019, Norphanphoun et al. 2019). Within the family, pestalotiopsis-like taxa (*Neopestalotiopsis*, *Pestalotiopsis* and *Pseudopestalotiopsis*) are the group that has received the most attention (Maharachchikumbura et al. 2014, Wang et al. 2019b, Gualberto et al. 2021). For example, *N. mangiferae* and *N. palmarum* cause leaf

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diseases on a variety of cash crops in Brazil, South Africa and India, weakening tree vigour, and even reducing yield in severe cases (Spaulding 1949, Mendes et al. 1998, Crous et al. 2000). *Pestalotiopsis pini* is an emerging pathogen causing shoot blight and stem necrosis on *Pinus pinea* (Silva et al. 2020), while in Australia, *Pes. telopeae* causes a serious leaf spot disease of *Telopea* spp. (Maharachchikumbura et al. 2014). Furthermore, pestalotiopsis-like fungi are widespread, occur on many hosts in *Proteaceae*, and are generally regarded to be saprobic or weakly pathogenic (Crous et al. 2013). *Neopestalotiopsis protearum* was recorded as causing leaf spots and blight on several *Protea* and *Leucospermum* hosts in Zimbabwe (Swart et al. 1999, Crous et al. 2011b). This species is also reported from Australia and *Proteaceae* in the Western Cape Province of South Africa (Crous et al. 2013). *Neopestalotiopsis protearum* is probably only a problem of commercial importance in summer rainfall areas and it has been intercepted at quarantine inspection points (Taylor 2000). *Pestalotiopsis montellicoides* was isolated from *Protea cynaroides* leaves from South Africa (Mordue 1986), and a *Pestalotiopsis* sp. (asexual *Pestalosphaeria leucospermi*), was described from living leaves of a *Leucospermum* sp. in New Zealand (Samuels et al. 1987). In Portugal and the Canary Islands, a species of *Pestalotiopsis* is commonly associated with tip blight and leaf spot symptoms on *Protea*, *Leucospermum* and *Leucadendron* species, although pathogenicity studies have not yet been conducted (Crous et al. 2013). Members of *Pseudopestalotiopsis* are cosmopolitan in distribution and have often been regarded as leaves spot pathogens occurring on a broad host range, e.g., *Pse. elaeidis* and *Pse. theae* cause foliar diseases in more than 60 hosts around the world in tropical and subtropical areas (Maharachchikumbura et al. 2014, Liu et al. 2019). In addition to pestalotiopsis-like species, the diseases caused by other groups of *Sporocadaceae* cannot be underestimated. Cypress canker is caused by several species of *Seiridium* (Bonthond et al. 2018), *Allelochaeta* is an important foliar pathogen of eucalypts (Crous et al. 2019b), and some species of *Distononappendiculata* and *Truncatella* cause diseases on a wide range of hosts (Crous et al. 2011a, 2013, Liu et al. 2019).

Sporocadaceae has an extremely rich species diversity in China. The investigation of the biodiversity of plant-associated pestalotioid fungi in China date back as far as 1886, when Patouillard collected and described many species from Yunnan (Patouillard 1886). With subsequent research, a total of 310 species belonging to 22 genera were reported in China, inhabiting many hosts, especially in *Juglandaceae*, *Myrtaceae*, *Pinaceae*, *Podocarpaceae*, *Rhododendronaceae*, *Rosaceae*, *Theaceae* and *Vitaceae* (Chen 2003, Ge et al. 2009, Liu et al. 2019). Most of the previous studies on *Sporocadaceae* in China focused on *Pestalotiopsis*. Previous investigations on *Pestalotiopsis* in China were summarised by Tai (1979), in which 38 species from 52 plant hosts were listed. A wider survey included 153 species obtained from at least 406 plant species, 67 of which are endemic to China (Ge et al. 2009). Hitherto 203 species have been reported in China, accounting for more than 65 % of the total records of this family in China. However, the distribution of 11 genera in China is still unknown, i.e., *Ciliochorella*, *Clypeosphaeria*, *Diploceras*, *Disaeta*, *Distononappendiculata*, *Heterotruncatella*, *Hyalotiella*, *Morinia*, *Nonappendiculata*, *Parabartalinia* and *Xenseimatosporium*. Furthermore, many species of *Sporocadaceae* can also cause serious plant diseases in China. *Pseudopestalotiopsis camelliae-sinensis* is responsible for grey blight of tea plants and causes serious losses in some tea-growing regions of China (Wang et al. 2019b), while *Pes. apiculata* causes severe top blight of cedar seedlings (Ge et al. 2009). *Monochaetia kansensis* and *M. monochaeta* cause leaf spots on a variety of *Quercus* and *Castanea* plants (Teng 1996, Chen et al. 2002, Chen 2003), and *Truncatella laurocerasi* causes grey blight and leaf spot on *Eriobotrya* in China (Tai 1979). Considering the importance of pestalotioid fungi, it is necessary to clarify the species diversity and distribution of *Sporocadaceae* in China in a modern taxonomic framework.

Rosa (*Rosaceae*) is widely distributed in tropical to cold temperate regions of the Northern Hemisphere, including approximately 200 species (Bruneau et al. 2007, Fougère-Danezan et al. 2015). China is the main distribution area of *Rosa* plants globally (Wu et al. 2003). There are currently 95 *Rosa* spp. in China (65 of which are endemic), accounting for about 41 % of the global total (Jin 2020). *Rosa* species are widely cultivated and are of immense economic importance in China (Liu 2016). As important ornamental plants, *Rosa* spp. play a key role in Chinese landscaping (Zhang et al. 2009). Furthermore, *Rosa* species are important raw materials for the spice and food industry, and a rose industry has been established in many parts of China, generating huge income for the local economy (Wang 2021). Most *Rosa* spp. can be used in traditional Chinese medicines, having great nutritional and medicinal value (Wang 2021). In addition to these, *Rosa* spp. are important resource species for ecological and vegetation restoration, having great ecological value in China, because many rose species have strong resistance to stress and can survive in harsh environments (Liu 2016).

Many fungal taxa such as *Botryosphaeria dothidea*, *Botrytis cinerea*, *Chaetomella raphigera*, *Colletotrichum siamense*, *Cytospora* spp., *Diplocarpon rosae*, *Elsinoe rosarum* and *Lasiodiplodia theobromae* have in the past been identified as the causal agents of various diseases of *Rosa* spp. in China, and severely limited their production. (Zhang et al. 2014, Bagsic et al. 2016, Chen et al. 2016, Debener 2019, Feng et al. 2019 Jia et al. 2019, Munoz et al. 2019, Pan et al. 2020). Members of *Sporocadaceae* have also been reported to cause diseases on *Rosa* spp. Examples include cankers caused by *N. rosicola*, dieback caused by *Ciliochorella mangiferae* and *Robillarda sessilis*, stem lesions caused by *N. rosae* and *R. sessilis*, and leaf spots caused by *Diploceras discosioides*, *Discosia artocreas* and *Truncatella angustata* (Weiss 1950, Mathur 1979, Peregrine & Ahmad 1982, Eken et al. 2009, Maharachchikumbura et al. 2014, Jiang et al. 2018). Furthermore, *Rosa* has proven to represent a rich niche of undescribed species of *Sporocadaceae*, with many remaining poorly identified, as the generic concepts have been in flux until recently (Liu et al. 2019). Therefore, conducting detailed surveys of pestalotioid fungi from *Rosa* spp. in China was necessary. The aims of the present study were thus to identify these fungi based on phylogenetic analyses and morphological comparisons, describe the species new to science, and gain a better understanding of the diversity and prevalence of *Sporocadaceae* associated with *Rosa* spp. in China.

MATERIALS AND METHODS

Sampling and isolation

A total of 295 *Rosa* samples (branches, fruits, leaves and spines) showing disease symptoms (Fig. 1) were collected from five provinces (Gansu, Henan, Hunan, Qinghai and Shaanxi) and the Ningxia Autonomous Region of China, which are the main production areas of *Rosa* plants in China. The *Rosa* species sampled include *R. chinensis, R. helenae, R. laevigata, R. multiflora, R. omeiensis, R. rugosa, R. spinosissima* and *R. xanthina*.

A total of 126 strains were obtained by removing the spore mass from conidiomata and generating single spore colonies, or plating superficially sterilised diseased tissue on potato

Fig. 1 Disease symptoms on *Rosa* associated with infection by *Sporocadaceae*. a–c. Leaves spots on *Rosa rugosa* caused by *Pestalotiopsis rhodomyrtus*; d–e. lesion developing on the fruits of *Rosa laevigata* infected by *Seimatosporium nonappendiculatum*; f. dying bush; g–h. dieback on (g) *Rosa rugosa* and (h) *Rosa xanthina* caused by *Seiridium rosae* and *Sporocadus sorbi*; i–j. sporocarps of *Pestalotiopsis chamaeropis* and *Seimatosporium centrale* on the spines of (i) *Rosa rugosa* and (j) *Rosa chinensis.*

Table 1 PCR reaction primers (forward and reverse) for amplification of gene loci of each fungal genus.

Genus	Loci used for amplification					References
	ITS	LSU	*RPB2*	*TEF*	*TUB*	
Monochaetia	ITS1/ITS4	LROR/LR5	RPB2-5F2/fRPB2-7cR			Liu et al. (2019), Jiang et al. (2021)
Neopestalotiopsis	ITS1/ITS4	LROR/LR5	RPB2-5F2/fRPB2-7cR	EF1-728F/EF-2	T1/Bt2b	Liu et al. (2019), Norphanphoun et al. (2019), Jiang et al. (2021)
Pestalotiopsis	ITS1/ITS4	LROR/LR5	RPB2-5F2/fRPB2-7cR	EF1-728F/EF-2	T1/Bt2b	Liu et al. (2019), Norphanphoun et al. (2019), Jiang et al. (2021)
Seimatosporium	ITS1/ITS4	LROR/LR5	RPB2-5F2/fRPB2-7cR			Goonasekara et al. (2016), Wijayawardene et al. (2016a), Liu et al. (2019)
Seiridium	ITS1/ITS4	LROR/LR5	RPB2-5F2/fRPB2-7cR	EF1-728F/EF-2	T1/Bt2b	Jiang et al. (2019), Liu et al. (2019), Marin-Felix et al. (2019)
Sporocadus	ITS1/ITS4	LROR/LR5	RPB2-5F2/fRPB2-7cR	EF1-728F/EF-2	T1/Bt2b	Liu et al. (2019)

Table 2 Isolates sequenced and used for phylogenetic analyses in the current study.

Species[1]	Culture no.	Status[2]	Host	Tissues	Origin	GenBank accession no.				
						ITS	LSU	*RPB2*	*TEF*	*TUB*
Monochaetia rosarum	**CFCC55172 = ROC 099**	**T**	***Rosa chinensis***	**branches**	**Nanyang, Henan**	**MZ292088**	**OK560346**	**OL742111**	**OL814484**	**OM103654**
	CFCC55173 = ROC 100		***Rosa chinensis***	**branches**	**Nanyang, Henan**	**MZ292089**	**OK560347**	**OL742112**	**OL814485**	**OM103655**
	ROC 098		***Rosa chinensis***	**branches**	**Nanyang, Henan**	**MZ292090**	**OK560348**	**OL742113**	**OL814486**	**OM103656**
	ROC 101		***Rosa chinensis***	**branches**	**Nanyang, Henan**	**MZ292091**	**OK560349**	**OL742114**	**OL814487**	**OM103657**
Neopestalotiopsis concentrica	**CFCC 55162 = ROC 53**	**T**	***Rosa rugosa***	**spines**	**Xinyang, Henan**	**OK560707**	**OK560440**	**OL742115**	**OM622433**	**OM117698**
	CFCC 55163 = ROC 64		***Rosa chinensis***	**spines**	**Xinyang, Henan**	**OK560708**	**OK560441**	**OL742116**	**OM622434**	**OM117699**
	ROC 135		***Rosa chinensis***	**spines**	**Xinyang, Henan**	**OK560709**	**OK560442**	**OL742117**	**OM622435**	**OM117700**
	ROC 136		***Rosa chinensis***	**spines**	**Xinyang, Henan**	**OK560710**	**OK560443**	**OL742118**	**OM622436**	**OM117701**
	ROC 137		***Rosa chinensis***	**spines**	**Nanyang, Henan**	**OK560711**	**OK560444**	**OL742119**	**OM622437**	**OM117702**
	ROC 138		***Rosa chinensis***	**spines**	**Nanyang, Henan**	**OK560712**	**OK560445**	**OL742120**	**OM622438**	**OM117703**
	ROC 140		***Rosa chinensis***	**spines**	**Nanyang, Henan**	**OK560713**	**OK560446**	**OL742121**	**OM622439**	**OM117704**
	ROC 141		***Rosa chinensis***	**spines**	**Nanyang, Henan**	**OK560714**	**OK560447**	**OL742122**	**OM622440**	**OM117705**
	ROC 142		***Rosa chinensis***	**spines**	**Nanyang, Henan**	**OK560715**	**OK560448**	**OL742123**	**OM622441**	**OM117706**
N. subepidermalis	**CFCC 55160 = ROC 161**	**T**	***Rosa rugosa***	**spines**	**Xinyang, Henan**	**OK560699**	**OK560432**	**–**	**OM622425**	**OM117690**
	ROC 162		***Rosa rugosa***	**spines**	**Xinyang, Henan**	**OK560700**	**OK560433**	**–**	**OM622426**	**OM117691**
	CFCC 55161 = ROC 169		***Rosa chinensis***	**spines**	**Xinyang, Henan**	**OK560701**	**OK560434**	**–**	**OM622427**	**OM117692**
	ROC 170		***Rosa chinensis***	**spines**	**Xinyang, Henan**	**OK560702**	**OK560435**	**–**	**OM622428**	**OM117693**
	ROC 171		***Rosa chinensis***	**branches**	**Xinyang, Henan**	**OK560703**	**OK560436**	**–**	**OM622429**	**OM117694**
	ROC 172		***Rosa chinensis***	**branches**	**Xinyang, Henan**	**OK560704**	**OK560437**	**–**	**OM622430**	**OM117695**
	ROC 173		***Rosa chinensis***	**branches**	**Xinyang, Henan**	**OK560705**	**OK560438**	**–**	**OM622431**	**OM117696**
	ROC 174		***Rosa chinensis***	**spines**	**Xinyang, Henan**	**OK560706**	**OK560439**	**–**	**OM622432**	**OM117697**
Pestalotiopsis chamaeropis	CFCC 55156 = ROC 23-1		*Rosa chinensis*	spines	Tianshui, Gansu	OK560574	OK560306	OL742124	OL814488	OM158138
	ROC 270		*Rosa chinensis*	spines	Tianshui, Gansu	OK560575	OK560307	OL742125	OL814489	OM158139
	ROC 272		*Rosa chinensis*	spines	Tianshui, Gansu	OK560576	OK560308	OL742126	OL814490	OM158140
	ROC 273		*Rosa chinensis*	spines	Tianshui, Gansu	OK560577	OK560309	OL742127	OL814491	OM158141
	ROC 275		*Rosa chinensis*	spines	Tianshui, Gansu	OK560578	OK560310	OL742128	OL814492	OM158142
	CFCC 55157 = ROC 23-2		*Rosa chinensis*	spines	Tianshui, Gansu	OK560579	OK560311	OL742129	OL814493	OM158143
	ROC 276		*Rosa chinensis*	spines	Tianshui, Gansu	OK560580	OK560312	OL742130	OL814494	OM158144
	ROC 278		*Rosa chinensis*	spines	Tianshui, Gansu	OK560581	OK560313	OL742131	OL814495	OM158145
	ROC 279		*Rosa chinensis*	spines	Tianshui, Gansu	OK560582	OK560314	OL742132	OL814496	OM158146
	ROC 280		*Rosa chinensis*	spines	Tianshui, Gansu	OK560583	OK560315	OL742133	OL814497	OM158147
	ROC 281		*Rosa chinensis*	spines	Tianshui, Gansu	OK560584	OK560316	OL742134	OL814498	OM158148
	ROC 282		*Rosa chinensis*	spines	Tianshui, Gansu	OK560585	OK560317	OL742135	OL814499	OM158149
	ROC 283		*Rosa chinensis*	spines	Tianshui, Gansu	OK560586	OK560318	OL742136	OL814500	OM158150
	ROC 286		*Rosa chinensis*	spines	Tianshui, Gansu	OK560587	OK560319	OL742137	OL814501	OM158151
	ROC 289		*Rosa chinensis*	spines	Tianshui, Gansu	OK560588	OK560320	OL742138	OL814502	OM158152
	ROC 290		*Rosa chinensis*	spines	Tianshui, Gansu	OK560589	OK560321	OL742139	OL814503	OM158153
	ROC 292		*Rosa chinensis*	spines	Tianshui, Gansu	OK560590	OK560322	OL742140	OL814504	OM158154
	ROC 293		*Rosa chinensis*	spines	Tianshui, Gansu	OK560591	OK560323	OL742141	OL814505	OM158155
Pes. rhodomyrtus	ROC 056		*Rosa rugosa*	leaves	Nanyang, Henan	OK560592	–	–	OL814506	OM158156
	ROC 057		*Rosa rugosa*	leaves	Nanyang, Henan	OK560593	–	–	OL814507	OM158157
	ROC 058		*Rosa rugosa*	leaves	Nanyang, Henan	OK560594	–	–	OL814508	OM158158
	ROC 059		*Rosa rugosa*	leaves	Nanyang, Henan	OK560595	–	–	OL814509	OM158159
	ROC 060		*Rosa rugosa*	leaves	Nanyang, Henan	OK560596	–	–	OL814510	OM158160
	ROC 061		*Rosa rugosa*	leaves	Nanyang, Henan	OK560597	–	–	OL814511	OM158161
	ROC 062		*Rosa rugosa*	leaves	Nanyang, Henan	OK560598	–	–	OL814512	OM158162
	ROC 303		*Rosa multiflora*	spines	Gannan, Gansu	OK560599	–	–	OL814513	OM158163
	ROC 304		*Rosa multiflora*	spines	Gannan, Gansu	OK560600	–	–	OL814514	OM158164
	ROC 305		*Rosa multiflora*	spines	Gannan, Gansu	OK560601	–	–	OL814515	OM158165
	ROC 306		*Rosa multiflora*	spines	Gannan, Gansu	OK560602	–	–	OL814516	OM158166
	ROC 307		*Rosa multiflora*	spines	Gannan, Gansu	OK560603	–	–	OL814517	OM158167
	ROC 309		*Rosa multiflora*	spines	Gannan, Gansu	OK560604	–	–	OL814518	OM158168
	ROC 311		*Rosa multiflora*	spines	Gannan, Gansu	OK560605	–	–	OL814519	OM158169

Table 2 (cont.)

Species[1]	Culture no.	Status[2]	Host	Tissues	Origin	GenBank accession no.				
						ITS	LSU	*RPB2*	*TEF*	*TUB*
Pes. rhodomyrtus (cont.)	ROC 356		*Rosa chinensis*	branches	Changsha, Hunan	OK560606	–	–	OL814520	OM158170
	ROC 357		*Rosa chinensis*	branches	Changsha, Hunan	OK560607	–	–	OL814521	OM158171
	ROC 358		*Rosa chinensis*	branches	Changsha, Hunan	OK560608	–	–	OL814522	OM158172
	ROC 359		*Rosa chinensis*	branches	Changsha, Hunan	OK560609	–	–	OL814523	OM158173
Pes. tumida	**CFCC 55158 = ROC 110**	**T**	***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560610**	**OK560324**	**OL742142**	**OL814524**	**OM158174**
	ROC 109		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560611**	**OK560325**	**OL742143**	**OL814525**	**OM158175**
	ROC 108		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560612**	**OK560326**	**OL742144**	**OL814526**	**OM158176**
	CFCC 55159 = ROC 234		***Rosa chinensis***	**branches**	**Tianshui, Gansu**	**OK560613**	**OK560327**	**OL742145**	**OL814527**	**OM158177**
	ROC 235		***Rosa chinensis***	**branches**	**Tianshui, Gansu**	**OK560614**	**OK560328**	**OL742146**	**OL814528**	**OM158178**
	ROC 236		***Rosa chinensis***	**branches**	**Tianshui, Gansu**	**OK560615**	**OK560329**	**OL742147**	**OL814529**	**OM158179**
	ROC 237		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560616**	**OK560330**	**OL742148**	**OL814530**	**OM158180**
	ROC 238		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560617**	**OK560331**	**OL742149**	**OL814531**	**OM158181**
	ROC 240		***Rosa chinensis***	**branches**	**Tianshui, Gansu**	**OK560618**	**OK560332**	**OL742150**	**OL814532**	**OM158182**
Seimatosporium centrale	**CFCC 55166 = ROC 003**	**T**	***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560629**	**OK560399**	**ON055447**	**OM986918**	**OM301641**
	ROC 001		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560630**	**OK560400**	**ON055448**	**OM986919**	**OM301642**
	ROC 002		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560631**	**OK560401**	**ON055449**	**OM986920**	**OM301643**
	CFCC 55169 =ROC 014		***Rosa chinensis***	**spines**	**Baoji, Shaanxi**	**OK560632**	**OK560402**	**ON055450**	**OM986921**	**OM301644**
	ROC 015		***Rosa chinensis***	**spines**	**Baoji, Shaanxi**	**OK560633**	**OK560403**	**ON055451**	**OM986922**	**OM301645**
	ROC 016		***Rosa chinensis***	**spines**	**Baoji, Shaanxi**	**OK560634**	**OK560404**	**ON055452**	**OM986923**	**OM301646**
	ROC 145		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560635**	**OK560405**	**ON055453**	**OM986924**	**OM301647**
	ROC 146		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560636**	**OK560406**	**ON055454**	**OM986925**	**OM301648**
	ROC 147		***Rosa chinensis***	**spines**	**Tianshui, Gansu**	**OK560637**	**OK560407**	**ON055455**	**OM986926**	**OM301649**
Seim. gracile	**CFCC 55167 = ROC 004**	**T**	***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560638**	**OK560408**	**ON055456**	**OM986927**	**OM301650**
	ROC 005		***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560639**	**OK560409**	**ON055457**	**OM986928**	**OM301651**
	ROC 006		***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560640**	**OK560410**	**ON055458**	**OM986929**	**OM301652**
	ROC 007		***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560641**	**OK560411**	**ON055459**	**OM986930**	**OM301653**
	ROC 008		***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560642**	**OK560412**	**ON055460**	**OM986931**	**OM301654**
	ROC 009		***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560643**	**OK560413**	**ON055461**	**OM986932**	**OM301655**
	ROC 010		***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560644**	**OK560414**	**ON055462**	**OM986933**	**OM301656**
	ROC 011		***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560645**	**OK560415**	**ON055463**	**OM986934**	**OM301657**
	ROC 012		***Rosa xanthina***	**spines**	**Tianshui, Gansu**	**OK560646**	**OK560416**	**ON055464**	**OM986935**	**OM301658**
Seim. nonappendiculatum	**CFCC 55168 = ROC 377**	**T**	***Rosa laevigata***	**fruits**	**Guyuan, Ningxia**	**OK560657**	**OK560427**	**ON055475**	**OM986946**	**OM301669**
	ROC 378		***Rosa laevigata***	**fruits**	**Guyuan, Ningxia**	**OK560658**	**OK560428**	**ON055476**	**OM986947**	**OM301670**
	ROC 379		***Rosa laevigata***	**fruits**	**Guyuan, Ningxia**	**OK560659**	**OK560429**	**ON055477**	**OM986948**	**OM301671**
	ROC 380		***Rosa laevigata***	**fruits**	**Guyuan, Ningxia**	**OK560660**	**OK560430**	**ON055478**	**OM986949**	**OM301672**
	ROC 381		***Rosa laevigata***	**fruits**	**Guyuan, Ningxia**	**OK560661**	**OK560431**	**ON055479**	**OM986950**	**OM301673**
Seim. parvum	**CFCC 55164 = ROC 038**	**T**	***Rosa spinosissima***	**spines**	**Huangnan, Qinghai**	**OK560647**	**OK560417**	**ON055465**	**OM986936**	**OM301659**
	ROC 039		***Rosa spinosissima***	**spines**	**Huangnan, Qinghai**	**OK560648**	**OK560418**	**ON055466**	**OM986937**	**OM301660**
	ROC 040		***Rosa spinosissima***	**spines**	**Huangnan, Qinghai**	**OK560649**	**OK560419**	**ON055467**	**OM986938**	**OM301661**
	ROC 041		***Rosa spinosissima***	**spines**	**Huangnan, Qinghai**	**OK560650**	**OK560420**	**ON055468**	**OM986939**	**OM301662**
	ROC 042		***Rosa spinosissima***	**spines**	**Huangnan, Qinghai**	**OK560651**	**OK560421**	**ON055469**	**OM986940**	**OM301663**
	ROC 043		***Rosa spinosissima***	**spines**	**Huangnan, Qinghai**	**OK560652**	**OK560422**	**ON055470**	**OM986941**	**OM301664**
	CFCC 55165 =ROC 017		***Rosa helenae***	**spines**	**Huangnan, Qinghai**	**OK560653**	**OK560423**	**ON055471**	**OM986942**	**OM301665**
	ROC 018		***Rosa helenae***	**spines**	**Huangnan, Qinghai**	**OK560654**	**OK560424**	**ON055472**	**OM986943**	**OM301666**
	ROC 019		***Rosa helenae***	**spines**	**Huangnan, Qinghai**	**OK560655**	**OK560425**	**ON055473**	**OM986944**	**OM301667**
	ROC 020		***Rosa helenae***	**spines**	**Huangnan, Qinghai**	**OK560656**	**OK560426**	**ON055474**	**OM986945**	**OM301668**
Seiridium rosae	**CFCC 55174 = ROC 208**	**T**	***Rosa rugosa***	**branches**	**Guyuan, Ningxia**	**OK560681**	**OK560394**	**OL742151**	**OL814533**	**OM313314**
	ROC 209		***Rosa rugosa***	**branches**	**Guyuan, Ningxia**	**OK560682**	**OK560395**	**OL742152**	**OL814534**	**OM313315**
	CFCC 55175 = ROC 267		***Rosa rugosa***	**branches**	**Guyuan, Ningxia**	**OK560683**	**OK560396**	**OL742153**	**OL814535**	**OM313316**
	ROC 268		***Rosa rugosa***	**branches**	**Guyuan, Ningxia**	**OK560684**	**OK560397**	**OL742154**	**OL814536**	**OM313317**
Sporocadus brevis	**CFCC 55170 = ROC 091**	**T**	***Rosa spinosissima***	**spines**	**Gannan, Gansu**	**OK655780**	**OK560371**	**OL742155**	**OL814537**	**OM401659**
	ROC 092		***Rosa spinosissima***	**spines**	**Gannan, Gansu**	**OK655781**	**OK560372**	**OL742156**	**OL814538**	**OM401660**
	ROC 093		***Rosa spinosissima***	**spines**	**Gannan, Gansu**	**OK655782**	**OK560373**	**OL742157**	**OL814539**	**OM401661**

Table 2 (cont.)

Species[1]	Culture no.	Status[2]	Host	Tissues	Origin	GenBank accession no.				
						ITS	LSU	*RPB2*	*TEF*	*TUB*
Sporocadus brevis (cont.)	**ROC 094**		***Rosa spinosissima***	**spines**	**Gannan, Gansu**	**OK655783**	**OK560374**	**OL742158**	**OL814540**	**OM401662**
	ROC 095		***Rosa spinosissima***	**spines**	**Gannan, Gansu**	**OK655784**	**OK560375**	**OL742159**	**OL814541**	**OM401663**
Spo. sorbi	ROC 105		*Rosa xanthina*	branches	Lanzhou, Gansu	OK655785	OK560376	OL742160	OL814542	OM401664
	ROC 102		*Rosa xanthina*	branches	Lanzhou, Gansu	OK655786	OK560377	OL742161	OL814543	OM401665
	ROC 103		*Rosa xanthina*	branches	Lanzhou, Gansu	OK655787	OK560378	OL742162	OL814544	OM401666
	ROC 159		*Rosa xanthina*	spines	Ganan, Gansu	OK655788	OK560379	OL742163	OL814545	OM401667
	ROC 160		*Rosa xanthina*	spines	Ganan, Gansu	OK655789	OK560380	OL742164	OL814546	OM401668
	ROC 161		*Rosa xanthina*	spines	Ganan, Gansu	OK655790	OK560381	OL742165	OL814547	OM401669
Spo. spiniger	**ROC 119**	**T**	***Rosa omeiensis***	**spines**	**Lanzhou, Gansu**	**OK655791**	**OK560382**	**OL742166**	**OL814548**	**OM401670**
	ROC 120		***Rosa omeiensis***	**spines**	**Lanzhou, Gansu**	**OK655792**	**OK560383**	**OL742167**	**OL814549**	**OM401671**
	ROC 121		***Rosa omeiensis***	**spines**	**Lanzhou, Gansu**	**OK655793**	**OK560384**	**OL742168**	**OL814550**	**OM401672**
	ROC 122		***Rosa omeiensis***	**spines**	**Lanzhou, Gansu**	**OK655794**	**OK560385**	**OL742169**	**OL814551**	**OM401673**
	ROC 123		***Rosa omeiensis***	**spines**	**Lanzhou, Gansu**	**OK655795**	**OK560386**	**OL742170**	**OL814552**	**OM401674**
	ROC 124		***Rosa omeiensis***	**spines**	**Lanzhou, Gansu**	**OK655796**	**OK560387**	**OL742171**	**OL814553**	**OM401675**
	ROC 125		***Rosa omeiensis***	**spines**	**Lanzhou, Gansu**	**OK655797**	**OK560388**	**OL742172**	**OL814554**	**OM401676**
Spo. trimorphus	CFCC 55171 = ROC 112		*Rosa xanthina*	branches	Lanzhou, Gansu	OK655798	OK560389	OL742173	OL814555	OM401677
	ROC 113		*Rosa xanthina*	branches	Lanzhou, Gansu	OK655799	OK560390	OL742174	OL814556	OM401678
	ROC 114		*Rosa xanthina*	branches	Lanzhou, Gansu	OK655800	OK560391	OL742175	OL814557	OM401679
	ROC 115		*Rosa xanthina*	branches	Lanzhou, Gansu	OK655801	OK560392	OL742176	OL814558	OM401680
	ROC 116		*Rosa xanthina*	branches	Lanzhou, Gansu	OK655802	OK560393	OL742177	OL814559	OM401681

[1] Newly described taxa and deposited sequences are in **bold**.
[2] T: ex-type.

dextrose agar (PDA, 20 % diced potatoes, 2 % agar and 2 % glucose) and incubating Petri dishes at 25 °C in the dark for 2–3 d. When colonies just formed, they were hyphal-tipped and transferred to fresh PDA Petri dishes (Crous et al. 2019a). Type specimens of new species from this study were deposited in the Museum of the Beijing Forestry University (BJFC), and ex-type living cultures were deposited in the China Forestry Culture Collection Centre (CFCC), Beijing, China.

Morphological analyses

Cultures were incubated on PDA at 25 °C in a 12 h day/night regime (Crous et al. 2019a). After 15 d, colony diameters were measured and colony colours were rated according to Rayner (1970). Slide preparations were mounted in lactic acid or water, from colonies sporulating on PDA, autoclaved pine needles on 2 % tap water agar (Smith et al. 1996), and incubated at 25 °C under continuous nuv-light to promote sporulation. Sections through stromata were made by hand. Observations were made with a Leica DM 2500 dissecting microscope (Wetzlar, Germany), and with a Nikon Eclipse 80i compound microscope using differential interference contrast (DIC) illumination and images recorded on a Nis DS-Ri2 camera with the Nikon Nis-Elements F4.30.01 software. Conidial length was measured from the base of the basal cell to the base of the apical appendage, and conidial width was measured at the widest point of the conidium (Bonthond et al. 2018). Taxonomic novelties were deposited in MycoBank (Crous et al. 2004).

DNA extraction, PCR amplification and sequencing

Total genomic DNA was extracted from axenic cultures using a modified cetyltrimethylammonium bromide (CTAB) protocol (Doyle & Doyle 1990). DNA products were stored at -20 °C. The extracted DNA was used as template for the polymerase chain reaction (PCR). PCR reaction primers (forward and reverse) of each fungal genus are found in Table 1. PCR parameters were initiated with 95 °C for 5 min, followed by 34 cycles of denaturation at 95 °C for 30 s, annealing at a suitable temperature for 30 s (56 °C for ITS and LSU, 52 °C for *TEF*, 52 °C for *RPB2* and 60 °C for *TUB*), and extension at 72 °C for 30 s, and terminated with a final elongation step at 72 °C for 10 min. The final PCR products were examined by electrophoresis in 2 % agarose gels. The amplified PCR products were sent to a commercial sequencing provider (Tsingke Biotechnology Co. Ltd, Beijing, China).

Phylogenetic analyses

All nucleotide sequences generated from different primer pairs in this study were deposited in GenBank (Table 2). Sequences were BLASTn searched in NCBI to obtain the related sequences from recent publications and were analysed (Table 3). Sequences were aligned in MAFFT v. 7 at the web server (http://mafft.cbrc.jp/alignment/server) (Katoh & Standley 2013, Katoh et al. 2019) and manually adjusted in MEGA v. 6 (Tamura et al. 2013).

Seven phylogenetic analyses were conducted based on both individual and combined loci for one family (*Sporocadaceae*) and six genera (*Monochaetia*, *Neopestalotiopsis*, *Pestalotiopsis*, *Seimatosporium*, *Seiridium* and *Sporocadus*). Maximum Parsimony (MP) was used to construct phylogenies using PAUP v. 4.0b10 (Swofford 2003), Maximum Likelihood (ML) was executed in RAxML (Dean et al. 2014) implemented in raxmlGUI v. 1.5b1 (Silvestro & Michalak 2012) and MrBayes v. 3.1.2 was used for Bayesian analyses (BA) (Huelsenbeck & Ronquist 2001).

Trees were visualised with FigTree v. 1.4.0 (http://tree.bio.ed.ac.uk software/figtree/), and additional layout was done with Adobe Illustrator CS v. 5. Maximum-likelihood bootstrap values (MLBP)

Table 3 Isolates from previous studies used in the phylogenetic analyses in the current study.

Species	Strain number[1]	Status[2]	Country	Substrate	GenBank accession no.					References
					ITS	LSU	*RPB2*	*TEF*	*TUB*	
Allelochaeta acuta	CPC 16629		Australia	*Eucalyptus dives*	MH554086	MH554297	MH555000	–	–	Crous et al. (2018)
All. elegans	CBS 187.81	ET	Australia	*Melaleuca lanceolata*	MH554014	MH554234	MH554927	–	–	Crous et al. (2018)
All. falcata	CPC 13580		Australia	*Eucalyptus alligatrix*	MH554073	MH554284	MH554985	–	–	Crous et al. (2018)
	CBS 131117	ET	Australia	*Eucalyptus alligatrix*	MH553999	MH554217	MH554907	–	–	Crous et al. (2018)
All. fusispora	CPC 17616		Australia	*Eucalyptus* sp.	MH554094	MH554304	MH555008	–	–	Crous et al. (2018)
	CBS 810.73	IT	Australia	*Eucalyptus polyanthemos*	MH554067	MH554279	MH554980	–	–	Crous et al. (2018)
All. kriegeriana	CBS 188.81		Australia	*Callistemon sieberi*	MH554015	MH554235	MH554928	–	–	Crous et al. (2018)
All. neoacuta	CBS 115131	T	South Africa	*Eucalyptus smithii*	JN871200	JN871209	MH554998	–	–	Crous et al. (2018)
	CBS 110733		South Africa	*Eucalyptus smithii*	JN871201	JN871210	MH554999	–	–	Crous et al. (2018)
All. neodilophospora	CPC 17161	T	Australia	*Callistemon pinifolius*	MH554090	MH554300	MH555004	–	–	Crous et al. (2018)
All. neoorbicularis	CPC 13581		Australia	*Eucalyptus regnans*	MH554074	MH554285	MH554986	–	–	Crous et al. (2018)
All. obliquae	CPC 20191	T	Australia	*Eucalyptus obliqua*	MH554105	MH554315	MH555018	–	–	Crous et al. (2018)
All. orbicularis	CBS 131118	ET	Australia	*Corymbia henryi*	MH554000	MH554218	MH554908	–	–	Crous et al. (2018)
All. paraelegans	CBS 150.71	T	Australia	*Melaleuca ericifolia*	MH554007	MH554228	MH554923	–	–	Crous et al. (2018)
All. pseudowalkeri	CPC 17043	T	Australia	*Eucalyptus* sp.	MH554089	MH554299	MH555003	–	–	Crous et al. (2018)
All. sparsifoliae	CPC 14529		Australia	*Eucalyptus sparsifolia*	MH554083	MH554294	MH554995	–	–	Crous et al. (2018)
	CPC 14502	T	Australia	*Eucalyptus sparsifolia*	MH554082	MH554293	MH554994	–	–	Crous et al. (2018)
Bartalinia bella	CBS 125525		South Africa	*Maytenus abbottii*	GU291796	MH554214	MH554904	–	–	Liu et al. (2019)
	CBS 464.61	T	Brazil	Air	MH554051	MH554264	MH554964	–	–	Liu et al. (2019)
Bar. pini	CBS 143891	T	Uganda	*Pinus patula*	MH554125	MH554330	MH555033	–	–	Liu et al. (2019)
	CBS 144141		USA	*Acacia koa*	MH554170	MH554364	MH555067	–	–	Liu et al. (2019)
Bar. robillardoides	CBS 122705	ET	Italy	*Leptoglossus occidentalis*	LT853104	KJ710438	LT853152	–	–	Liu et al. (2019)
	CBS 122615		South Africa	*Cupressus lusitanica*	MH553989	MH554207	MH554897	–	–	Liu et al. (2019)
Beltrania pseudorhombica	CPC 23656		China	*Pinus tabulaeformis*	MH554124	KJ869215	MH555032	–	–	Crous et al. (2014a), Liu et al. (2019)
Bel. rhombica	CBS 123.58	T	Mozambique	Sand near mangrove swamp	MH553990	MH554209	MH554899	–	–	Liu et al. (2019)
Broomella vitalbae	HPC 1154		–	–	MH554173	MH554367	–	–	–	Liu et al. (2019)
	MFLUCC 13-0798	ET	Italy	*Clematis vitalba*	NR_153610	KP757749	–	–	–	Liu et al. (2019)
Ciliochorella phanericola	MFLUCC 12-0310		Thailand	Dead leaves	KF827444	KF827445	KF827479	–	–	Hyde et al. (2016)
	MFLUCC 14-0984	T	Thailand	*Phanera purpurea*	KX789680	KX789681	–	–	–	Hyde et al. (2016)
Clypeosphaeria uniseptata	CBS 114967		Hong Kong, China	Wood	MH553979	MH554197	MH554878	–	–	Liu et al. (2019)
Diploceras hypericinum	CBS 109058		New Zealand	*Hypericum* sp.	MH553955	MH554178	MH554852	–	–	Liu et al. (2019)
	CBS 492.97		Netherlands	*Hypericum perforatum*	MH554054	MH554267	MH554967	–	–	Liu et al. (2019)
	CBS 197.36		Switzerland	*Hypericum* sp.	MH554017	MH554237	MH554930	–	–	Liu et al. (2019)
	CBS 143885	ET	Netherlands	*Hypericum perforatum*	MH554108	MH554316	MH555019	–	–	Liu et al. (2019)
Disaeta arbuti	CBS 143903		Australia	*Acacia pycnantha*	MH554148	MH554346	MH555050	–	–	Liu et al. (2019)
Discosia artocreas	CBS 124848	ET	Germany	*Fagus sylvatica*	MH553994	MH554213	MH554903	–	–	Liu et al. (2019)
Dis. brasiliensis	NTCL095		Thailand	Dead leaf	KF827433	KF827437	KF827474	–	–	Liu et al. (2019)
	NTCL097-2		Thailand	Dead leaf	KF827434	KF827438	KF827475	–	–	Liu et al. (2019)
	NTCL094-2		Thailand	Dead leaf	KF827432	KF827436	KF827473	–	–	Liu et al. (2019)
Discosia sp. 6	CBS 241.66		South Africa	*Acacia karroo*	MH554022	MH554244	MH554933	–	–	Liu et al. (2019)
Discosia sp. 7	CBS 684.70		Netherlands	*Aesculus hippocastanu*	MH554064	MH554277	MH554978	–	–	Liu et al. (2019)
Distononappendiculata banksiae	CPC 17658		Australia	*Banksia marginata*	MH554097	MH554307	MH555011	–	–	Liu et al. (2019)
	CBS 131308	T	Australia	*Banksia marginata*	JQ044422	JQ044442	MH554909	–	–	Liu et al. (2019)
	CPC 20185		Australia	*Banksia marginata*	MH554104	MH554314	MH555017	–	–	Liu et al. (2019)
	CBS 143906		Australia	*Banksia marginata*	MH554158	MH554354	MH555057	–	–	Liu et al. (2019)
Dist. casuarinae	CBS 143884	T	Australia	*Casuarina* sp.	MH554093	MH554303	MH555007	–	–	Liu et al. (2019)
Dist. verrucata	CBS 144032	T	Australia	*Banksia repens*	MH554163	MH554359	MH555062	–	–	Liu et al. (2019)
Diversimediispora humicola	CBS 302.86	T	USA	Soil	MH554028	MH554247	MH554941	–	–	Liu et al. (2019)
Heterotruncatella lutea	CBS 349.73	IT	Australia	*Acacia pycnantha*	LT853099	DQ414533	LT853146	–	–	Liu et al. (2019)
Het. proteicola	CBS 123029		South Africa	*Protea acaulis*	MH553993	MH554212	MH554902	–	–	Liu et al. (2019)

Table 3 (cont.)

Species	Strain number[1]	Status[2]	Country	Substrate	GenBank accession no.					References
					ITS	LSU	*RPB2*	*TEF*	*TUB*	
Het. restionacearum	CBS 119210		South Africa	*Ischyrolepis* cf. *gaudichaudiana*	DQ278915	DQ278929	MH554892	–	–	Liu et al. (2019)
	CBS 118150		South Africa	*Restio filiformis*	DQ278914	MH554203	MH554889	–	–	Liu et al. (2019)
Het. spadicea	CBS 118148		South Africa	*Rhodocoma capensis*	DQ278913	DQ278928	MH554888	–	–	Liu et al. (2019)
	CBS 118144		South Africa	*Ischyrolepis* sp.	DQ278921	DQ278926	MH554886	–	–	Liu et al. (2019)
Hyalotiella spartii	MFLUCC 13-0397	T	Italy	*Spartium junceum*	KP757756	KP757752	–	–	–	Li et al. (2015)
Hyalotiella transvalensis	CBS 303.65	T	South Africa	Soil	MH554029	MH554248	MH554942	–	–	Liu et al. (2019)
Hymenopleella austroafricana	CBS 143886	T	South Africa	*Gleditsia triacanthos*	MH554115	MH554320	MH555023	–	–	Liu et al. (2019)
	CBS 144027		Zambia	*Combretum hereroense*	MH554119	MH554324	MH555027	–	–	Liu et al. (2019)
	CBS 144026		South Africa	*Bridelia mollis*	MH554117	MH554322	MH555025	–	–	Liu et al. (2019)
Hym. endophytica	EML AS5-1	T	Korea	*Abies firma*	KX216520	KX216518	–	–	–	Liu et al. (2019)
Hym. hippophaëicola	CBS 113687		Sweden	*Hippophae rhamnoides*	MH553969	MH554188	MH554863	–	–	Jaklitsch et al. (2016)
	CBS 140410	ET	Austria	*Hippophae rhamnoides*	KT949901	MH554224	MH554919	–	–	Jaklitsch et al. (2016)
Hym. lakefuxianensis	HKUCC 7303	T	China	Submerged wood	–	AF452047	–	–	–	Liu et al. (2019)
Hym. polyseptata	CBS 143887	T	South Africa	*Combretum* sp.	MH554116	MH554321	MH555024	–	–	Liu et al. (2019)
Hym. subcylindrica	CBS 164.77		India	*Cocos nucifera*	MH554009	MH554230	MH554925	–	–	Liu et al. (2019)
	CBS 647.74	T	India	*Gypsophilla seeds*	MH554062	MH554275	MH554976	–	–	Liu et al. (2019)
Immersidiscosia eucalypti	MAFF 242781		Japan	Unknown dead leaves	AB594793	AB593725	–	–	–	Tanaka et al. (2011)
	NBRC 104197		Japan	*Ardisia japonica*	AB594792	AB593724	–	–	–	Tanaka et al. (2011)
Lepteutypa fuckelii	CBS 140409	NT	Belgium	*Tilia cordata*	NR_154123	KT949902	MH554918	–	–	Liu et al. (2019)
Lep. sambuci	CBS 131707	T	UK	*Sambucus nigra*	NR_154124	MH554219	MH554911	–	–	Liu et al. (2019)
Microdochium lycopodinum	CBS 125585	T	Austria	*Lycopodium annotinum*	KP859016	KP858952	KP859125	–	–	Hernández-Restrepo et al. (2016), Liu et al. (2019)
Mic. phragmitis	CBS 285.71	ET	Poland	*Puccinia teleutosorus*	KP859013	KP858949	KP859122	–	–	Liu et al. (2019)
Mic. seminicola	CBS 139951	T	Switzerland	*Maize kernels*	NR_155375	KP858974	KP859147	–	–	Hernández-Restrepo et al. (2016), Liu et al. (2019)
Monochaetia camelliae	PSH2000I-151		China	*Camellia hongkongensis*	AY682948	–	–	–	–	Liu et al. (2019)
	PSH2000I-146		China	*Camellia pitardii*	AY682947	–	–	–	–	Liu et al. (2019)
M. castaneae	CFCC 54354 = SM9-1	T	China	*Castanea mollissima*	MW166222	–	–	–	–	Jiang et al. (2021)
	SM9-2		China	*Castanea mollissima*	MW166223	–	–	–	–	Jiang et al. (2021)
M. dimorphospora	NBRC 9980		Japan	*Castanea pubinervis*	LC146750	–	–	–	–	De Silva et al. (2018)
	NNIBRFG396		Korea	Fresh water	MT271967	–	–	–	–	De Silva et al. (2018)
M. ilicis	CBS 101009		Japan	Air	MH553953	MH554176	MH554849	–	–	Liu et al. (2019)
	KUMCC 15-0520	T	China	*Ilex* sp.	KX984153	–	–	–	–	Liu et al. (2019)
M. junipericola	CBS:143391		Germany	*Juniperus communis*	MH107900	–	–	–	–	Liu et al. (2019)
M. kansensis	ZJLQ468		China	*Pseudotaxus chienii*	KC345692	–	–	–	–	De Silva et al. (2018)
	PSHI2004Endo1030		China	*Cyclobalaopsis* sp.	DQ534044	–	–	–	–	De Silva et al. (2018)
	PSHI2004Endo1031		China	*Quercus aliena*	DQ534045	–	–	–	–	De Silva et al. (2018)
M. mochaeta	CBS 315.54		England	*Quercus* sp.	MH554030	MH554249	MH554943	–	–	Liu et al. (2019)
	CBS 658.95		Netherlands	*Quercus robur*	MH554063	MH554276	MH554977	–	–	Liu et al. (2019)
	CBS 115004		Netherlands	*Quercus robur*	AY853243	MH554198	MH554879	–	–	Liu et al. (2019)
	CBS 546.80		Netherlands	Culture contaminant	MH554056	MH554270	MH554969	–	–	Liu et al. (2019)
	CBS 199.82	ET	Italy	*Quercus pubescens*	MH554018	MH554238	MH554931	–	–	Liu et al. (2019)
	M18		Italy	Unknown plant	JX262802	–	–	–	–	Liu et al. (2019)
M. quercus	CBS 144034 = CPC 29514	T	Mexico	*Quercus eduardi*	MH554171	MH554365	MH555068	–	–	De Silva et al. (2018)
	CBS 144034 = CPC 29515		Mexico	*Quercus eduardi*	NR_161110	–	–	–	–	De Silva et al. (2018)
M. schimae	SAUCC212201	T	China	*Schima superba*	MZ577565	–	–	OK104874	OK104867	Zhang et al. (2022)
	SAUCC212202		China	*Schima superba*	MZ577566	–	–	OK104875	OK104868	Zhang et al. (2022)
	SAUCC212203		China	*Schima superba*	MZ577567	–	–	OK104876	OK104869	Zhang et al. (2022)
M. sinensis	HKAS 10065		China	*Quercus* sp.	NR_161064	–	–	–	–	De Silva et al. (2019)
	KUMCC 15-0517		China	*Quercus* sp.	MH115996	–	–	–	–	De Silva et al. (2020)

Table 3 (cont.)

Species	Strain number[1]	Status[2]	Country	Substrate	GenBank accession no.					References
					ITS	LSU	*RPB2*	*TEF*	*TUB*	
Morinia acaciae	CBS 100230		New Zealand	*Prunus salicina* cv. 'Omega'	MH553950	MH554174	MH554847	–	–	Liu et al. (2019)
	CBS 137994	T	France	*Acacia melanoxylon*	MH554002	MH554221	MH554914	–	–	Liu et al. (2019)
Mor. crini	CBS 143888	T	South Africa	*Crinum bulbispermum*	MH554118	MH554323	MH555026	–	–	Liu et al. (2019)
Mor. longiappendiculata	CBS 117603	T	Spain	*Calluna vulgaris*	AY929324	MH554202	MH554885	–	–	Collado et al. (2006), Liu et al. (2019)
Mor. pestalozzioides	F090354	ET	Spain	*Sedum sediforme*	AY929325	–	–	–	–	Liu et al. (2019)
Neopestalotiopsis acrostichi	MFLUCC 17-1754	T	Thailand	*Acrostichum aureum*	MK764272	–	–	MK764316	MK764338	Norphanphoun et al. (2019)
	MFLUCC 17-1755		Thailand	*Acrostichum aureum*	MK764273	–	–	MK764317	MK764339	Norphanphoun et al. (2019)
N. alpapicalis	MFLUCC 17-2544	T	Thailand	*Rhizophora mucronata*	MK357772	–	–	MK463547	MK463545	Kumar et al. (2019)
	MFLUCC 17-2545		Thailand	*Rhizophora apiculata*	MK357773	–	–	MK463548	MK463546	Kumar et al. (2019)
N. aotearoa	CBS 367.54	T	New Zealand	Canvas	KM199369	–	–	KM199526	KM199454	Maharachchikumbura et al. (2014)
N. asiatica	MFLUCC 12-0286	T	China	Leaves	JX398983	–	–	JX399049	JX399018	Maharachchikumbura et al. (2014)
N. australis	CBS 114159	T	Australia	*Telopea* sp.	KM199348	–	–	KM199537	KM199432	Maharachchikumbura et al. (2014)
N. brachiata	MFLUCC 17-1555	T	Thailand	*Rhizophora apiculata*	MK764274	–	–	MK764318	MK764340	Norphanphoun et al. (2019)
N. brasiliensis	COAD 2166	T	Brazil	*Psidium guajava*	MG686469	–	–	MG692402	MG692400	Bezerra et al. (2018)
N. camelliae-oleiferae	CSUFTCC81	T	China	*Camellia oleifera*	OK493585	–	–	OK507955	OK562360	Li et al. (2021)
N. cavernicola	KUMCC 20-0269	T	China	Cave rock surface	MW545802	–	–	MW550735	MW557596	Liu et al. (2021)
N. chiangmaiensis	MFLUCC 18-0113		Thailand	Dead leaves	–	–	–	MH388404	MH412725	Tibpromma et al. (2018)
N. chrysea	MFLUCC 12-0261	T	China	*Pandanus* sp.	JX398985	–	–	JX399051	JX399020	Maharachchikumbura et al. (2014)
N. clavispora	MFLUCC 12-0281	T	China	*Magnolia* sp.	JX398979	–	–	JX399045	JX399014	Maharachchikumbura et al. (2014)
N. cocoes	MFLUCC 15-0152		Thailand	*Cocos nucifera*	KX789687	–	–	KX789689	–	Hyde et al. (2016)
N. coffeae-arabicae	HGUP 4019	T	China	*Coffea arabica*	KF412649	–	–	KF412646	KF412643	Song et al. (2013)
N. cubana	CBS 600.96	T	Cuba	Leaf litter	KM199347	KM116253	MH554973	KM199521	KM199438	Maharachchikumbura et al. (2014)
N. dendrobii	MFLUCC 14-0106		Thailand	*Dendrobium cariniferum*	MK993571	–	–	MK975829	MK975835	Ma et al. (2019)
N. drenthii	BRIP 72264a	T	Australia	*Macadamia integrifolia*	MZ303787	–	–	MZ344172	MZ312680	Prasannath et al. (2021)
N. egyptiaca	CBS 140162	T	Egypt	*Mangifera indica*	KP943747	–	–	KP943748	KP943746	Crous et al. (2015b)
N. ellipsospora	CBS 115113	T	China	Dead plant material	KM199343	–	–	KM199544	KM199450	Maharachchikumbura et al. (2014)
	MFLUCC 12-0283		China	Dead plant material	JX398980	–	–	JX399047	JX399016	Maharachchikumbura et al. (2014)
N. eucalypticola	CBS 264.37	T	–	*Eucalyptus globulus*	KM199376	KM116256	MH554935	KM199551	KM199431	Maharachchikumbura et al. (2014)
N. eucalyptorum	CBS 147684	T	Portugal	*Eucalyptus globulus*	MW794108	–	–	MW805397	MW802841	Diogo et al. (2021)
N. foedans	CGMCC 3.9123	T	China	Mangrove plant	JX398987	–	–	JX399053	JX399022	Maharachchikumbura et al. (2014)
N. formicarum	CBS 362.72	T	Cuba	Plant debris	MH860500	–	–	KM199517	KM199455	Maharachchikumbura et al. (2014)
N. guajavae	FMBCC 11.1	T	Pakistan	*Psidium guajava*	MF783085	–	–	MH460868	MH460871	Ul Haq et al. (2021)
N. guajavicola	FMBCC 11.4	T	Pakistan	*Psidium guajava*	MH209245	–	–	MH460870	MH460873	Ul Haq et al. (2021)
N. hadrolaeliae	COAD 2637	T	Brazil	*Hadrolaelia jongheana*	MK454709	–	–	MK465122	MK465120	Freitas et al. (2019)
N. haikouensis	SAUCC212271	T	China	*Ilex chinensis*	OK087294	–	–	OK104877	OK104870	Zhang et al. (2022)
	SAUCC212272		China	*Ilex chinensis*	OK087295	–	–	OK104878	OK104871	Zhang et al. (2022)
N. hispanica	CBS 147686	T	Portugal	*Eucalyptus globulus*	MW794107	–	–	MW805399	MW802840	Diogo et al. (2021)
N. honoluluana	CBS 114495	T	USA	*Telopea* sp.	KM199364	–	–	KM199548	KM199461	Maharachchikumbura et al. (2014)
N. hydeana	MFLUCC 20-0132	T	Thailand	*Artocarpus heterophyllus*	MW266069	–	–	MW251129	MW251119	Huanluek et al. (2021)
N. iberica	CBS 147688	T	Portugal	*Eucalyptus globulus*	MW794111	–	–	MW805402	MW802844	Diogo et al. (2021)
N. iraniensis	CBS 137768		Iran	*Fragaria* x *ananassa*	KM074045	–	–	KM074051	KM074056	Norphanphoun et al. (2019)
N. javaensis	CBS 257.31	T	Indonesia	*Cocos nucifera*	KM199357	–	–	KM199543	KM199437	Maharachchikumbura et al. (2014)
N. longiappendiculata	CBS 147690	T	Portugal	*Eucalyptus globulus*	MW794112	–	–	MW805404	MW802845	Diogo et al. (2021)
N. lusitanica	CBS 147692	T	Portugal	*Eucalyptus globulus*	MW794110	–	–	MW805406	MW802843	Diogo et al. (2021)
N. macadamiae	BRIP 63737c	T	New South Wales	*Macadamia integrifolia*	KX186604	–	–	KX186627	KX186654	Akinsanmi et al. (2017)
N. maddoxii	BRIP 72266a	T	Australia	*Macadamia integrifolia*	MZ303782	–	–	MZ344167	MZ312675	Prasannath et al. (2021)
N. magna	MFLUCC 12-0652	T	France	*Pteridium* sp.	KF582795	–	–	KF582791	KF582793	Maharachchikumbura et al. (2014)
N. mesopotamica	CBS 336.86	T	Iraq	*Pinus brutia*	KM199362	KM116271	MH554944	KM199555	KM199441	Maharachchikumbura et al. (2014)
N. musae	MFLU 16-1279	T	Thailand	*Musa* sp.	KX789683	–	–	KX789685	KX789686	Hyde et al. (2016)
N. natalensis	CBS 138.41	T	South Africa	*Acacia mollissima*	KM199377	–	–	KM199552	KM199466	Maharachchikumbura et al. (2014)

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					ITS	LSU	*RPB2*	*TEF*	*TUB*	
N. nebuloides	BRIP 66617	T	Australia	*Sporobolus elongatus*	MK966338	–	–	MK977633	MK977632	Crous et al. (2020)
N. olumideae	BRIP 72273a	T	Australia	*Macadamia integrifolia*	MZ303790	–	–	MZ344175	MZ312683	Prasannath et al. (2021)
N. palmarum	PSHI2004Endo458		Cuba	*Zalacca wallichiana*	DQ813426	–	–	–	DQ787836	Liu et al. (2010)
	PSHI2004Endo454		Cuba	*Roystonea regia*	DQ813427	–	–	–	DQ787837	Liu et al. (2010)
N. pandanicola	KUMCC 17-0175		–	*Pandanus* sp.	–	–	–	MH388389	MH412720	Tibpromma et al. (2018)
N. pernambucana	URM 7148-01	T	Brazil	*Vismia guianensis*	KJ792466	–	–	KU306739	–	Silvério et al. (2016)
N. perukae	FMBCC 11.3	T	Pakistan	*Psidium guajava*	MH209077	–	–	MH523647	MH460876	Ul Haq et al. (2021)
N. petila	MFLUCC 17-1738	T	Thailand	*Rhizophora mucronata*	MK764275	–	–	MK764319	MK764341	Norphanphoun et al. (2019)
	MFLUCC 17-1737		Thailand	*Rhizophora mucronata*	MK764276	–	–	MK764320	MK764342	Norphanphoun et al. (2019)
N. phangngaensis	MFLUCC 18-0119		–	*Pandanus* sp.	MH388354	–	–	MH388390	MH412721	Tibpromma et al. (2018)
N. piceana	CBS 394.48	T	UK	*Picea* sp.	KM199368	–	–	KM199527	KM199453	Maharachchikumbura et al. (2014)
N. protearum	CBS 114178	T	Zimbabwe	*Leucospermum cuneiforme*	JN712498	JN712564	MH554873	LT853201	KM199463	Maharachchikumbura et al. (2014)
N. psidii	FMBCC 11.2	T	Pakistan	*Psidium guajava*	MF783082	–	–	MH460874	MH477870	Ul Haq et al. (2021)
N. rhapidis	GUCC 21501	T	China	*Rhododendron simsii*	MW931620	–	–	MW980442	MW980441	Yang et al. (2021)
N. rhizophorae	MFLUCC 17-1551	T	Thailand	*Rhizophora mucronata*	MK764277	–	–	MK764321	MK764343	Norphanphoun et al. (2019)
	MFLUCC 17-1550		Thailand	*Rhizophora mucronata*	MK764278	–	–	MK764322	MK764344	Norphanphoun et al. (2019)
N. rhododendri	GUCC 21504	T	China	*Rhododendron simsii*	MW979577	–	–	MW980444	MW980443	Yang et al. (2021)
N. rosae	CBS 101057	T	New Zealand	*Rosa* sp.	KM199359	KM116245	MH554850	KM199524	KM199430	Maharachchikumbura et al. (2014)
	CBS 124745		USA	*Paeonia suffruticosa*	KM199360	–	–	KM199524	KM199430	Maharachchikumbura et al. (2014)
	CRM-FRC		Mexico	*Fragaria* × *ananassa*	MN385718	–	–	MN268532	MN268529	Rebollar-Alviter et al. (2020)
	AC50		Italy	*Persea americana*	ON117810	–	–	ON107276	ON209165	Alberto et al. (2022)
N. rosicola	CFCC 51992	T	China	*Rosa chinensis*	KY885239	–	–	KY885243	KY885245	Jiang et al. (2018)
	CFCC 51993		China	*Rosa chinensis*	KY885240	–	–	KY885244	KY885246	Jiang et al. (2018)
N. samaragenensis	MFLUCC 12-0233	T	Thailand	*Syzygium samarangense*	KM199365	–	–	KM199556	KM199447	Norphanphoun et al. (2019)
N. saprophytica	MFLUCC 12-0282	T	China	*Magnolia* sp.	KY606286	–	–	JX399048	JX399017	Maharachchikumbura et al. (2014)
N. scalabiensis	CAA1029	T	Portugal	*Vaccinium corymbosum*	MW969748			MW959100	MW934611	Santos et al. (2022)
N. sichuanensis	CFCC 54338 = SM15-1	T	China	*Castanea mollissima*	MW166231	–	–	MW199750	MW218524	Jiang et al. (2021)
	SM15-1C		China	*Castanea mollissima*	MW166232	–	–	MW199751	MW218525	Jiang et al. (2021)
N. siciliana	AC46		Italy	*Persea americana*	ON117813	–	–	ON107273	ON209162	Alberto et al. (2022)
	AC48		Italy	*Persea americana*	ON117812	–	–	ON107274	ON209163	Alberto et al. (2022)
	AC49		Italy	*Persea americana*	ON117811	–	–	ON107275	ON209164	Alberto et al. (2022)
N. sonneratae	MFLUCC 17-1744	T	Thailand	*Sonneronata alba*	MK764279	–	–	MK764323	MK764345	Norphanphoun et al. (2019)
	MFLUCC 17-1745		Thailand	*Sonneronata alba*	MK764280	–	–	MK764324	MK764346	Norphanphoun et al. (2019)
Neopestalotiopsis sp.1	VRes4		Colombia	Scab disease of Guava	KR493566	–	–	KR493638	–	Kumar et al. (2019)
Neopestalotiopsis sp.2	BPca2		Colombia	Scab disease of Guava	KR493559	–	–	KR493627	KR493666	Kumar et al. (2019)
Neopestalotiopsis sp.3	VrleP		Colombia	Scab disease of Guava	KR493520	–	–	KR493660	KR493719	Kumar et al. (2019)
Neopestalotiopsis sp.4	VTman4		Colombia	Scab disease of Guava	KR493554	–	–	KR493611	KR493724	Kumar et al. (2019)
Neopestalotiopsis sp.5	BVayr1		Colombia	Scab disease of Guava	KR493545	–	–	KR493629	KR493739	Kumar et al. (2019)
Neopestalotiopsis sp.6	BRIP 63740a		Australia	Dry flower	KX186617	–	–	KX186628	KX186656	Kumar et al. (2019)
Neopestalotiopsis sp.7	BRIP 63745a		Australia	Dry flower	KX186614	–	–	KX186633	KX186660	Kumar et al. (2019)
Neopestalotiopsis sp.8	CBS 119.75		India	*Achras sapota*	KM199356	–	–	KM199531	KM199439	Kumar et al. (2019)
Neopestalotiopsis sp.9	CMM1363		Brazil	*Opuntia stricta*	KY549599	–	–	KY549596	KY549634	Kumar et al. (2019)
Neopestalotiopsis sp.10	LC6489		China	*Camellia* sp.	KX895020	–	–	KX895239	KX895353	Kumar et al. (2019)
Neopestalotiopsis sp.11	MFLUCC 12-0614		Midi-pyrénées	Unidentified host	KX816919	–	–	KX816889	KX816947	Kumar et al. (2019)
Neopestalotiopsis sp.12	MMf0011		Japan	*Lilium speciosum*	LC184188	–	–	LC184190	LC184189	Kumar et al. (2019)
Neopestalotiopsis sp.13	SC2A3		China	Tea plant	KU252210	–	–	KU252390	KU252477	Kumar et al. (2019)
Neopestalotiopsis sp.14	CBS 164.42		France	Sand dune	KM199367	–	–	KM199520	KM199434	Kumar et al. (2019)
Neopestalotiopsis sp.15	CBS 266.80		India	*Vitis vinifera*	KM199352	–	–	KM199532	–	Kumar et al. (2019)
Neopestalotiopsis sp.16	CBS 360.61		Guinea	*Cinchona* sp.	KM199346	–	–	KM199522	KM199440	Kumar et al. (2019)
Neopestalotiopsis sp.17	CBS 361.61		Netherlands	*Cissus* sp.	KM199355	–	–	KM199549	KM199460	Kumar et al. (2019)
N. steyaertii	IMI 192475		Australia	*Eucalyptus viminalis*	KF582796	–	–	KF582792	KF582794	Maharachchikumbura et al. (2014)

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					ITS	LSU	*RPB2*	*TEF*	*TUB*	
N. surinamensis	CBS 450.74	T	Suriname	Soil	KM199351	KM116258	MH554962	KM199518	KM199465	Maharachchikumbura et al. (2014)
N. thailandica	MFLUCC 17-1730	T	Thailand	*Rhizophora mucronata*	MK764281	–	–	MK764325	MK764347	Norphanphoun et al. (2019)
N. umbrinospora	MFLUCC 12-0285	T	China	Dead leaves	JX398984	–	–	JX399050	JX399019	Norphanphoun et al. (2019)
N. vaccinii	CAA1059	T	Portugal	*Vaccinium corymbosum*	MW969747	–	–	MW959099	MW934610	Santos et al. (2022)
N. vacciniicola	CAA1055	T	Portugal	*Vaccinium corymbosum*	MW969751	–	–	MW959103	MW934614	Santos et al. (2022)
N. versicolor	CBS 303.49		China	*Myrica rubra*	MH856535	–	–	–	–	Vu et al. (2019)
N. vheenae	BRIP 72293a	T	Australia	*Macadamia integrifolia*	MZ303792	–	–	MZ344177	MZ312685	Prasannath et al. (2021)
N. vitis	MFLUCC 15-1265		China	*Vitis vinifera*	KU140694	–	–	KU140676	KU140685	Jayawardena et al. (2016)
N. zakeelii	BRIP 72282a	T	Australia	*Macadamia integrifolia*	MZ303789	–	–	MZ344174	MZ312682	Prasannath et al. (2021)
N. zimbabwana	CBS H-21769		Zimbabwe	*Leucospermum cuncifome*	–	JX556249	MH554855	KM199545	KM199456	Maharachchikumbura et al. (2014)
Nonappendiculata quercina	CBS 116061	T	Italy	*Quercus suber*	MH553982	MH554199	MH554882	–	–	Liu et al. (2019)
	CBS 270.82		Italy	*Quercus pubescens*	MH554025	MH554246	MH554937	–	–	Liu et al. (2019)
Parabartalinia lateralis	CBS 399.71	T	South Africa	*Acacia karroo*	MH554043	MH554256	MH554954	–	–	Liu et al. (2019)
Pestalotiopsis abietis	CFCC 53011	T	China	*Abies fargesii*	MK397013	–	–	MK622277	MK622280	Gu et al. (2021)
	CFCC 53012		China	*Abies fargesii*	MK397014	–	–	MK622278	MK622281	Gu et al. (2021)
	CFCC 53013		China	*Abies fargesii*	MK397015	–	–	MK622279	MK622282	Gu et al. (2021)
Pes. adusta	ICMP 6088	T	Fiji	Refrigerator door PVC gasket	JX399006	–	–	JX399070	JX399037	Norphanphoun et al. (2019)
	CBS 263.33		Netherlands	*Rhododendron ponticum*	KM199316	–	–	KM199489	KM199414	Norphanphoun et al. (2019)
Pes. aggestorum	LC6301	T	China	*Camellia sinensis*	KX895015	–	–	KX895234	KX895348	Liu et al. (2017)
Pes. anacardiacearum	IFRDCC 2397	T	China	*Mangifera indica*	KC247154	–	–	KC247156	KC247155	Maharachchikumbura et al. (2013b)
Pes. arceuthobii	CBS 433.65		USA	*Arceuthobium campylopodum*	MH554046	–	–	MH554481	MH554722	Maharachchikumbura et al. (2014)
	CBS 434.65	T	USA	*Arceuthobium campylopodum*	KM199341	–	–	KM199516	KM199427	Maharachchikumbura et al. (2014)
Pes. arengae	CBS 331.92	T	Singapore	*Arenga undulatifolia*	KM199340	–	–	KM199515	KM199426	Maharachchikumbura et al. (2014)
Pes. australasiae	CBS 114126	T	New Zealand	*Knightia* sp.	KM199297	KM116218	MH554867	KM199499	KM199409	Maharachchikumbura et al. (2014)
	CBS 114141		Australia	*Protea* cv. 'Pink Ice'	KM199298	–	–	KM199501	KM199410	Maharachchikumbura et al. (2014)
Pes. australis	CBS 114193	T	Australia	*Grevillea* sp.	KM199332	KM116197	MH554875	KM199475	KM199383	Maharachchikumbura et al. (2014)
	CBS 119350		South Africa	*Brabejum stellatifolium*	KM199333	–	–	KM199476	KM199384	Maharachchikumbura et al. (2014)
	MEAN 1096 = CPC 36750 = CBS 146843		Portugal	*Pinus pinea*	MT374679	–	–	MT374692	MT374704	Silva et al. (2020)
	MEAN 1109		Portugal	*Pinus pinea*	MT374683	–	–	–	MT374708	Silva et al. (2020)
	MEAN 1110		Portugal	*Pinus pinea*	MT374684	–	–	MT374696	MT374709	Silva et al. (2020)
	MEAN 1111		Portugal	*Pinus pinea*	MT374685	–	–	MT374697	MT374710	Silva et al. (2020)
	MEAN 1112		Portugal	*Pinus pinea*	MT374686	–	–	MT374698	MT374711	Silva et al. (2020)
Pes. biciliata	CBS 124463	T	Slovakia	*Platanus* × *hispanica*	KM199308	–	–	KM199505	KM199399	Maharachchikumbura et al. (2014)
	CBS 236.38		Italy	*Paeonia* sp.	KM199309	–	–	KM199506	KM199401	Maharachchikumbura et al. (2014)
	MEAN 1168		Portugal	*Pinus pinea*	MT374690	–	–	MT374702	MT374715	Maharachchikumbura et al. (2014)
Pes. brachiata	LC2988	T	China	*Camellia* sp.	KX894933	–	–	KX895150	KX895265	Maharachchikumbura et al. (2014)
Pes. brassicae	CBS 170.26	T	New Zealand	*Brassica napus*	KM199379	–	–	KM199558	–	Maharachchikumbura et al. (2014)
Pes. camelliae	CBS 443.62		Turkey	*Camellia sinensis*	KM199336	–	–	KM199512	KM199424	Zhang et al. (2012b)
	MFLUCC 12-0277	T	China	*Camellia japonica*	JX399010	–	–	JX399074	JX399041	Zhang et al. (2012b)
Pes. camelliae-oleiferae	CSUFTCC08	T	China	*Camellia oleifera*	OK493593			OK507963	OK562368	Li et al. (2021)
	CSUFTCC09		China	*Camellia oleifera*	OK493594			OK507964	OK562369	Li et al. (2021)
	CSUFTCC10		China	*Camellia oleifera*	OK493595			OK507965	OK562370	Li et al. (2021)
Pes. chamaeropis	CBS 113607		–	–	KM199325	–	–	KM199472	KM199390	Maharachchikumbura et al. (2014)
	CBS 186.71	T	Italy	*Chamaerops humilis*	KM199326	–	–	KM199473	KM199391	Maharachchikumbura et al. (2014)
Pes. chiaroscuro	BRIP 72970	T	Australia	*Sporobolus natalensis*	OK422510	–	–	–	–	Crous et al. (2022)
Pes. clavata	MFLUCC 12-0268	T	China	*Buxus* sp.	JX398990	–	–	JX399056	JX399025	Maharachchikumbura et al. (2012)
Pes. colombiensis	CBS 118553	T	Colombia	*Eucalyptus eurograndis*	KM199307	–	–	KM199488	KM199421	Maharachchikumbura et al. (2014)
Pes. digitalis	ICMP 5434	T	New Zealand	*Digitalis purpurea*	KP781879	–	–	–	KP781883	Liu et al. (2015)
Pes. diploclisiae	CBS 115587	T	Hong Kong, China	*Diploclisia glaucescens*	KM199320	–	–	KM199486	KM199419	Maharachchikumbura et al. (2014)

Table 3 (cont.)

Species	Strain number[1]	Status[2]	Country	Substrate	GenBank accession no.					References
					ITS	LSU	*RPB2*	*TEF*	*TUB*	
Pes. disseminata	CBS 118552		New Zealand	*Eucalyptus botryoides*	MH553986	–	–	MH554410	MH554652	Maharachchikumbura et al. (2014)
	CBS 143904		New Zealand	*Persea americana*	MH554152	–	–	MH554587	MH554825	Maharachchikumbura et al. (2014)
	MEAN 1165		Portugal	*Pinus pinea*, blighted shoot	MT374687	–	–	MT374699	MT374712	Silva et al. (2020)
	MEAN 1166		Portugal	*Pinus pinea*, blighted shoot	MT374688	–	–	MT374700	MT374713	Silva et al. (2020)
Pes. distincta	LC3232	T	China	*Camellia sinensis*	KX894961	–	–	KX895178	KX895293	Silva et al. (2020)
	LC8184		China	*Camellia sinensis*	KY464138	–	–	KY464148	KY464158	Silva et al. (2020)
Pes. diversiseta	MFLUCC 12-0287	T	China	*Rhododendron* sp.	JX399009	–	–	JX399073	JX399040	Maharachchikumbura et al. (2012)
Pes. doitungensis	MFLUCC 14-0115	T	Thailand	*Dendrobium* sp.	MK993574	–	–	MK975832	MK975837	Ma et al. (2019)
Pes. dracaenicola	MFLUCC 18-0913	T	Thailand	*Dracaena* sp.	MN962731	–	–	MN962732	MN962733	Chaiwan et al. (2020)
Pes. dracontomelonis	MFLUCC 10-0149	T	Thailand	*Dracontomelon dao*	KP781877	–	–	KP781880	–	Liu et al. (2015)
Pes. ericacearum	IFRDCC 2439	T	China	*Rhododendron delavayi*	KC537807	–	–	KC537814	KC537821	Zhang et al. (2013b)
Pes. etonensis	BRIP 66615	T	Australia	*Sporobolus jacquemontii*	MK966339	–	–	MK977635	MK977634	Crous et al. (2020)
Pes. formosana	NTUCC 17-009	T	Taiwan,China	On dead grass	MH809381	–	–	MH809389	MH809385	Ariyawansa & Hyde (2018)
Pes. furcata	MFLUCC 12-0054	T	Thailand	*Camellia sinensis*	JQ683724	–	–	JQ683740	JQ683708	Maharachchikumbura et al. (2013a)
Pes. gaultheriae	IFRD 411-014	T	China	*Gaultheria forrestii*	KC537805	–	–	KC537812	KC537819	Zhang et al. (2013)
Pes. gibbosa	NOF 3175	T	Canada	*Gaultheria shallon*	LC311589	–	–	LC311591	LC311590	Watanabe et al. (2018)
Pes. grevilleae	CBS 114127	T	Australia	*Grevillea* sp.	KM199300	KM116212	MH554868	KM199504	KM199407	Maharachchikumbura et al. (2014)
Pes. hawaiiensis	CBS 114491	T	USA	*Leucospermum* cv. 'Coral'	KM199339	–	–	KM199514	KM199428	Maharachchikumbura et al. (2014)
Pes. hispanica	CBS 115.391	T	Spain	*Protea* cv. 'Susara'	MH553981	–	–	MH554399	MH554640	Liu et al. (2019)
Pes. hollandica	CBS 265.33	T	Netherlands	*Sciadopitys verticillata*	KM199328	KM116228	MH554936	KM199481	KM199388	Maharachchikumbura et al. (2014)
	MEAN 1091 = CPC 36745 = CBS 146839		Portugal	*Pinus pinea*, blighted shoot	MT374678	–	–	MT374691	MT374703	Maharachchikumbura et al. (2014)
Pes. humicola	CBS 115450	T	Hong Kong, China	*Ilex cinerea*	KM199319	KM116208	MH554881	KM199487	KM199418	Maharachchikumbura et al. (2014)
	CBS 336.97		Papua New Guinea	Soil	KM199317	–	–	KM199484	KM199420	Maharachchikumbura et al. (2014)
Pes. hunanensis	CSUFTCC15	T	China	*Camellia oleifera*	OK493599	–	–	OK507969	OK562374	Li et al. (2021)
	CSUFTCC18		China	*Camellia oleifera*	OK493600	–	–	OK507970	OK562375	Li et al. (2021)
	CSUFTCC19		China	*Camellia oleifera*	OK493601	–	–	OK507971	OK562376	Li et al. (2021)
Pes. hydei	MFLUCC 20-0135	T	Thailand	*Litsea petiolata*	NR_172003	–	–	MW251113	MW251112	Huanluek et al. (2021)
Pes. inflexa	MFLUCC 12-0270	T	China	Unidentified tree	JX399008	–	–	JX399072	JX399039	Maharachchikumbura et al. (2012)
Pes. intermedia	MFLUCC 12-0259	T	China	Unidentified tree	JX398993	–	–	JX399059	JX399028	Maharachchikumbura et al. (2012)
Pes. italiana	MFLUCC 12-0657	T	Italy	*Cupressus glabra*	KP781878	–	–	KP781881	KP781882	Liu et al. (2015)
Pes. jesteri	CBS 109350	T	Papua New Guinea	*Fragraea bodenii*	KM199380	–	–	KM199554	KM199468	Strobel et al. (2000)
Pes. jiangxiensis	LC4399	T	China	*Camellia* sp.	KX895009	–	–	KX895227	KX895341	Liu et al. (2017)
Pes. jinchanghens	LC6636	T	China	*Camellia sinensis*	KX895028	–	–	KX895247	KX895361	Liu et al. (2017)
Pes. kandelicola	NCYUCC 19-0355		Taiwan,China	*Kandelia candel*	MT560722	–	–	MT563101	MT563099	Hyde et al. (2020)
	NCYUCC 19-0354		Taiwan,China	*Kandelia candel*	MT560723	–	–	MT563102	MT563100	Hyde et al. (2020)
Pes. kenyana	CBS 442.67	T	Kenya	*Coffea* sp.	KM199302	KM116234	MH554958	KM199502	KM199395	Maharachchikumbura et al. (2014)
Pes. knightiae	CBS 114138	T	New Zealand	*Knightia* sp.	KM199310	KM116227	MH554870	KM199497	KM199408	Maharachchikumbura et al. (2014)
Pes. leucadendri	CBS 121417	T	South Africa	*Leucadendron* sp.	MH553987	–	–	MH554412	MH554654	Liu et al. (2019)
Pes. licualicola	HGUP 4057	T	China	*Licuala grandis*	KC492509	–	–	KC481684	KC481683	Geng et al. (2013)
Pes. linearis	MFLUCC 12-0271	T	China	*Trachelospermum* sp.	JX398992	–	–	JX399058	JX399027	Maharachchikumbura et al. (2012)
Pes. longiappendiculata	LC3013	T	China	*Camellia sinensis*	KX894939	–	–	KX895156	KX895271	Liu et al. (2017)
Pes. lushanensis	LC4344	T	China	*Camellia* sp.	KX895005	–	–	KX895223	KX895337	Liu et al. (2017)
Pes. macadamiae	BRIP 63738b	T	Australia	*Macadamia integrifolia*	KX186588	–	–	KX186621	KX186680	Akinsanmi et al. (2017)
Pes. malayana	CBS 102220	T	Malaysia	*Macaranga triloba*	KM199306	–	–	KM199482	KM199411	Maharachchikumbura et al. (2014)
Pes. monochaeta	CBS 144.97	T	Netherlands	*Quercus robur*	KM199327	–	–	KM199479	KM199386	Maharachchikumbura et al. (2014)
Pes. nanjingensis	CSUFTCC16	T	China	*Camellia oleifera*	OK493602	–	–	OK507972	OK562377	Li et al. (2021)
	CSUFTCC20		China	*Camellia oleifera*	OK493603	–	–	OK507973	OK562378	Li et al. (2021)
	CSUFTCC04		China	*Camellia oleifera*	OK493604	–	–	OK507974	OK562379	Li et al. (2021)
Pes. nanningensis	CSUFTCC10	T	China	*Camellia oleifera*	OK562371	–	–	OK507966	OK562371	Li et al. (2021)
	CSUFTCC11		China	*Camellia oleifera*	OK562372	–	–	OK507967	OK562372	Li et al. (2021)
	CSUFTCC12		China	*Camellia oleifera*	OK562373	–	–	OK507968	OK562373	Li et al. (2021)

Table 3 (cont.)

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					ITS	LSU	*RPB2*	*TEF*	*TUB*	
Pes. neolitseae	NTUCC 17-011	T	Taiwan,China	*Neolitsea villosa*	MH809383	–	–	MH809391	MH809387	Ariyawansa & Hyde (2018)
Pes. novae-hollandiae	CBS 130973	T	Australia	*Banksia grandis*	KM199337	–	–	KM199511	KM199425	Maharachchikumbura et al. (2014)
Pes. oryzae	CBS 353.69	T	Denmark	*Oryza sativa*	KM199299	KM116221	MH554947	KM199496	KM199398	Maharachchikumbura et al. (2014)
Pes. pallidotheae	MAFF 240993	T	Japan	*Pieris japonica*	NR111022	–	–	LC311585	LC311584	Watanabe et al. (2010)
Pes. pandanicola	MFLUCC 16-0255	T	Thailand	*Pandanus* sp.	MH388361	–	–	MH388396	MH412723	Li et al. (2021)
Pes. papuana	CBS 331.96	T	Papua New Guinea	Soil	KM199321	–	–	KM199491	KM199413	Maharachchikumbura et al. (2014)
Pes. parva	CBS 114972		Hong Kong, China	Leaf	MH553980	–	–	MH554397	MH704625	Maharachchikumbura et al. (2014)
	CBS 278.35	T	–	*Leucothoe fontanesiana*	KM199313	KM116205	MH554939	KM199509	KM199405	Maharachchikumbura et al. (2014)
Pes. photinicola	GZCC 16-0028	T	China	*Photinia serrulata*	KY092404	–	–	KY047662	KY047663	Chen et al. (2017)
Pes. pini	MEAN 1092 = CPC 36746 = CBS 146840		Portugal	*Pinus pinea*	MT374680	–	–	MT374693	MT374705	Silva et al. (2020)
	MEAN 1094 = CPC 36748 = CBS 146841	T	Portugal	*Pinus pinea*	MT374681	–	–	MT374694	MT374706	Silva et al. (2020)
	MEAN 1095 = CPC 36749 = CBS 146842		Portugal	*Pinus pinea*	MT374682	–	–	MT374695	MT374707	Silva et al. (2020)
	MEAN 1167		Portugal	*Pinus pinaster*	MT374689	–	–	MT374701	MT374714	Silva et al. (2020)
Pes. pinicola	KUMCC 19-0183	T	China	*Pinus armandii*	MN412636	–	–	MN417509	MN417507	Tibpromma et al. (2019)
Pes. portugallica	CBS 684.85		New Zealand	*Camellia japonica*	MH554065	–	–	MH554501	MH554741	Maharachchikumbura et al. (2014)
	CBS 393.48	T	Portugal	–	KM199335	KM116233	MH554951	KM199510	KM199422	Maharachchikumbura et al. (2014)
Pes. rhizophorae	MFLUCC 17-0416	T	Thailand	*Rhizophora apiculata*	MK764283	–	–	MK764327	MK764349	Norphanphoun et al. (2019)
Pes. rhododendri	IFRDCC 2399	T	China	*Rhododendron sinogrande*	KC537804	–	–	KC537811	KC537818	Norphanphoun et al. (2019)
	CBS 144024		Zimbabwe	*Pinus* sp.	MH554109	–	–	MH554543	MH554782	Norphanphoun et al. (2019)
Pes. rhodomyrtus	HGUP 4230	T	China	*Rhodomyrtus tomentosa*	KF412648	–	–	KF412645	KF412642	Norphanphoun et al. (2019)
	LC3413		China	*Camellia sinensis*	KX894981	–	–	KX895198	KX895313	Norphanphoun et al. (2019)
Pes. rosea	MFLUCC 12-0258	T	China	*Pinus* sp.	JX399005	–	–	JX399069	JX399036	Maharachchikumbura et al. (2012)
Pes. scoparia	CBS 176.25	T	–	*Chamaecyparis* sp.	KM199330	–	–	KM199478	KM199393	Maharachchikumbura et al. (2014)
Pes. sequoiae	MFLUCC 13-0399	T	Italy	*Sequoia sempervirens*	KX572339	–	–	–	–	Maharachchikumbura et al. (2014)
Pes. shorea	MFLUCC 12-0314	T	Thailand	*Shorea obtusa*	KJ503811	–	–	KJ503817	KJ503814	Song et al. (2013)
Pestalotiopsis 7 FL_2019	CBS 110326		USA	*Pinus* sp.	MH553957	–	–	MH554375	MH554616	Silva et al. (2020)
Pestalotiopsis 7 FL_2019	CBS 127.80		Chile	*Pinus radiata*	MH553995	–	–	MH554422	MH554664	Silva et al. (2020)
Pes. spathulata	CBS 356.86	T	Chile	*Guevina avellana*	KM199338	–	–	KM199513	KM199423	Maharachchikumbura et al. (2014)
Pes. spathuliappendiculata	CBS 144035	T	Australia	*Phoenix canariensis*	MH554172	MH554366	–	MH554607	MH554845	Liu et al. (2019)
Pes. telopeae	CBS 114137		Australia	*Protea* cv. 'Pink Ice'	KM199301	–	–	KM199559	KM199469	Maharachchikumbura et al. (2014)
	CBS 114161	T	Australia	*Telopea* sp.	KM199296	–	–	KM199500	KM199403	Maharachchikumbura et al. (2014)
Pes. terricola	CBS 141.69	T	Pacific Islands	Soil	MH554004	–	–	MH554438	MH554680	Maharachchikumbura et al. (2014)
Pes. thailandica	MFLUCC 17-1616	T	Thailand	*Rhizophora apiculata*	MK764285	–	–	MK764329	MK764351	Maharachchikumbura et al. (2014)
Pes. trachycarpicola	IFRDCC 2440	T	China	*Trachycarpus fortunei*	JQ845947	–	–	JQ845946	JQ845945	Zhang et al. (2012a)
Pes. unicolor	MFLUCC 12-0275		China	Unidentified tree	JX398998	–	–	JX399063	JX399029	Maharachchikumbura et al. (2012)
	MFLUCC 12-0276	T	China	*Rhododendron* sp.	JX398999	–	–	–	JX399030	Maharachchikumbura et al. (2012)
Pes. verruculosa	MFLUCC 12-0274	T	China	*Rhododendron* sp.	JX398996	–	–	JX399061	–	Maharachchikumbura et al. (2012)
Pes. cf. *verruculosa*	CBS 365.54		Netherlands	*Chamaecyparis lawsoniana*	MH554037	–	–	MH554472	MH554713	Maharachchikumbura et al. (2012)
Pes. yanglingensis	LC3412		China	*Camellia sinensis*	KX894980	–	–	KX895197	KX895312	Liu et al. (2017)
	LC4553	T	China	*Camellia sinensis*	KX895012	–	–	KX895231	KX895345	Liu et al. (2017)
Pes. yunnanensis	HMAS 96359	T	China	*Podocarpus macrophyllus*	AY373375	–	–	–	–	Wei et al. (2013)
Phlogicylindrium eucalypti	CBS 120080	T	Australia	*Eucalyptus globulus*	NR_132813	DQ923534	MH554893	–	–	Liu et al. (2019)
Phlogicylindrium eucalyptorum	CBS 120221	T	Australia	*Eucalyptus globus*	EU040223	MH554204	MH554894	–	–	Liu et al. (2019)
Phlogicylindrium uniforme	CBS 131312	T	Australia	*Eucalyptus globus*	JQ044426	JQ044445	MH554910	–	–	Crous et al. (2011a)
Pseudopestalotiopsis cocos	CBS 272.29	T	Indonesia	*Cocos nucifera*	KM199378	KM116276	MH554938	–	–	Maharachchikumbura et al. (2014)
Pse. elaeidis	CBS 413.62	IT	Nigeria	*Elaeis guineensis*	MH554044	MH554257	MH554955	–	–	Liu et al. (2019)
Pse. indica	CBS 459.78	T	India	*Rosa sinensis*	KM199381	MH554263	MH554963	–	–	Maharachchikumbura et al. (2014)
Pseudosarcostroma osyridicola	CBS 103.76	T	France	*Osyris alba*	MH553954	MH554177	MH554851	–	–	Liu et al. (2019)

Table 3 (cont.)

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					ITS	LSU	*RPB2*	*TEF*	*TUB*	
Robillarda africana	CBS 122.75	T	South Africa	–	KR873253	KR873281	MH554896	–	–	Crous et al. (2015a)
Rob. australiana	CBS 143882	T	Australia	–	MH554091	MH554301	MH555005	–	–	Liu et al. (2019)
Rob. roystoneae	CBS 115445	T	Hong Kong, China	*Roystonea regia*	KR873254	KR873282	MH554880	–	–	Crous et al. (2015a)
Rob. sessilis	CBS 114312	ET	Germany	Dust	KR873256	KR873284	MH554877	–	–	Liu et al. (2019)
Rob. terrae	CBS 587.71	T	India	Soil	KJ710484	KJ710459	MH554971	–	–	Crous et al. (2015a)
Sarcostroma australiense	CBS 144160	T	Australia	*Daviesia latifolia*	MH554138	MH554340	MH555044	–	–	Liu et al. (2019)
Sar. diversiseptatum	CBS 189.81	T	Australia	*Correa reflexa*	MH554016	MH554236	MH554929	–	–	Liu et al. (2019)
Sar. grevilleae	CBS 143418		Australia	*Grevillea* sp.	MH554006	MH554227	MH554922	–	–	Liu et al. (2019)
Sar. leucospermi	CBS 111290	T	South Africa	*Leucospermum* cv. 'High Gold'	MH554081	MH554292	MH554993	–	–	Liu et al. (2019)
	CBS 111309		South Africa	*Leucospermum* cv. 'High Gold'	MH554079	MH554290	MH554991	–	–	Liu et al. (2019)
Sar. longiappendiculatum	CBS 111308		South Africa	*Leucospermum* cv. 'High Gold'	MH554080	MH554291	MH554992	–	–	Liu et al. (2019)
Sar. paragrevilleae	CBS 114142	T	Australia	*Grevillea* sp.	MH553974	MH554193	MH554871	–	–	Liu et al. (2019)
Sar. proteae	CBS 113610	T	Australia	*Protea magnifica*	MH553968	MH554187	MH554862	–	–	Liu et al. (2019)
	CBS 114189		Australia	*Protea magnifica*	MH553976	MH554195	MH554874	–	–	Liu et al. (2019)
Sar. restionis	CBS 118153		South Africa	*Ischyrolepis* cf. *sieberi*	DQ278923	DQ278925	MH554890	–	–	Liu et al. (2019)
	CBS 282.65		UK	*Pteridium aquilinum*	AB594804	AB593736	MH554940	–	–	Liu et al. (2019)
	CBS 118154	T	South Africa	*Restio filiformis*	DQ278922	DQ278924	MH554891	–	–	Liu et al. (2019)
	CBS 111311		New Zealand	–	MH553958	MH554180	MH554854	–	–	Liu et al. (2019)
	CBS 114130		South Africa	*Leucospermum* sp.	MH553973	MH554192	MH554869	–	–	Liu et al. (2019)
Seimatosporium botan	HMUC-sei-302PD		Chile	*Vitis vinifera*	JN088482	–	–	–	–	Hatakeyama & Harada (2004)
	NBRC 104200 = H4619	T	Japan	*Paeonia suffruticosa*	AB594799	AB593731	–	–	LC047770	Hatakeyama & Harada (2004)
Seim. discosioides	NBRC 104201		Canada	*Punica granatum*	AB594800	AB593732	–	–		Tanaka et al. (2011)
Seim. elegans	NBRC 32674		Japan	*Melaleuca ericifolia*	AB594801	AB593733	–	–	–	Wijayawardene et al. (2016a)
Seim. eucalypti	CPC 156		South Africa	*Eucalyptus smithii*	JN871200	JN871209	–	–	–	Wijayawardene et al. (2016a)
Seim. falcatum	CPC 13578		Australia	*Eucalyptus* sp.	JN871204	JN871213	–	–	–	Wijayawardene et al. (2016a)
Seim. ficeae	MFLUCC 15-0519	T	Italy	*Rubus* sp.	KR092800	KR920686	–	–	–	Wijayawardene et al. (2016a)
Seim. foliicola	NBRC 32676		Japan	*Juniperus phoenicea*	AB594802	AB593734	–	–	–	Wijayawardene et al. (2016a)
Seim. germanicum	CBS 437.87	T	Germany	–	MH554047	MH554259	MH554957	MH554482	MH554723	Liu et al. (2019)
Seim. glandigenum	NBRC 32677		Japan	*Fagus sylvatica*	AB594803	AB593735	–	–	–	Liu et al. (2019)
Seim. grevilleae	ICMP 10981		South Africa	*Protea* sp.	AF405304	AF382372	–	–	–	Wijayawardene et al. (2016a)
Seim. hakeae	NBRC 32678		Japan	*Pteridium aquilinum*	AB594804	AB593736	–	–	–	Wijayawardene et al. (2016a)
Seim. hypericinum	NBRC 32647		Japan	*Hypericum* sp.	AB594805	AB593737	–	–	–	Wijayawardene et al. (2016a)
Seim. luteosporum	Napa754		USA	*Prunus persica*	KY706283	KY706308	–	KY706333	KY706258	Liu et al. (2019)
	CBS 142599	T	USA	*Vitis vinifera*	KY706284	KY706309	–	KY706334	KY706259	Liu et al. (2019)
Seim. mariae	NBRC 32681		Japan	*Correa reflexa*	AB594807	AB593740	–	–	–	Wijayawardene et al. (2016a)
Seim. marivanicum	IRAN 2310CT = CBS 143781	T	Iran	*Vitis vinifera*	MW361952	MW361960	–	MW375358	MW375352	Moghadam et al. (2022)
	IRAN 2300C = CBS 143780		Iran	*Vitis vinifera*	MW361951	MW361959	–	MW375357	MW375351	Moghadam et al. (2022)
Seim. obtusum	CPC 12935	T	Australia	*Corymbia henryi*	JN871206	JN871215	–	–	–	Barber et al. (2011)
Seim. parasiticum	NBRC 32682		Japan	*Physocarpus amurensis*	AB594808	AB593741	–	–	–	Wijayawardene et al. (2016a)
Seim. pezizoides	71TB		Unknown	Unknown	KF573991	–	–	–	–	Lawrence et al. (2018)
Seim. physocarpi	CBS 139968 = MFLUCC 14-0625	T	Russia	*Physocarpus opulifolius*	KT198722	KT198723	MH554917	MH554434	MH554676	Liu et al. (2019)
	CBS 789.68 = NBRC 32682		Netherlands	*Physocarpus amurensis*	MH554066	MH554278	MH554979	MH554502	MH554742	Liu et al. (2019)
Seim. pistaciae	CBS 138865 = CPC 24455	T	Iran	*Pistacia vera*	KP004463	KP004491	MH554915	MH554432	MH554674	Crous et al. (2014b)
	CPC 24457		Iran	*Pistacia vera*	MH554126	MH554331	MH555035	MH554561	MH554799	Crous et al. (2014b)
Seim. pseudorosae	MFLUCC 14-0468	T	Italy	*Rosa villosa*	–	KU359035	–	–	–	Li et al. (2016)
Seim. quercinum	MFLUCC 14-1198	T	Germany	*Quercus robur*	KU974965	KU974964	–	–	–	Goonasekara et al. (2016)
Seim. restionis	CBS 118154		South Africa	*Restio filiformis*	DQ278922	DQ278924	–	–	–	Lawrence et al. (2018)
Seim. rhombisporium	MFLUCC 15-0727	T	Italy	*Vaccinium myrtillus*	KR092792	KR092780	–	–	–	Wijayawardene et al. (2016a)
Seim. rosae	CBS 139823 = MFLUCC 14-0621	ET	Russia	*Rosa kalmiussica*	KT198726	KT198727	LT853153	LT853203	LT853253	Liu et al. (2019)

Table 3 (cont.)

Species	Strain number[1]	Status[2]	Country	Substrate	GenBank accession no.					References
					ITS	LSU	*RPB2*	*TEF*	*TUB*	
Seim. soli	CBS 941.69	T	Denmark	Soil	MH554071	MH554282	MH554983	MH554507	–	Liu et al. (2019)
Seim. vitifusiforme	CBS 142600	T	USA	*Vitis vinifera*	KY706296	KY706321	–	KY706346	KY706271	Lawrence et al. (2018)
	Napa751		USA	*Vitis vinifera*	KY706289	KY706314	–	KY706339	KY706264	Lawrence et al. (2018)
Seim. vitis	MFLUCC 14-0051	T	Italy	*Vitis vinifera*	KR920363	KR920362	–	–	–	Senanayake et al. (2015)
Seim. vitis-viniferae	CBS 123004	T	Spain	*Vitis vinifera*	MH553992	MH554211	MH554901	MH554418	MH554660	Liu et al. (2019)
	CBS 116499		Iran	*Vitis vinifera*	MH553984	MH554201	MH554884	MH554402	MH554643	Liu et al. (2019)
Seim. walkeri	CPC 17644		Australia	*Eucalyptus* sp.	JN871207	JN871216	–	–	–	Barber et al. (2011)
Seiridium aquaticum	MFLUCC 17-0474	T	China	Decaying wood	MK828605	–	–	–	–	Luo et al. (2019)
	S-136		China	Decaying wood	MK828606	–	–	–	–	Luo et al. (2019
Seir. camelliae	MFLUCC 12-0647	T	China	*Camellia reticula*	JQ683725	–	–	JQ683741	JQ683709	Maharachchikumbura et al. (2015)
Seir. cancrinum	CBS 226.55 = IMI 052256	T	Kenya	*Cupressus macrocarpa*	LT853089	MH554241	LT853137	LT853186	LT853236	Bonthond et al. (2018)
	CBS 907.85		South Africa	*Cupressus lustinaca*	LT853090	–	LT853138	LT853187	LT853237	Bonthond et al. (2018)
Seir. cardinale	CBS 909.85	T	South Africa	*Cupressus lustinaca*	LT853064	–	LT853113	LT853161	LT853211	Marin-Felix et al. (2019)
	CBS 910.85		South Africa	*Cupressus sempervirens*	LT853065	–	LT853114	LT853162	LT853212	Marin-Felix et al. (2019)
	CBS 523.82		New Zealand	*Cupressocyparis* sp.	LT853062	–	LT853111	LT853159	LT853209	Marin-Felix et al. (2019)
Seir. ceratosporum	PHSI2001Pathcw07		China	*Vitis vinifera*	AY687314	–	–	–	–	Jiang et al. (2019)
Seir. chinense	CFCC 53031	T	China	*Trachycarpus fortunei*	MK353158	–	MK351796	MK351799	MK351802	Jiang et al. (2019)
	CFCC 53032		China	*Trachycarpus fortunei*	MK353159	–	MK351797	MK351800	MK351803	Jiang et al. (2019)
	CFCC 53033		China	*Trachycarpus fortunei*	MK353160	–	MK351798	MK351801	MK351804	Jiang et al. (2019)
Seir. cupressi	CBS 122616		Greece	*Cupressus* sp.	LT853082	–	LT853130	LT853179	LT853229	Jiang et al. (2019)
	CBS 224.55 = IMI 052254	ET	Kenya	*Cupressus macrocarpa*	LT853083	–	LT853131	LT853180	LT853230	Jiang et al. (2019)
Seir. eucalypti	CBS 343.97	ET	Australia	*Eucalyptus delegatensis*	LT853099	MH554251	LT853146	LT853196	LT853246	Jiang et al. (2019)
Seir. kartense	CBS 142629 = CPC 20183	T	Australia	*Eucalyptus cladocalyx*	LT853100	–	LT853147	LT853197	LT853247	Bonthond et al. (2018)
Seir. kenyanium	CBS 228.55 = IMI 052257	T	Kenya	*Juniperus procera*	LT853098	MH554242	LT853145	LT853195	LT853245	Jiang et al. (2019)
Seir. marginatum	CBS 140403	ET	France	*Rosa canina*	KT949914	MH554223	LT853149	LT853199	LT853249	Jaklitsch et al. (2016)
Seir. neocupressi	CBS 142625 = CPC 23786	T	Italy	*Cupressus sempervirens*	LT853079	MH554329	LT853127	LT853176	LT853226	Bonthond et al. (2018)
	CBS 142626		Italy	*Cupressus sempervirens*	LT853080	–	LT853128	LT853177	LT853227	Bonthond et al. (2018)
Seir. papillatum	CBS 340.97 = VPRI 20827	T	Australia	*Eucalyptus delegatensis*	LT853102	DQ414531	LT853150	LT853200	LT853250	Jiang et al. (2019)
Seir. pezizoides	CBS 145115		Italy	*Vitis vinifera*	MK079342	–	MK058475	MK058480	MK058485	Marin-Felix et al. (2019)
Seir. phylicae	CBS 133587 = CPC 19964	T	Tristan da Cunha	*Phylica arborea*	LT853091	–	LT853139	LT853188	–	Crous et al. (2012)
	CPC 19962		Tristan da Cunha	*Phylica arborea*	LT853092	–	LT853140	LT853189	–	Crous et al. (2012)
Seir. podocarpi	CBS 137995	T	South Africa	*Podocarpus latifolus*	LT853101	–	LT853148	LT853198	LT853248	Crous et al. (2014a)
Seir. pseudocardinale	MFLUCC 13-0525		Italy	*Cupressus arizonica*	KU848210	–	–	–	–	Wijayawardene et al. (2016b)
	CBS 122613 = CMW 1648		Portugal	*Cupressus* sp.	LT853096	MH554206	LT853143	LT853193	LT853243	Wijayawardene et al. (2016b)
Seir. rosarum	MFLUCC 17-0654	T	Italy	*Rosa* sp.	MG828961	–	–	–	–	Wanasinghe et al. (2018)
Seir. spyridicola	CBS 142628	T	Australia	*Spyridium globosum*	LT853095	–	LT853142	LT853192	LT853242	Bonthond et al. (2018)
Seir. unicorne	CBS 120306		South Africa	*Cupressus sempervirens*	LT853087	–	LT853135	LT853184	LT853234	Bonthond et al. (2018)
	CBS 538.82 = NBRC 32684	T	New Zealand	*Cryptomeria japonica*	LT853088	MH554269	LT853136	LT853185	LT853235	Bonthond et al. (2018)
Seir. venetum	MFLU 14-0265	T	Italy	*Cornus mas*	KT438836	–	–	–	KT438837	Maharachchikumbura et al. (2015)
Sporocadus biseptatus	CBS 110324 = MYC 754	T	–	–	MH553956	MH554179	MH554853	MH554374	MH554615	Liu et al. (2019)
Spo. cornicola	CBS 143889 = CPC 23235		Germany	*Cornus sanguinea*	MH554121	MH554326	MH555029	MH554555	MH554794	Liu et al. (2019)
	MFLUCC 14-0448	T	Italy	*Cornus sanguinea*	KU974967	–	–	–	–	Liu et al. (2019)
Spo. cornii	MFLUCC 14-0467	T	Italy	*Cornus* sp.	KT162918	KR559739	–	–	–	Moghadam et al. (2022)
Spo. cotini	CBS 139966 = MFLUCC 14-0623	T	Russia	*Cotinus coggygria*	MH554003	MH554222	MH554916	MH554433	MH554675	Liu et al. (2019)
Spo. incanus	CBS 123003	T	Spain	*Prunus dulcis*	MH553991	MH554210	MH554900	MH554417	MH554659	Liu et al. (2019)
Spo. italicus	MFLUCC 14-1196	T	Italy	*Crategus* sp.	MF614829	MF614829	–	–	–	Moghadam et al. (2022)
Spo. kurdistanicus	IRAN 2356C = CBS 143778	T	Iran	*Vitis vinifera*	MW361950	MW361958	–	MW375356	MW375350	Moghadam et al. (2022)
	IRAN 2355C		Iran	*Vitis vinifera*	MW361949	–	–	–	–	Moghadam et al. (2022)
	IRAN 2354C		Iran	*Vitis vinifera*	MW361948	MW361957	–	MW375355	MW375349	Moghadam et al. (2022)
	IRAN 2313C = CBS 143777		Iran	*Vitis vinifera*	MW361947	MW361956	–	MW375354	MW375348	Moghadam et al. (2022)

Table 3 (cont.)

Species	Strain number[1]	Status[2]	Country	Substrate	GenBank accession no.					References
					ITS	LSU	*RPB2*	*TEF*	*TUB*	
Spo. lichenicola	CBS 354.90 = NBRC 32677		Germany	*Fagus sylvatica*	MH554035	MH554252	MH554948	MH554470	MH554711	Liu et al. (2019)
	CPC 24528		Germany	*Juniperus communis*	MH554127	MH554332	MH555036	MH554562	MH554800	Liu et al. (2019)
	NBRC 32625 = IMI 079706	ET	UK	*Rosa canina*	MH883643	MH883646	MH883647	MH883644	MH883645	Liu et al. (2019)
Spo. mali	CBS 446.70	T	Netherlands	*Malus sylvestris*	MH554049	MH554261	MH554960	MH554484	MH554725	Liu et al. (2019)
Spo. microcyclus	CBS 424.95	T	Germany	*Sorbus aria*	MH554045	MH554258	MH554956	MH554480	MH554721	Liu et al. (2019)
	CBS 887.68 = NBRC 32680		Netherlands	*Ribes* sp.	MH554068	MH554280	MH554981	MH554504	MH554744	Liu et al. (2019)
Spo. multiseptatus	CBS 143899 = CPC 26606	T	Serbia	*Viburnum* sp.	MH554141	MH554343	MH555047	MH554576	MH554814	Liu et al. (2019)
Spo. pseudocorni	MFLU 13-0529	T	Italy	*Cornus* sp.	–	KU359033	–	–	–	Moghadam et al. (2022)
Spo. rosarum	CBS 113832 = UPSC 2172		Sweden	*Rosa canina*	MH553970	MH554189	MH554864	MH554388	MH554629	Liu et al. (2019)
	MFLUCC 15-0563	T	Italy	*Rosa canina*	MG828960	MG829071	–	–	–	Liu et al. (2019)
	MFLUCC 14-0466	T	Italy	*Rosa canina*	KT284775	KT281912	–	–	–	Liu et al. (2019)
Spo. rosigena	CBS 116498		Iran	*Vitis vinifera*	MH553983	MH554200	MH554883	MH554401	MH554642	Liu et al. (2019)
	CBS 129166 = MSCL 860		Latvia	*Rhododendron*	MH553996	MH554215	MH554905	MH554423	MH554665	Liu et al. (2019)
	CBS 182.50		Netherlands	*Pyrus communis*	MH554013	MH554233	MH554926	MH554447	MH554689	Liu et al. (2019)
	CBS 250.49		Netherlands	*Rubus fruticosus*	MH554023	MH554245	MH554934	MH554457	MH554699	Liu et al. (2019)
	CBS 466.96		Netherlands	*Rubus* sp.	MH554052	MH554265	MH554965	MH554487	MH554728	Liu et al. (2019)
	MFLU 16-0239	T	Italy	*Rosa canina*	MG828958	MG829069	–	–	–	Liu et al. (2019)
Spo. rotundatus	CBS 616.83	T	Canada	*Arceuthobium pussilum*	MH554060	MH554273	MH554974	MH554496	MH554737	Liu et al. (2019)
Spo. sorbi	CBS 160.25		–	–	MH554008	MH554229	MH554924	MH554442	MH554684	Liu et al. (2019)
	MFLUCC 14-0469	T	Italy	*Sorbus torminalis*	KT284774	KT281911	–	–	–	Liu et al. (2019)
Sporocadus sp.	CBS 506.71		Italy	*Euphorbia* sp.	MH554055	MH554268	MH554968	MH554490	MH554731	Liu et al. (2019)
Spo. trimorphus	CBS 114203 = UPSC 2430	T	Sweden	*Rosa canina*	MH553977	MH554196	MH554876	MH554395	MH554636	Liu et al. (2019)
Strickeria kochii	CBS 140411	ET	Austria	*Robinia pseudoacacia*	NR_154423	KT949918	MH554920	–	–	Liu et al. (2019)
Synnemapestaloides juniperi	CBS 477.77	T	France	*Juniperus phoenicea*	MH554053	MH554266	MH554966	–	–	Liu et al. (2019)
Syn. rhododendri	MAFF 239201	T	Japan	*Rhododendron brachycarpum*	LC047753	LC047744	–	–	–	Liu et al. (2019)
	MAFF 243052		Japan	*Rhododendron brachycarpum*	LC047757	LC047748	–	–	–	Liu et al. (2019)
Truncatella angustata	CBS 398.71		Turkey	Soil	MH554042	MH554255	MH554953	–	–	Liu et al. (2019)
	CBS 231.77		Turkey	*Gossypium* sp.	MH554021	MH554243	MH554932	–	–	Liu et al. (2019)
	CPC 21354		France	*Vitis vinifera* cv. 'Prunelard'	MH554111	MH554317	MH555020	–	–	Liu et al. (2019)
	CBS 642.97		Switzerland	*Heterodera carotae*	MH554061	MH554274	MH554975	–	–	Liu et al. (2019)
	CBS 393.80		Chile	*Gevuina avellana*	MH554041	MH554254	MH554952	–	–	Liu et al. (2019)
	CBS 938.70		Netherlands	*Prunus laurocerasus*	MH554070	MH554281	MH554982	–	–	Liu et al. (2019)
	CBS 356.33		–	*Prunus* sp.	MH554036	MH554253	MH554949	–	–	Liu et al. (2019)
	CBS 144025	NT	France	*Vitis vinifera* cv. 'Prunelard	MH554112	MH554318	MH555021	–	–	Liu et al. (2019)
	CBS 338.32		Netherlands	*Lupinus* sp.	MH554033	MH554250	MH554945	–	–	Liu et al. (2019)
	CBS 165.25		–	*Prunus armeniaca*	MH554010	MH554231	–	–	–	Liu et al. (2019)
undetermined sp. 1	CBS 113991		Sweden	*Salix caprea*	MH553971	MH554190	MH554865	–	–	Liu et al. (2019)
undetermined sp. 2	CBS 387.77		Finland	Skin of man	MH554040	KM116277	MH554950	–	–	Liu et al. (2019)
Xenoseimatosporium quercinum	MFLUCC 14-1198	T	Germany	*Quercus robur*	NR_155804	NG_059681	–	–	–	Liu et al. (2019)
	CBS 129171			*Rhododendron* sp.	MH553997	MH554216	MH554906	–	–	Liu et al. (2029)

[1] BRIP: Queensland Plant Pathology Herbarium, Australia; CBS: Culture collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CFCC: China Forestry Culture Collection Center, China; CMW: Culture Collection of the Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa; CPC: Culture collection of Pedro Crous, housed at the Westerdijk Institute; HGUP: Plant Pathology Herbarium of Guizhou University; HHUF: herbarium of Hirosaki University; HKUCC: The University of Hong Kong Culture Collection; HPC: Herbarium of Pedro Crous, housed at the Westerdijk Institute; ICMP: International Collection of Micro-organisms from Plants, Landcare Research, Private Bag 92170, Auckland, New Zealand; IFRDCC: International Fungal Research and Development Culture Collection; IMI: International Mycological Institute, CABI-Bioscience, Egham, Bakeham Lane, United Kingdom; LC: working collection of Lei Cai, housed at the Institute of Microbiology, Chinese Academy of Sciences, Beijing, China; MAFF: Ministry of Agriculture, Forestry and Fisheries, Tsukuba, Ibaraki, Japan; MEAN: culture collection of INIAV Institute, Oeiras, Portugal; MFLUCC: Mae Fah Luang University Culture Collection; NOF: The Fungus Culture Collection of the Northern Forestry Centre, Alberta, Canada; MSCL: Microbial Strain Collection of Latvia; NBRC: Biological Resource Center; NTUCC: National Taiwan University Culture Collection, Taiwan; UPSC: Uppsala University Culture Collection of Fungi, Sweden; VPRI: Victorian Plant Disease Herbarium, Australia.

[2] Status: status of the strains. ET: ex-epitype; IT: ex-isotype; NT: ex-neotype; R: reference strain; ST: ex-syntype; T: ex-type.

[3] MFLUCC 15-0563: Type of *Seimatosporium rosigenum*; MFLUCC 14-0466: Type of *Seimatosporium pseudorosarum*.

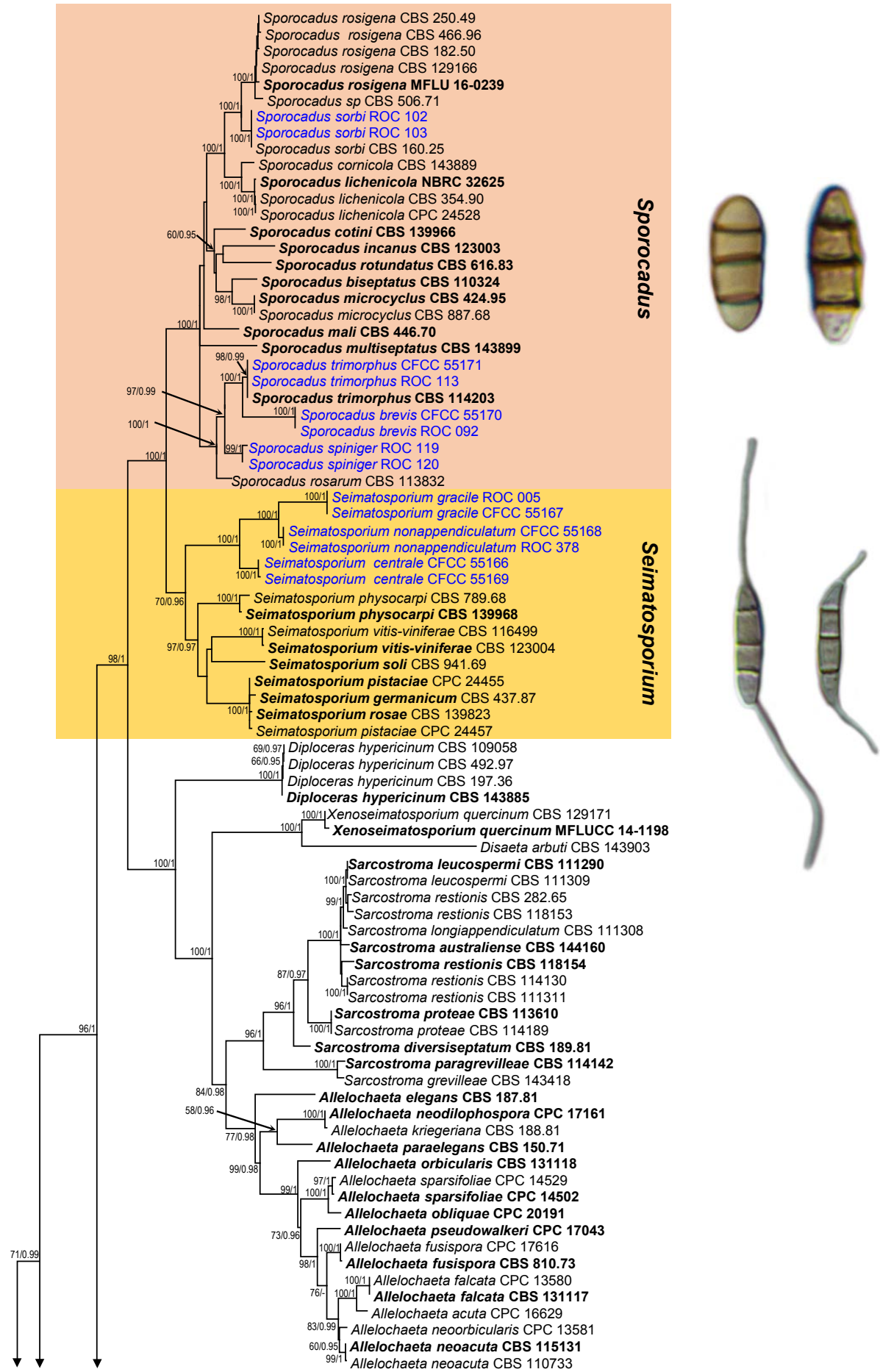
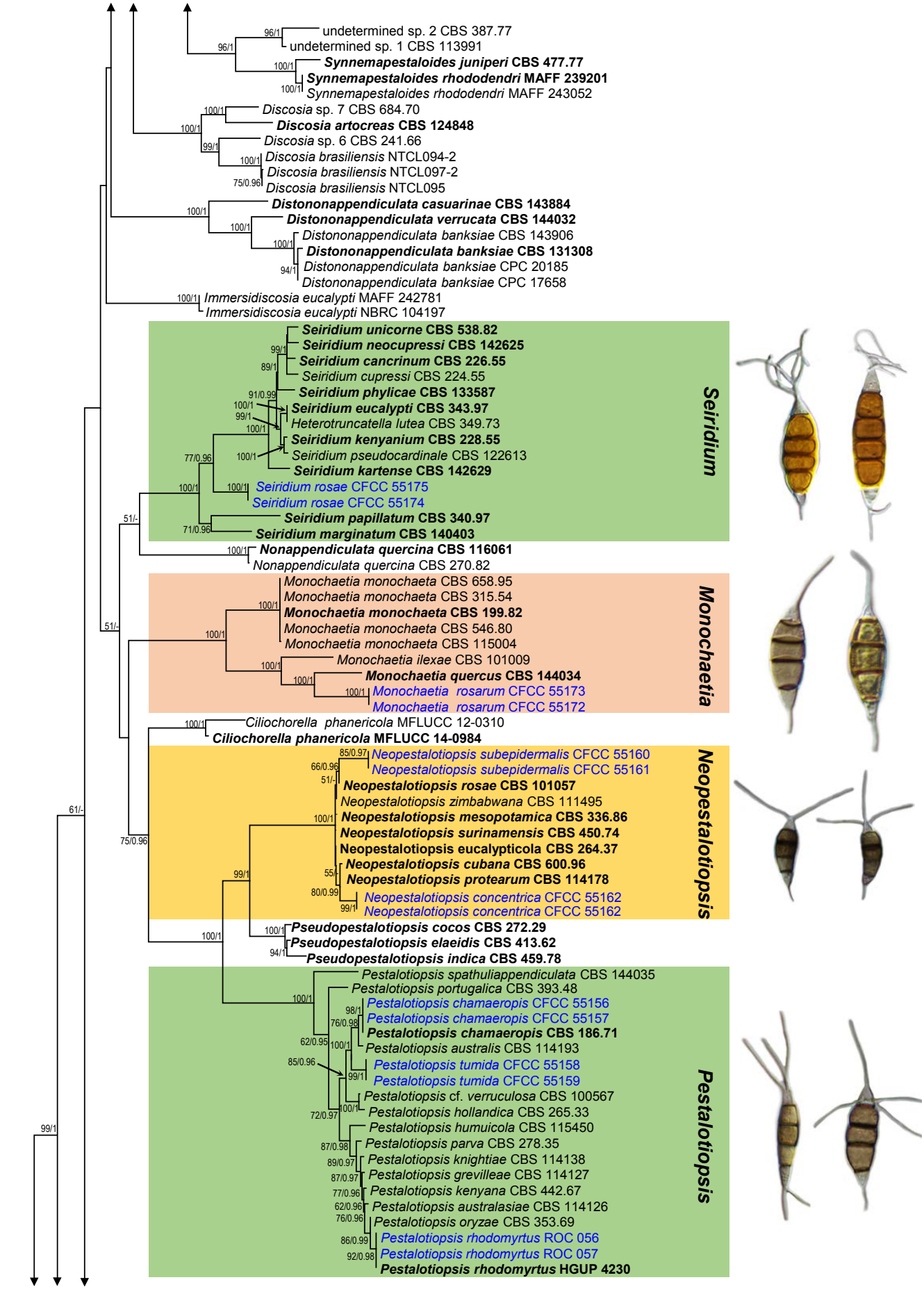


Fig. 2 Phylogenetic tree of *Sporocadaceae* (50 % majority rule consensus) based on maximum likelihood (ML) analysis of the combined LSU, ITS and *RPB2* sequence alignment. Nodes are labelled with bootstrap values from RAxML/Bayesian posterior probabilities. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Genera in this study are delimited in coloured boxes and isolates collected in this study are in **bold**. Ex-type strains are represented in **bold**.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undetermined sp. 1 CBS 113991
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Synnemapestaloides rhododendri MAFF 239201
Synnemapestaloides rhododendri MAFF 243052
Discosia sp. 7 CBS 684.70
Discosia artocreas CBS 124848
Discosia sp. 6 CBS 241.66
Discosia brasiliensis NTCL094-2
Discosia brasiliensis NTCL097-2
Discosia brasiliensis NTCL095
Distononappendiculata casuarinae CBS 143884
Distononappendiculata verrucata CBS 144032
Distononappendiculata banksiae CBS 143906
Distononappendiculata banksiae CBS 131308
Distononappendiculata banksiae CPC 20185
Distononappendiculata banksiae CPC 17658
Immersidiscosia eucalypti MAFF 242781
Immersidiscosia eucalypti NBRC 104197
Seiridium unicorne CBS 538.82
Seiridium neocupressi CBS 142625
Seiridium cancrinum CBS 226.55
Seiridium cupressi CBS 224.55
Seiridium phylicae CBS 133587
Seiridium eucalypti CBS 343.97
Heterotruncatella lutea CBS 349.73
Seiridium kenyanium CBS 228.55
Seiridium pseudocardinale CBS 122613
Seiridium kartense CBS 142629
Seiridium rosae CFCC 55175
Seiridium rosae CFCC 55174
Seiridium papillatum CBS 340.97
Seiridium marginatum CBS 140403
Seiridium
Nonappendiculata quercina CBS 116061
Nonappendiculata quercina CBS 270.82
Monochaetia monochaeta CBS 658.95
Monochaetia monochaeta CBS 315.54
Monochaetia monochaeta CBS 199.82
Monochaetia monochaeta CBS 546.80
Monochaetia monochaeta CBS 115004
Monochaetia ilexae CBS 101009
Monochaetia quercus CBS 144034
Monochaetia rosarum CFCC 55173
Monochaetia rosarum CFCC 55172
Monochaetia
Ciliochorella phanericola MFLUCC 12-0310
Ciliochorella phanericola MFLUCC 14-0984
Neopestalotiopsis subepidermalis CFCC 55160
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Neopestalotiopsis rosae CBS 101057
Neopestalotiopsis zimbabwana CBS 111495
Neopestalotiopsis mesopotamica CBS 336.86
Neopestalotiopsis surinamensis CBS 450.74
Neopestalotiopsis eucalypticola CBS 264.37
Neopestalotiopsis cubana CBS 600.96
Neopestalotiopsis protearum CBS 114178
Neopestalotiopsis concentrica CFCC 55162
Neopestalotiopsis concentrica CFCC 55162
Neopestalotiopsis
Pseudopestalotiopsis cocos CBS 272.29
Pseudopestalotiopsis elaeidis CBS 413.62
Pseudopestalotiopsis indica CBS 459.78
Pestalotiopsis spathuliappendiculata CBS 144035
Pestalotiopsis portugalica CBS 393.48
Pestalotiopsis chamaeropis CFCC 55156
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Pestalotiopsis tumida CFCC 55158
Pestalotiopsis tumida CFCC 55159
Pestalotiopsis cf. verruculosa CBS 100567
Pestalotiopsis hollandica CBS 265.33
Pestalotiopsis humuicola CBS 115450
Pestalotiopsis parva CBS 278.35
Pestalotiopsis knightiae CBS 114138
Pestalotiopsis grevilleae CBS 114127
Pestalotiopsis kenyana CBS 442.67
Pestalotiopsis australasiae CBS 114126
Pestalotiopsis oryzae CBS 353.69
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Pestalotiopsis rhodomyrtus ROC 057
Pestalotiopsis rhodomyrtus HGUP 4230
Pestalotiopsis

Fig. 2 (cont.)

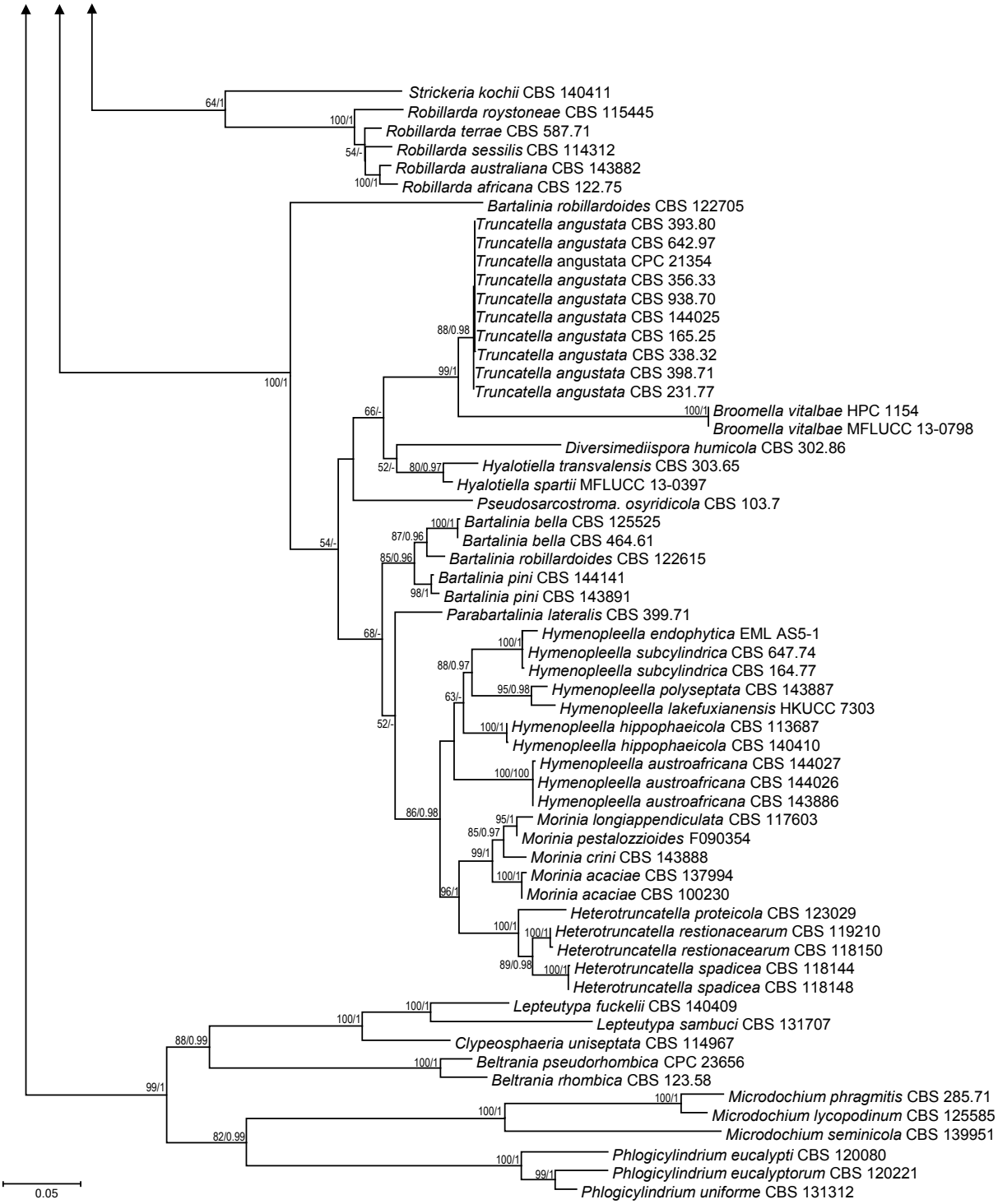


Fig. 2 (cont.)

and Maximum-parsimony bootstrap values (MPBP) equal or greater than 50 % are provided for each tree. Bayesian posterior probabilities (BYPP) > 0.90 are indicated as thickened lines.

Prevalence

To determine the prevalence of *Sporocadaceae* genera and species on *Rosa* spp. and plant parts (branches, fruits, leaves or spines), the Isolation Rate (RI) was calculated for each species with the formula: RI % = (NS / NI) × 100, where NS was the number of isolates from the same genera or species, and NI was the total number of isolates from each *Rosa* sp. or plant part. The overall RI was calculated using the NI value equal to the total number of isolates obtained from *Rosa* plants (Vieira et al. 2014, Fu et al. 2019, Guo et al. 2020).

RESULTS

Phylogenetic analyses

The concatenated DNA sequence dataset (ITS, LSU and *RPB2*) was used to infer delimitation at the family level. The concatenated alignment had a total length of 2 419 characters including alignment gaps (659 for ITS, 890 for LSU and 832 for *RPB2*). Of these, 1 401 characters were constant, 144 variable characters were parsimony-uninformative and 874 characters were parsimony informative. The ML search resolved a best tree with an lnL of -36418.696700. The BA lasted for 1 855 000 generations and the 50 % consensus tree and posterior probabilities were calculated from 2 784 trees from two runs. The ML tree confirmed the same tree topology and the clades as those presented in the Bayesian phylogeny (Fig. 2).

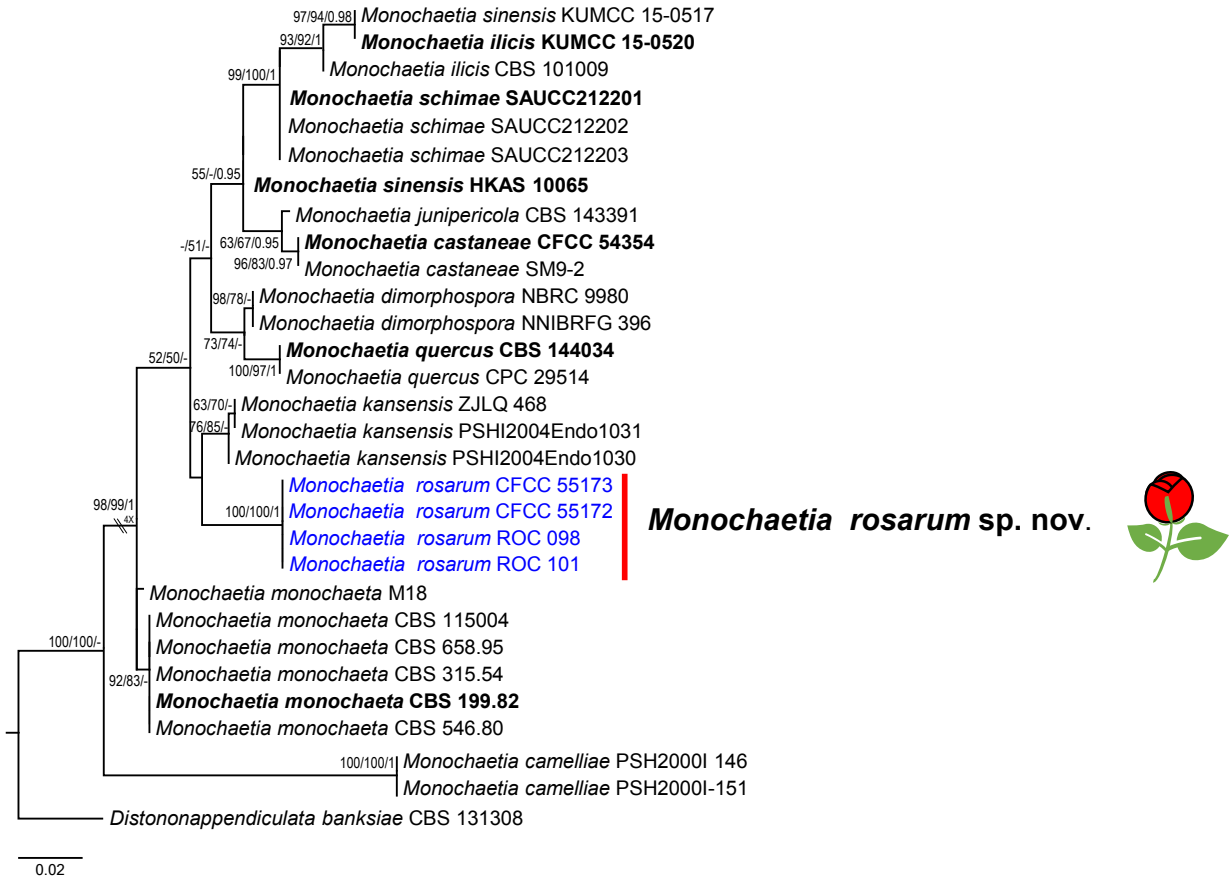


Fig. 3 Phylogenetic tree of *Monochaetia* resulting from maximum likelihood (ML) analysis of the ITS sequence alignment. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Ex-type strains are represented in **bold**; strains obtained in the current study in blue. The flower symbol represents species that have been recorded from *Rosa*.

Following alignment of *Monochaetia*, the ITS sequence data with a total of 599 characters including gaps, of which 496 characters were constant, 15 variable characters were parsimony uninformative, and 88 characters were variable and parsimony informative. The parsimony analysis resulted in 1 000 equally parsimonious trees, one of which is in Fig. 3 (CI = 0.780, RI = 0.887, RC = 0.692, HI = 0.220). The topology of the phylogenetic trees generated from the MP, ML and BA methods were congruent.

In the phylogenetic tree constructed for *Neopestalotiopsis* and *Pestalotiopsis*, sequences of the combined ITS, *TEF* and *TUB* were aligned. In *Neopestalotiopsis*, the alignment comprises 2 263 characters including alignment gaps after alignment (580 for ITS, 592 for *TEF* and 787 for *TUB*). Of these, 1 647 characters were constant, 383 variable characters were parsimony-uninformative and 233 characters were parsimony informative. The MP analysis resulted in a single equally most parsimonious tree (CI = 0.672, RI = 0.659, RC = 0.442, HI = 0.328). In *Pestalotiopsis*, the alignment comprises 2 183 characters including alignment gaps after alignment (590 for ITS, 670 for *TEF* and 909 for *TUB*), of which 1 165 characters were constant, 384 variable characters were parsimony-uninformative and 634 characters were parsimony informative. The MP analysis resulted in a single equally most parsimonious tree (CI = 0.565, RI = 0.845, RC = 0.478, HI = 0.435). MP was similar to the topology from ML and BA (Fig. 4, 5).

In *Seimatosporium*, the combined ITS + LSU dataset had an aligned length of 1 495 characters in the dataset (601 for ITS and 887 for LSU), of which 1 181 characters are constant, 118 are variable and parsimony-uninformative, and 196 are parsimony informative. Maximum Parsimony analysis yielded 750 equally parsimonious trees (CI = 0.674, RI = 0.738, RC = 0.497, HI = 0.326), and a strict consensus tree is shown in Fig. 6.

In *Seiridium*, the combined ITS, *RPB2*, *TEF* and *TUB* dataset consists of 2 897 characters including alignment gaps (598 for ITS, 818 for *RPB2*, 606 for *TEF* and 829 for *TUB*), of which 1 637 are constant, 454 are variable parsimony uninformative characters and 806 are parsimony-informative characters. The MP analysis resulted in a single equally most parsimonious tree (CI = 0.664, RI = 0.689, RC = 0.457, HI = 0.336) (Fig. 7).

In *Sporocadus*, the combined sequences of ITS, LSU, *RPB2*, *TEF* and *TUB* were aligned. The combined data comprises 3 619 characters including alignment gaps (566 for ITS, 900 for LSU, 869 for *RPB2*, 496 for *TEF* and 760 for *TUB*). Of these, 2 671 characters were constant, 263 variable characters were parsimony-uninformative and 685 characters were parsimony informative. The MP analysis resulted in a single equally most parsimonious tree (CI = 0.657, RI = 0.808, RC = 0.531, HI = 0.343) (Fig. 8).

All the MP analyses resulted in a tree with the same topology and terminal clades as the ML and BA trees. The new species from the present study appeared in distinct clades with high bootstrap support.

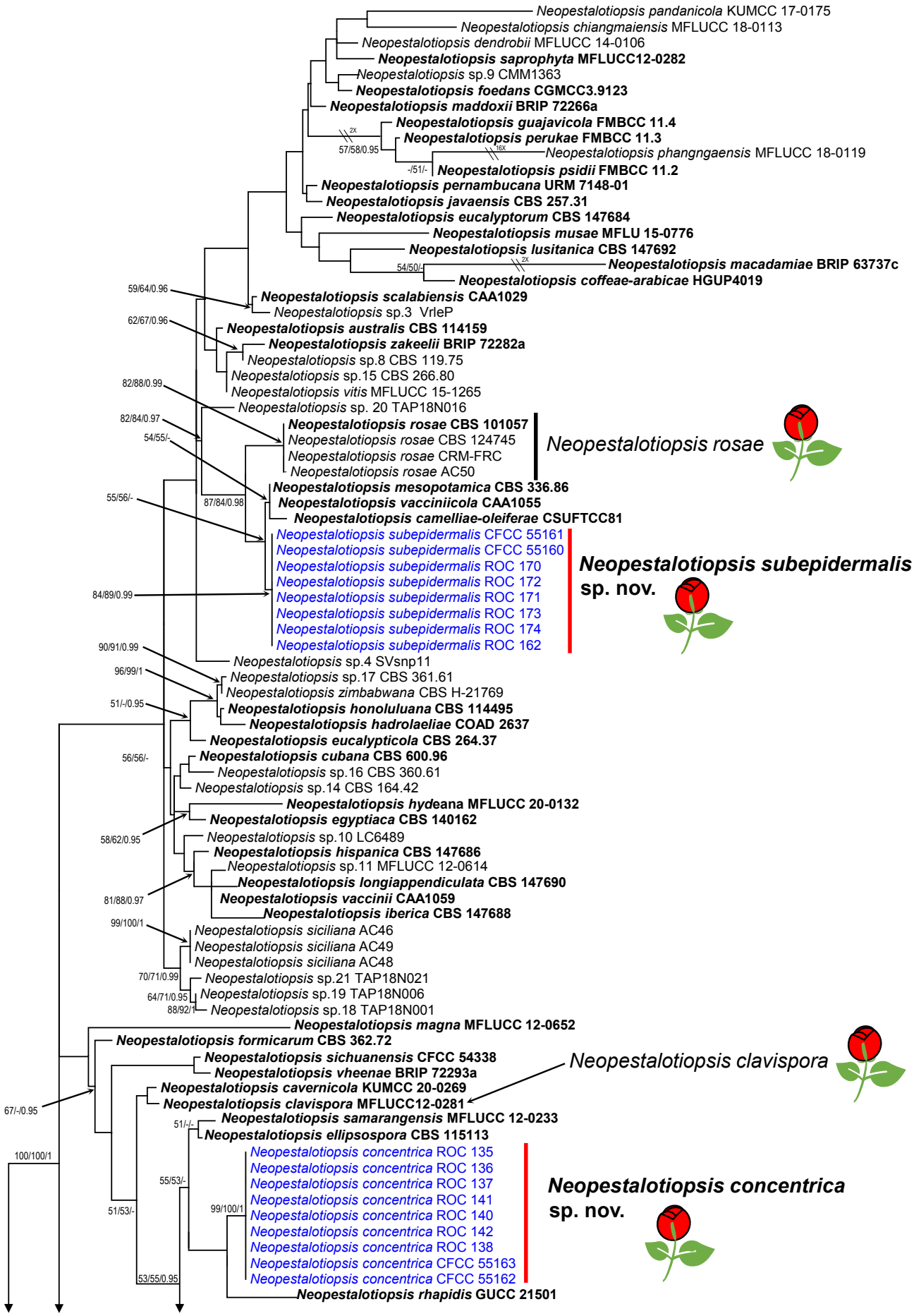


Fig. 4 The best Maximum Likelihood tree from the multi-gene alignment (ITS, *TUB* and *TEF*) for the *Neopestalotiopsis*. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Ex-type strains are represented in **bold**; strains obtained in the current study in blue. The flower symbol represents species that have been recorded from *Rosa*.

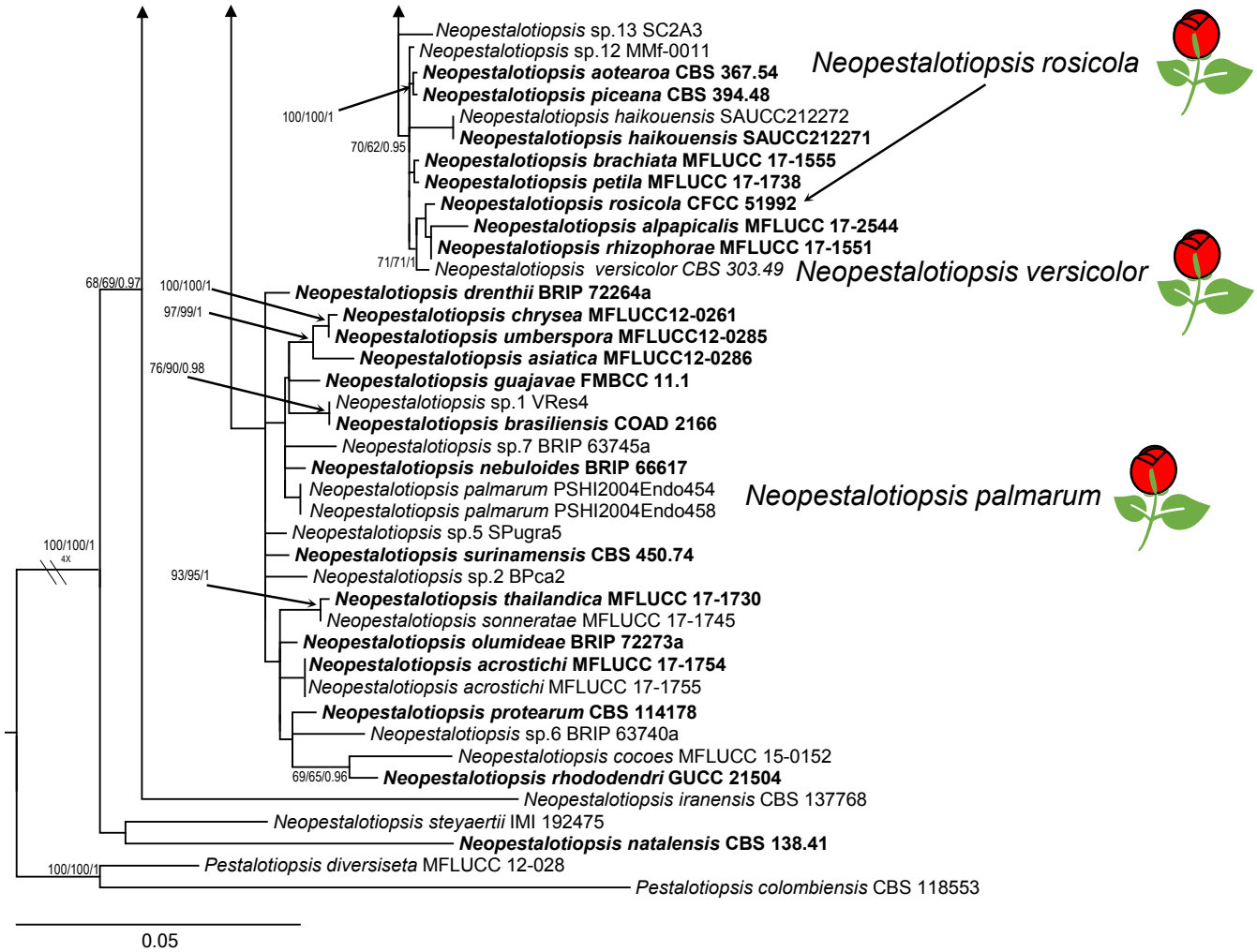


Fig. 4 (cont.)

Taxonomy

Based on the morphology and multi-locus phylogeny, 126 isolates were assigned to 15 species belonging to six genera in *Sporocadaceae*, including 11 species newly described below.

Monochaetia rosarum C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843811; Fig. 9

Etymology. The species epithet reflects the name of the host plant genus *Rosa*.

Typus. China, Henan Province, Nanyang City, Neixiang county, Baotianman Nature Reserve, N33°29'29" E111°55'50", alt. 1311 m, on branches of *R. chinensis*, 7 Aug. 2020, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (holotype BJFC-S1877, ex-type culture CFCC 55172 = ROC 099).

Symptoms appeared as circular to irregular, red or dark brown and raised, dehiscent lesions on twigs and branches (Fig. 9b–c). Sexual morph not observed. Asexual morph: *Acervular conidiomata* visible on the host, globose or irregular, superficial to semi-immersed, scattered or aggregated, black or red, 76–118 µm diam. *Conidiophores* septate and branched, hyaline, smooth-walled or verruculose. *Conidiogenous cells* annellidic, discrete or integrated, cylindrical, subcylindrical, hyaline or pale brown, smooth, 6.5–14(–15) × (1–)1.5–2 µm (av. = 10.7 ± 2.84 × 1.7 ± 0.26 µm). *Conidia* fusoid, straight or slightly curved, 4-septate, wall smooth, not constricted at the septa, (17.5–)18–20(–21) × 5–6(–7) µm (av. = 19.5 ± 0.95 × 5.4 ± 0.37 µm); basal cell obconic with or without truncate base, thin-walled, hyaline, 2.5–3(–3.5) µm (av. = 2.6 ± 0.27 µm) long; three median cells, doliiform or subcylindrical, mid-brown, thick-walled, the first median cell from base (3–)3.5–5 µm (av. = 4.2 ± 0.42 µm) long, the second cell (2.5–)3–3.5(–4.5) µm (av. = 3.4 ± 0.27 µm) long, the third cell (3–)3.5–4(–5) µm (av. = 3.7 ± 0.36 µm) long, together (10.5–)11.5–12.5(–13) µm (av. = 12.1 ± 0.47 µm) long; apical cell conic with an acute apex, thin-walled, hyaline, 2–2.5(–3) µm (av. = 2.4 ± 0.31 µm) long; apical appendage single, tubular, attenuated, unbranched, variously bent; (8–)9–12(–12.5) µm (av. = 10.8 ± 1.36 µm) long; basal appendage single, unbranched, centric, 4.5–6(–6.5) µm (av. = 5.5 ± 0.48 µm); mean conidium length/width ratio = 3.25 : 1.

Culture characteristics — On PDA, colonies slowly growing, up to 10 mm diam after 3 d and reaching 38–40 mm after 15 d, white to pale grey with a uniform texture, with an irregular margin, lacking aerial mycelium, becoming greyish and yellowish after 30 d, reverse yellowish brown. Conidiomata globose, distributed irregularly on the medium surface, exuding globose, dark brown to black conidial masses.

Additional materials examined. China, Henan Province, Nanyang City, Neixiang county, Baotianman Nature Reserve, N33°29'68" E111°55'16", alt. 1329 m, on branches of *R. chinensis*, 7 Aug. 2020, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (BJFC-S1878, cultures CFCC 55173 = ROC 100, ROC 98, ROC 101).

Notes — *Monochaetia rosarum* forms an independent clade and is phylogenetically distinct from *M. kansensis* (Fig. 3). *Monochaetia rosarum* can be distinguished from *M. kansensis* in ITS loci by 13 bp differences (from 561 characters, with 97.6 % sequence identity, including 3 bp gaps). In addition, *M. rosarum* differs from *M. kansensis* in producing thinner conidia (5–6 µm

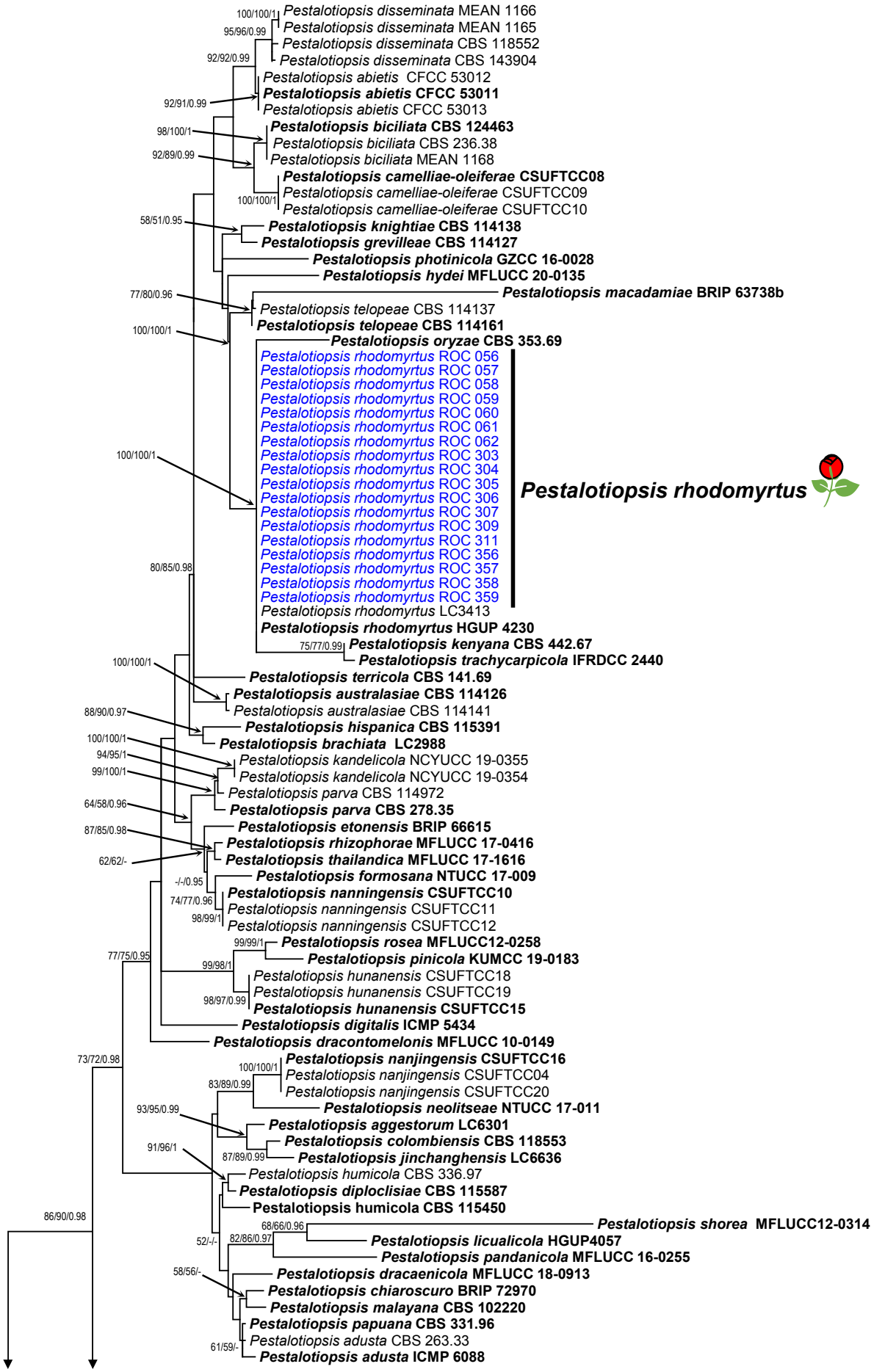
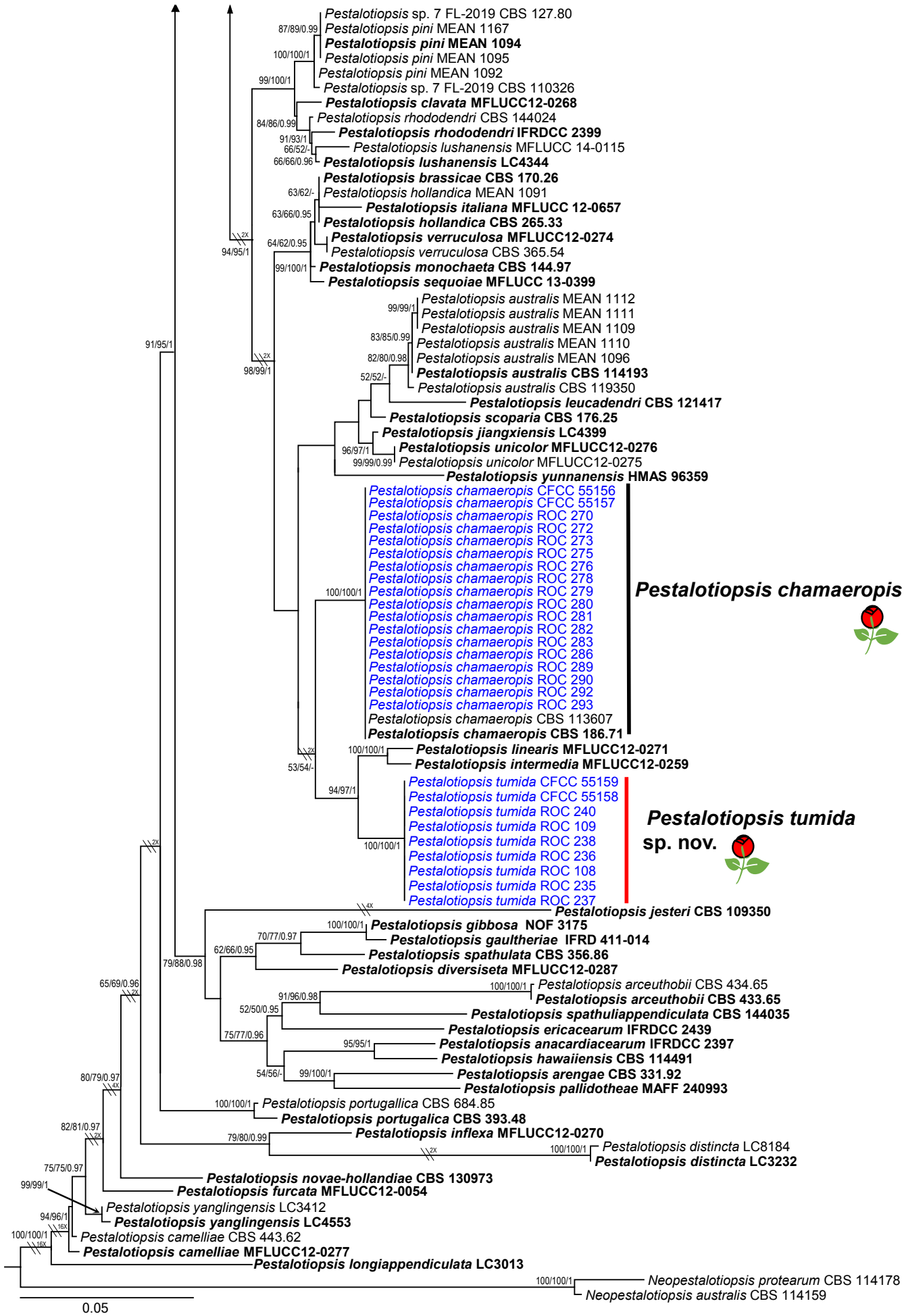


Fig. 5 The best Maximum Likelihood tree from the multi-gene alignment (ITS, *TUB* and *TEF*) for the *Pestalotiopsis*. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Ex-type strains are represented in **bold**; strains obtained in the current study in blue. The flower symbol represents species that have been recorded from *Rosa*.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Pestalotiopsis pini MEAN 1094
Pestalotiopsis pini MEAN 1095
Pestalotiopsis pini MEAN 1092
Pestalotiopsis sp. 7 FL-2019 CBS 110326
Pestalotiopsis clavata MFLUCC12-0268
Pestalotiopsis rhododendri CBS 144024
Pestalotiopsis rhododendri IFRDCC 2399
Pestalotiopsis lushanensis MFLUCC 14-0115
Pestalotiopsis lushanensis LC4344
Pestalotiopsis brassicae CBS 170.26
Pestalotiopsis hollandica MEAN 1091
Pestalotiopsis italiana MFLUCC 12-0657
Pestalotiopsis hollandica CBS 265.33
Pestalotiopsis verruculosa MFLUCC12-0274
Pestalotiopsis verruculosa CBS 365.54
Pestalotiopsis monochaeta CBS 144.97
Pestalotiopsis sequoiae MFLUCC 13-0399
Pestalotiopsis australis MEAN 1112
Pestalotiopsis australis MEAN 1111
Pestalotiopsis australis MEAN 1109
Pestalotiopsis australis MEAN 1110
Pestalotiopsis australis MEAN 1096
Pestalotiopsis australis CBS 114193
Pestalotiopsis australis CBS 119350
Pestalotiopsis leucadendri CBS 121417
Pestalotiopsis scoparia CBS 176.25
Pestalotiopsis jiangxiensis LC4399
Pestalotiopsis unicolor MFLUCC12-0276
Pestalotiopsis unicolor MFLUCC12-0275
Pestalotiopsis yunnanensis HMAS 96359
Pestalotiopsis chamaeropis CFCC 55156
Pestalotiopsis chamaeropis CFCC 55157
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Pestalotiopsis intermedia MFLUCC12-0259
Pestalotiopsis tumida CFCC 55159
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Pestalotiopsis tumida ROC 235
Pestalotiopsis tumida ROC 237
Pestalotiopsis tumida sp. nov.
Pestalotiopsis jesteri CBS 109350
Pestalotiopsis gibbosa NOF 3175
Pestalotiopsis gaultheriae IFRD 411-014
Pestalotiopsis spathulata CBS 356.86
Pestalotiopsis diversiseta MFLUCC12-0287
Pestalotiopsis arceuthobii CBS 434.65
Pestalotiopsis arceuthobii CBS 433.65
Pestalotiopsis spathuliappendiculata CBS 144035
Pestalotiopsis ericacearum IFRDCC 2439
Pestalotiopsis anacardiacearum IFRDCC 2397
Pestalotiopsis hawaiiensis CBS 114491
Pestalotiopsis arengae CBS 331.92
Pestalotiopsis pallidotheae MAFF 240993
Pestalotiopsis portugallica CBS 684.85
Pestalotiopsis portugalica CBS 393.48
Pestalotiopsis inflexa MFLUCC12-0270
Pestalotiopsis distincta LC8184
Pestalotiopsis distincta LC3232
Pestalotiopsis novae-hollandiae CBS 130973
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Pestalotiopsis yanglingensis LC4553
Pestalotiopsis camelliae CBS 443.62
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Neopestalotiopsis australis CBS 114159
0.05

Fig. 5 (cont.)

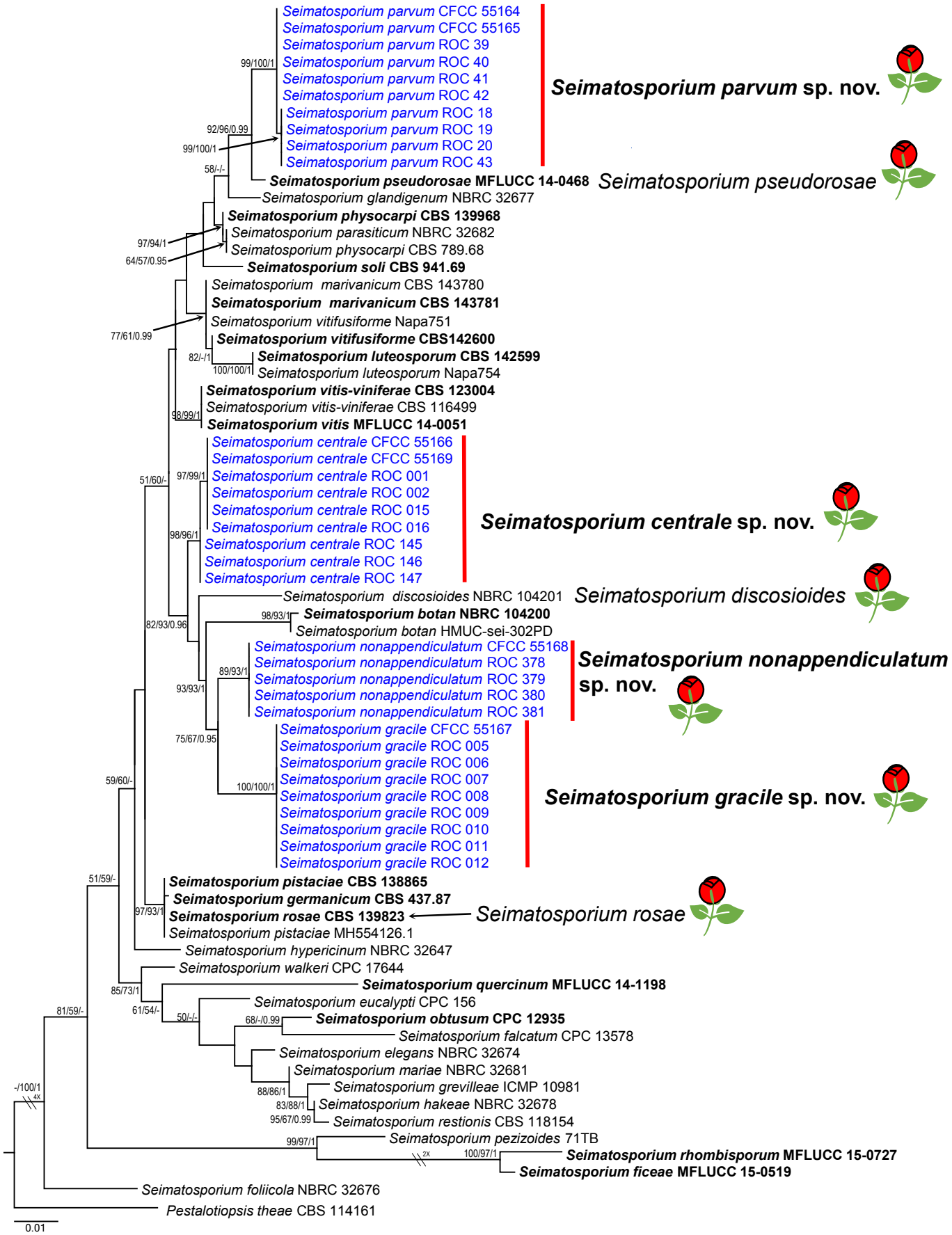

Fig. 6 The best Maximum Likelihood tree from the multi-gene alignment (ITS and LSU) for the *Seimatosporium*. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Ex-type strains are represented in **bold**; strains obtained in the current study in blue. The flower symbol represents species that have been recorded from *Rosa*.

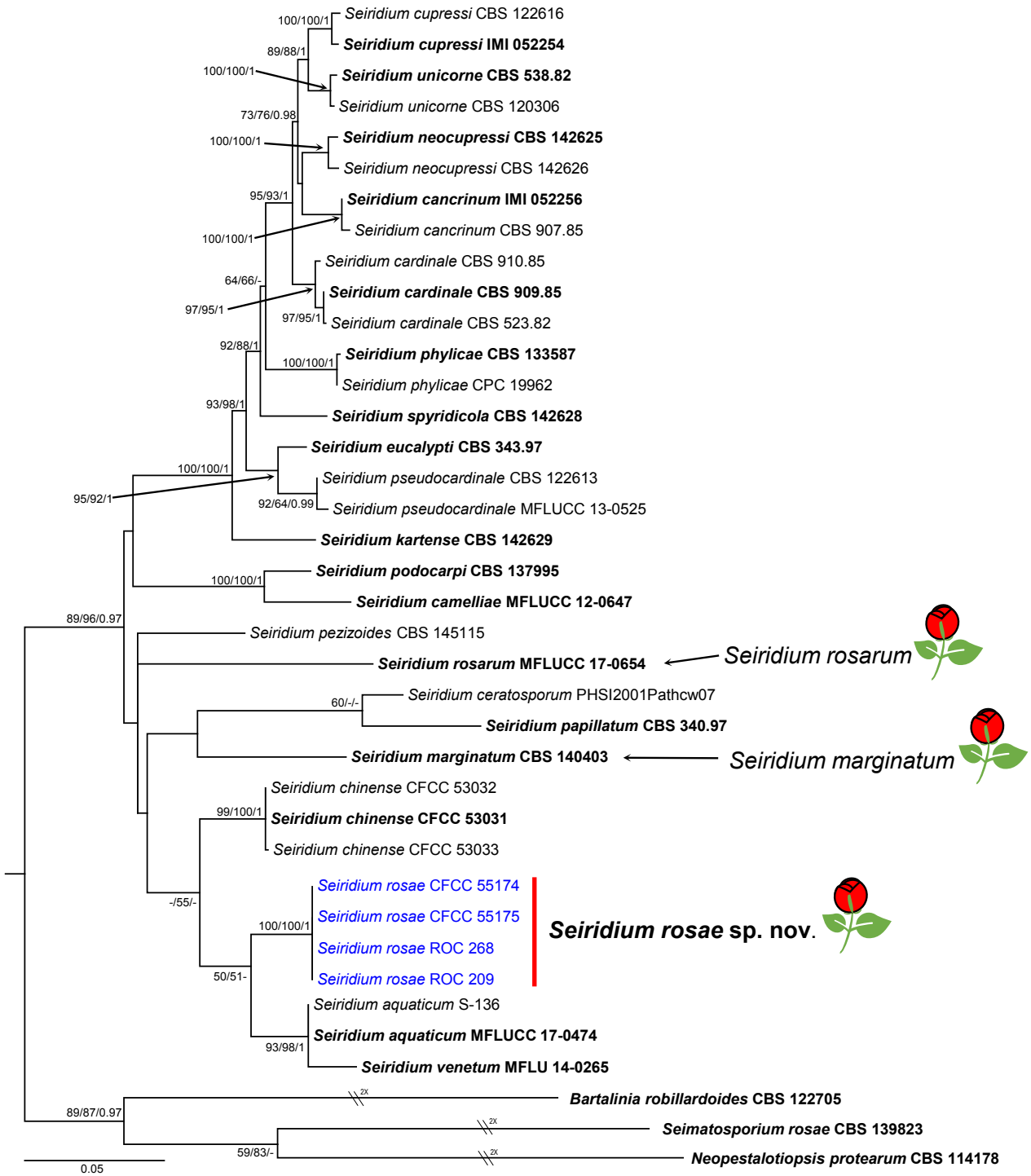

Fig. 7 The best Maximum Likelihood tree from the multi-gene alignment (ITS, *RPB2*, *TEF* and *TUB*) for the *Seiridium*. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Ex-type strains are represented in **bold**; strains obtained in the current study in blue. The flower symbol represents species that have been recorded from *Rosa*.

vs 6–8 µm). Furthermore, the apical and basal appendages of *M. rosarum* are significantly shorter than those of *M. kansensis* (9–12 µm vs 15–26 µm and 4.5–6 µm vs 10–38 µm).

Four *Monochaetia* species have been reported from *Rosa* spp., i.e., *M. concentrica*, *M. rosae-caninae*, *M. seiridioides* and *M. turgida* (Guba 1961, Tai 1979, Nag Raj 1993, Chen 2003). These four species are easily distinguishable from our new species based on conidial dimensions. *Monochaetia concentrica* and *M. seiridioides* have longer conidia than *M. rosarum* (20–26 µm vs 18–20 µm and 26–28 µm vs 18–20 µm). *Monochaetia turgida* has wider conidia than *M. rosarum* (7.6–8.3 µm vs 5–6 µm).

Although *M. rosarum* and *M. rosae-caninae* have similar conidial width (5–6 µm vs 5–7 µm), the conidia of *M. rosarum* is significantly longer than those of *M. rosae-caninae* (18–20 µm vs 16–18 µm). In addition, *M. rosarum* is similar to *M. camelliae* in conidial dimensions (18–20 × 5–6 µm vs 18–20 × 4–7 µm), the latter having been previously reported from *Camellia*, *Eucalyptus* and *Peltophorum*. However, based on the combined gene phylogenetic analysis, *M. rosarum* is separated from *M. camelliae* and the apical appendages of *M. rosarum* are shorter than those of *M. camelliae* (9–12 µm vs 12–14 µm).

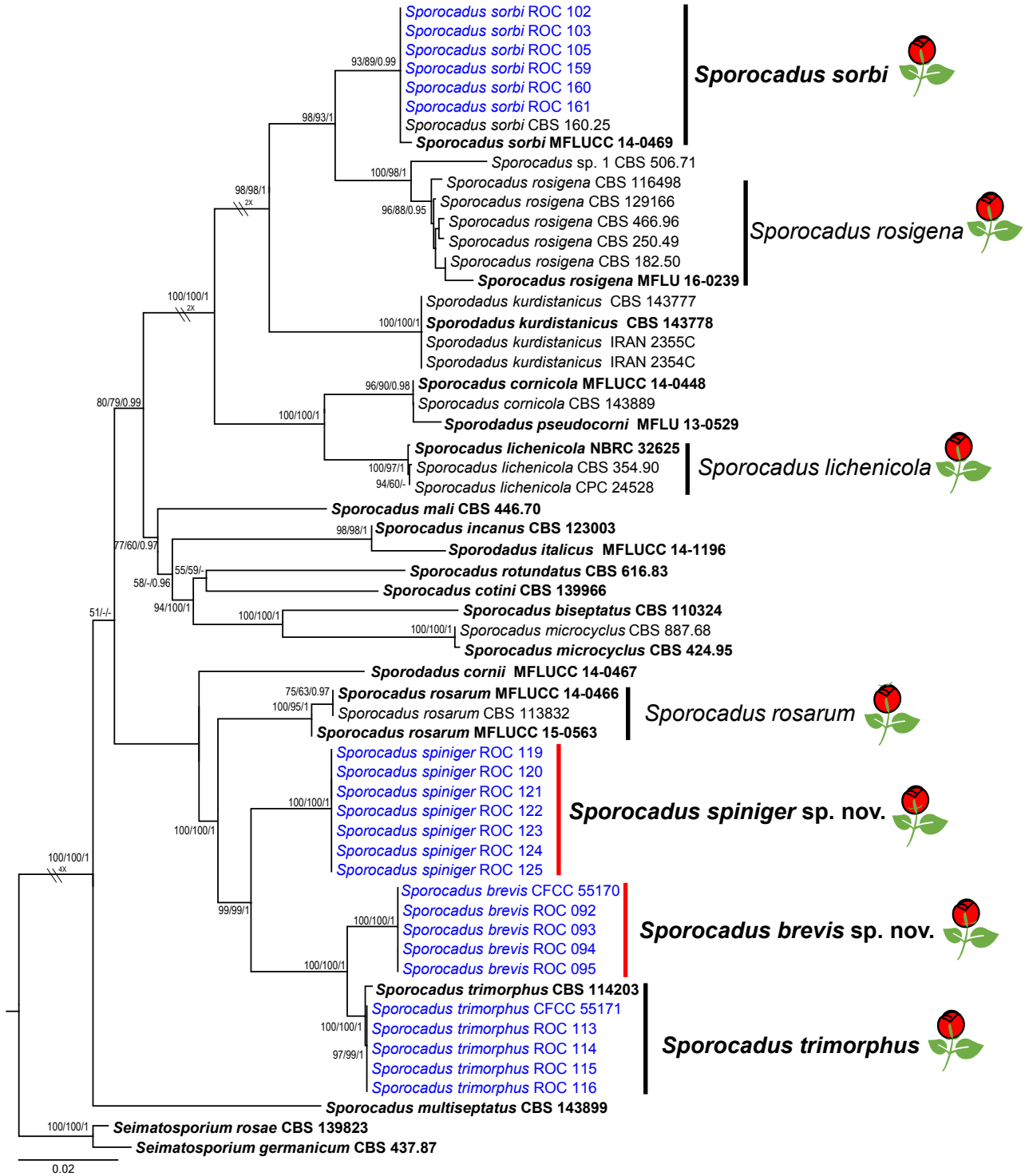

Fig. 8 The best Maximum Likelihood tree from the multi-gene alignment (ITS, LSU, *RPB2*, *TEF* and *TUB*) for the *Sporocadus*. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Ex-type strains are represented in **bold**; strains obtained in the current study in blue. The flower symbol represents species that have been recorded from *Rosa*.

Key to Monochaetia species on Rosa spp.

1. Conidial length more than 20 µm 2
1. Conidial length less than 20 µm 3
2. Conidia 20–26 × 6.5–8.5 µm, apical appendage 15 µm long . . . . . *M. concentrica*
2. Conidia 26–28 × 6–7 µm, apical appendage 12 µm long . . . . . *M. seiridioides*
3. Conidial width more than 8 µm . . . . . *M. turgida*
3. Conidial width less than 8 µm 4
4. Conidia 16–18 × 5–7 µm . . . . . *M. rosae-caninae*
4. Conidia 18–20 × 5–6 µm . . . . . *M. rosarum*

Neopestalotiopsis concentrica C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843813; Fig. 10

Etymology. Name refers to the concentric circles formed by colonies on PDA.

Typus. China, Henan Province, Xinyang City, Jigong Mountain, N31°49'3" E114°4'33", alt. 717 m, on spines of *R. rugosa*, 6 Aug. 2020, *C. Peng* & *S. Jia* (holotype BJFC-S1882, ex-type culture CFCC 55162 = ROC 053).

Sexual morph not observed. Asexual morph: *Acervular conidiomata* globose or irregular, superficial to semi-immersed, scattered or aggregated, visible as black acervuli on the host, 93–117 µm diam. *Conidiophores* often reduced to conidiogenous

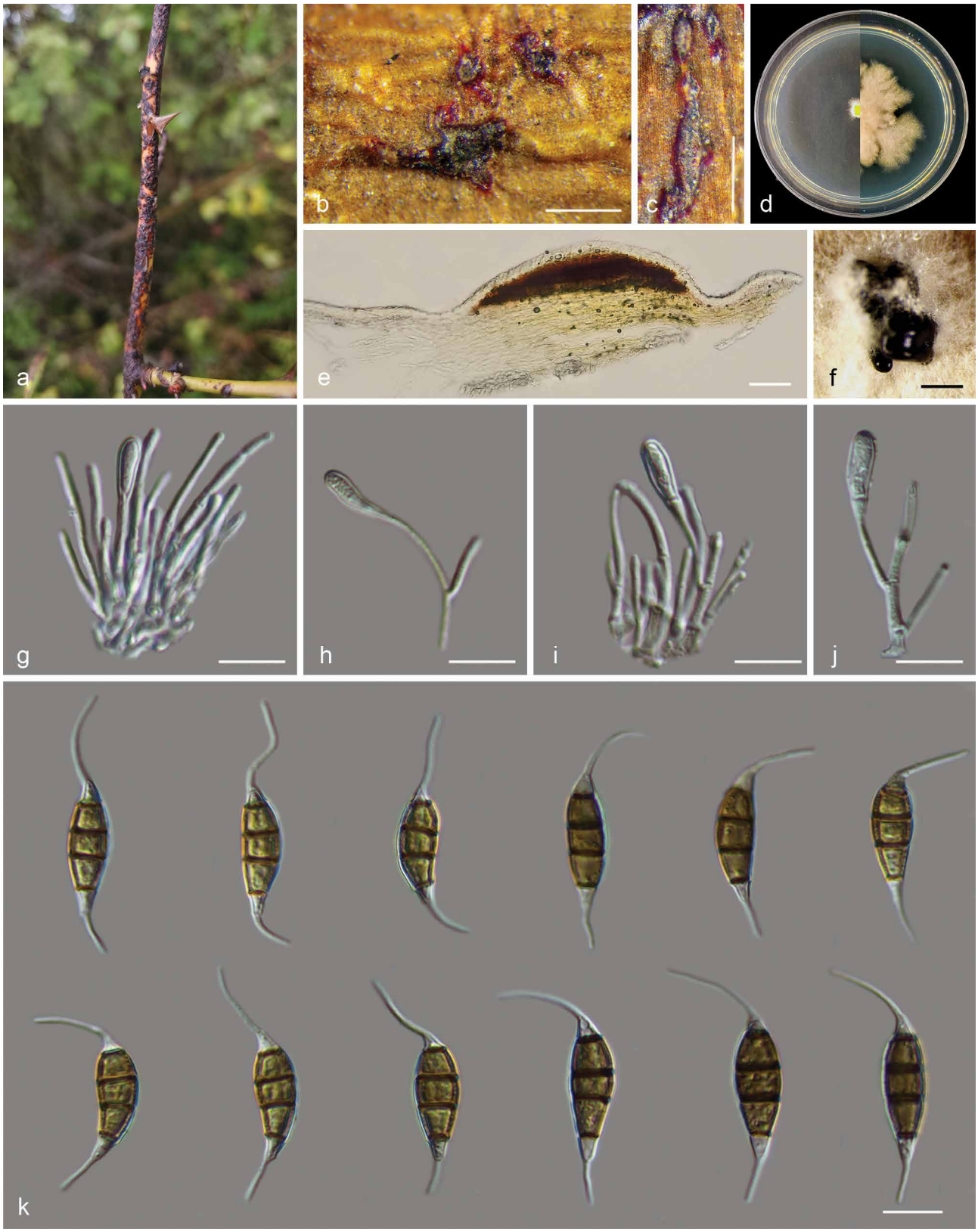

Fig. 9 *Monochaetia rosarum* (BJFC-S1877, holotype). a. Disease symptoms; b–c. habit of conidiomata on branch; d. colonies on PDA at 3 d (left) and 15 d (right); e. longitudinal section through conidioma; f. conidiomata on PDA; g–i. conidiogenous cells with attached conidia; k. conidia. — Scale bars: b–c, e = 50 µm; f = 200 µm; g–k = 10 µm.

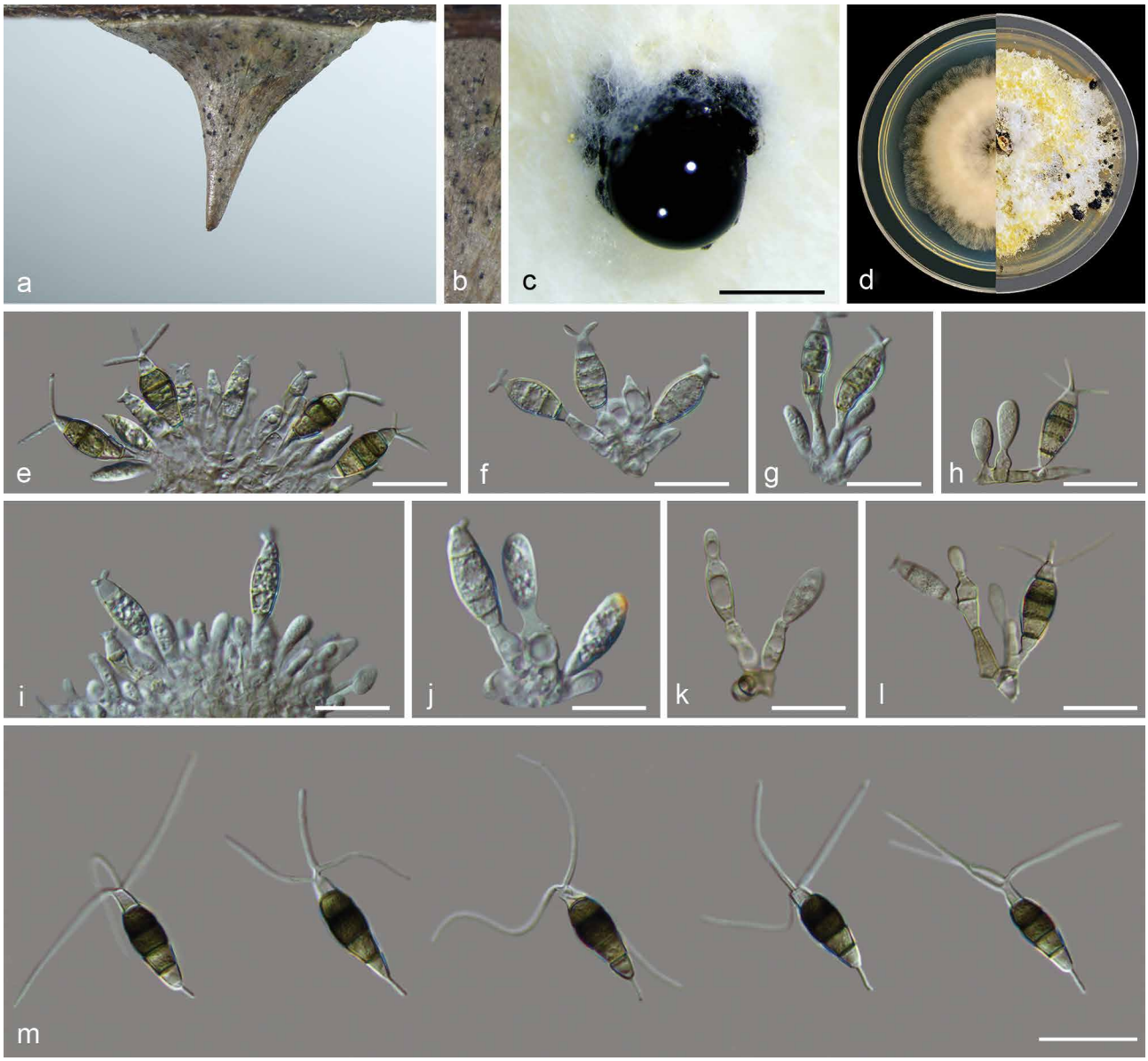

Fig. 10 *Neopestalotiopsis concentrica* (BJFC-S1882, holotype). a–b. Appearance of conidiomata on host substrate; c. conidiomata on PDA; d. colonies on PDA at 3 d (left) and 15 d (right); e–l. conidiogenous cells with attached conidia; m. conidia. — Scale bars: c = 200 µm; e–l = 10 µm.

cells. *Conidiogenous cells* discrete, ampulliform or irregular, variable in size, (3–)3.5–14.5(–15) × 3–5(–5.5) µm (av. = 7.8 ± 4.96 × 4.0 ± 1.21 µm), hyaline to subhyaline. *Conidia* fusoid, ellipsoid, straight to slightly curved, 4-septate, 14–18.5(–19) × 4.5–5(–6) µm (av. = 15.7 ± 1.06 × 4.9 ± 0.69 µm); basal cell conic to obconic with a truncate base, hyaline and thin-walled, 3–3.5(–4.0) µm (av. = 4.3 ± 0.21 µm) long; three median cells doliiform, (9–)9.5–10.5(–11) µm (av. = 10.0 ± 0.96 µm) long, wall rugose, versicoloured, septa darker than the rest of the cell, second cell from the base pale brown, 3–3.5 µm (av. = 3.3 ± 0.28 µm) long; third cell honey brown, 3–4 µm (av. = 3.74 ± 0.44 µm) long; fourth cell brown, 3–3.5 µm (av. = 3.1 ± 0.31 µm) long; apical cell (2.5–)3–3.5(–4) µm (av. = 3.4 ± 0.86 µm) long, hyaline, cylindrical, thin- and smooth-walled; with 2–3 tubular apical appendages (mostly three), branched or unbranched, filiform, 19–26(–26.5) µm (av. = 22.6 ± 2.14 µm) long; basal appendage single, tubular, unbranched, centric, (3–)3.5–5.5(–6.0) µm (av. = 4.1 ± 0.95 µm) long.

Culture characteristics — Colony on PDA with flattened mycelium, white, smoke grey in the centre, reverse with smoke grey pigments formed a concentric ring pattern, reaching at 58–62 mm diam in 15 d at 28 °C. Conidiomata globose, irregularly distributed on the medium surface, exuding globose, dark brown to black conidial masses.

Additional materials examined. China, Henan Province, Xinyang City, Jigong Mountain, N31°49'1" E114°4'12", alt. 723 m, on spines of *R. chinensis*, 6 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1883, living culture CFCC 55163 = ROC 064, ROC 135, ROC 136); Henan Province, Nanyang City, Xinyang City, Shihe District, N31°49'8" E114°3'58", alt. 727 m, on spines of *R. chinensis*, 6 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1884, cultures ROC 137, ROC 138, ROC 140, ROC 141, ROC 142).

Notes — This species is most closely related to *N. ellipsospora*, *N. rhapidis* and *N. samarangensis* (Fig. 4), but distinguished from *N. ellipsospora* by 15 bp difference in the concatenated alignment (two in the ITS region (482/484, 99.5 % with no gaps), nine *TEF* (531/540, 98.3 % with four gaps) and four *TUB* (436/440, 99.0 % with four gaps)), from *N. rhapidis* by 13 bp difference (six in the ITS region (507/513, 98.8 % with no gaps), three *TEF* (499/502, 99.4 % with three gaps) and four *TUB* (743/747, 99.4 % with no gaps)) and from *N. samarangensis* by 12 bp difference (three in the ITS region (481/484, 99.3 % with two gaps), three *TEF* (537/540, 99.4 % with three gaps) and six *TUB* (434/440, 98.6 % with no gaps)). Moreover, *N. concentrica* differs from these two species in morphology, namely by having longer apical appendages than *N. ellipsospora* (19–26 µm vs 5–12 µm), *N. rhapidis* (19–26 µm vs 11–16 µm) and *N. samarangensis* (19–26 µm vs 12–18 µm). However, its conidia are shorter than those of *N. ellipsospora* (14–18.5 µm

vs 19–25 µm), *N. rhapidis* (14–18.5 µm vs 22–25.5 µm) and *N. samarangensis* (14–18.5 µm vs 18–21 µm).

Neopestalotiopsis concentrica is phylogenetically and morphologically distinct from *N. clavispora*, *N. palmarum*, *N. rosae*, *N. rosicola* and *N. versicolor*, which were previously also reported from *Rosa* (Liu et al. 2010, Feng et al. 2014, Maharachchikumbura et al. 2014, Jiang et al. 2018, Vu et al. 2019). Its conidia are smaller than *N. clavispora* (14–18.5 × 4.5–5 µm vs 20–24 × 6.5–8.5 µm), *N. palmarum* (14–18.5 × 4.5–5 µm vs 19–23.6 × 5.6–6.6 µm), *N. rosae* (14–18.5 × 4.5–5 µm vs 22–37 × 7.5–9.5 µm), *N. rosicola* (14–18.5 × 4.5–5 µm vs 20.2–25.5 × 5.5–8 µm) and *N. versicolor* (14–18.5 × 4.5–5 µm vs 21.2–28.3 × 7.1–8.3 µm).

Neopestalotiopsis subepidermalis C. Peng & C.M. Tian, *sp. nov*. — MycoBank MB 843812; Fig. 11

Etymology. Referring to the conidioma occurring under the epidermis of spines, not breaking through the epidermis.

Typus. China, Henan Province, Xinyang City, Jigong Mountain, N31°49'15" E114°3'31", alt. 163.4 m, on spines of *R. rugosa*, 5 Aug. 2020, *C. Peng* & *S. Jia* (holotype BJFC-S1879, ex-type culture CFCC 55160 = ROC 161, ROC 162).

Sexual morph not observed. Asexual morph: *Acervular conidiomata* globose or irregular, superficial to semi-immersed, scattered or aggregated, visible as black acervuli on the host, 80–122 µm diam. *Conidiophores* septate, branched, subcylindrical, hyaline to subhyaline, often reduced to conidiogenous cells. *Conidiogenous cells* discrete, collarette present and not

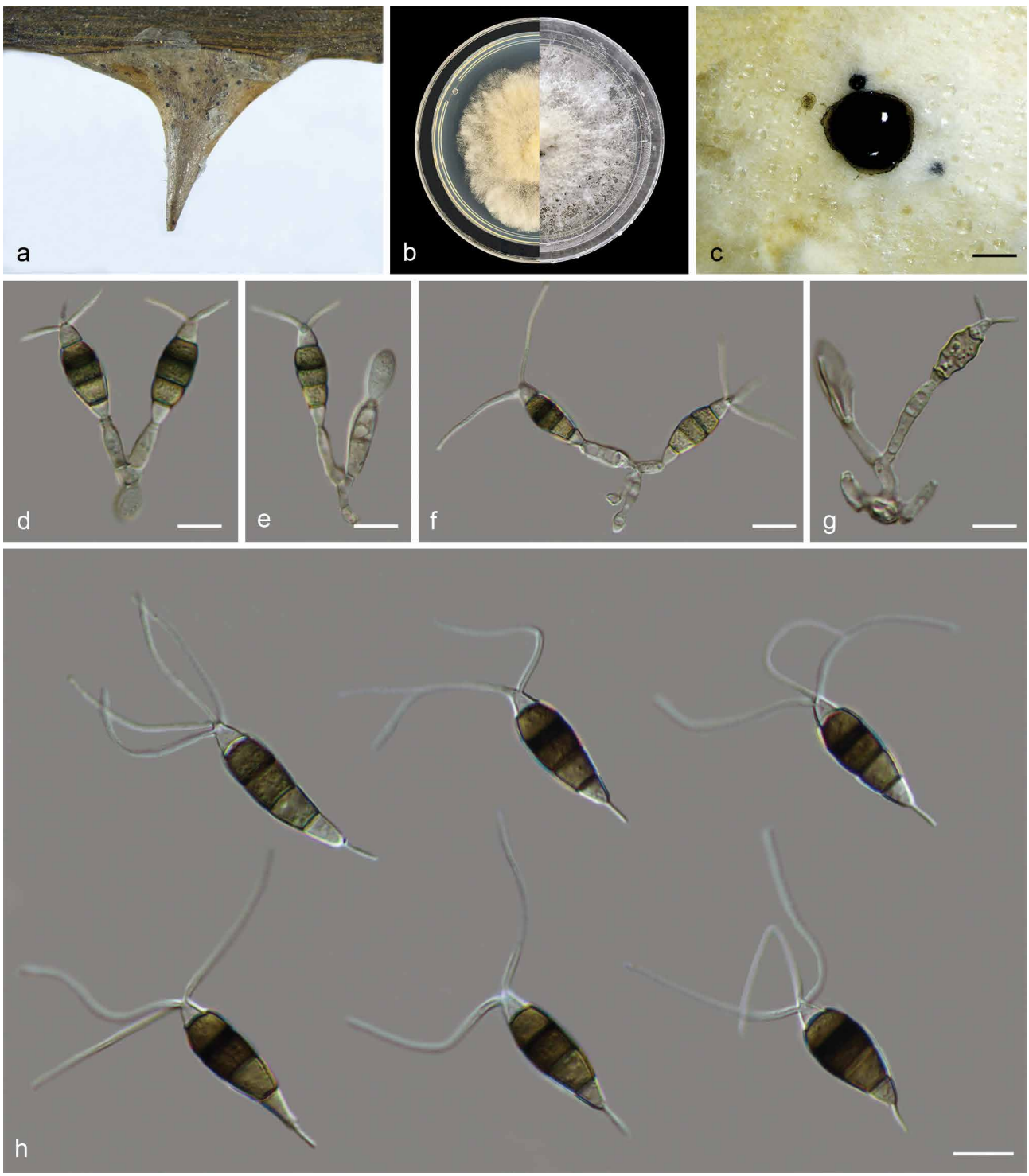

Fig. 11 *Neopestalotiopsis subepidermalis* (BJFC-S1879, holotype). a. Appearance of conidiomata on host substrate; b. colonies on PDA at 3 d (left) and 15 d (right); c. conidiomata on PDA; d–g. conidiogenous cells with attached conidia; h. conidia. — Scale bars: c = 200 µm; d–h = 10 µm.

flared, cylindrical, hyaline to subhyaline, (5.5–)6–18(–18.5) × 3–5 µm (av. = 11.2 ± 2.90 × 3.8 ± 0.60 µm). *Conidia* fusoid, ellipsoid, straight to slightly curved, 4-septate, (19.5–)20–25(–26) × 7.5–9(–9.5) µm (av. = 22.6 ± 2.10 × 8.4 ± 0.95 µm); basal cell conic to obconic with a truncate base, hyaline and thin-walled, 4.0–5.5 µm (av. = 4.6 ± 0.64 µm) long; three median cells doliiform, 14–16 µm (av. = 15.0 ± 1.06 µm) long, wall rugose, versicoloured, septa darker than the rest of the cell, second cell from the base pale brown, (4.5–)5–6 µm (av. = 5.7 ± 0.44 µm) long; third cell honey brown, (4.5–)5–6 µm (av. = 5.4 ± 0.36 µm) long; fourth cell brown, (3.5–)4–5 µm (av. = 4.5 ± 0.72 µm) long; apical cell 3–3.5(–4) µm (av. = 3.2 ± 0.27 µm) long, hyaline, cylindrical, thin- and smooth-walled; with 2–4 tubular apical appendages, branched or unbranched, filiform, (26.5–)27–32.5(–33.5) µm (av. = 29.2 ± 1.79 µm) long; basal appendage single, tubular, unbranched, centric, (6.5–)7–7.5(–8) µm (av. = 7.3 ± 0.58 µm) long.

Culture characteristics — Colonies on PDA with aerial mycelium white, fluffy, reverse yellowish pigment accumulation in the centre, surrounded by amber, pure white at the colony margin, reaching at 58–60 mm diam in 15 d at 28 °C. Conidiomata globose, irregularly distributed on the medium surface, exuding globose, dark brown to black conidial masses.

Additional materials examined. China, Henan Province, Xinyang City, Jigong Mounta, N31°49'20" E114°32'6", alt. 220.1 m , on spines of *R. chinensis*, 5 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1880, cultures CFCC 55161 = ROC 169, ROC 170); Henan Province, Xinyang City, Shihe District, N31°49'23" E114°3'24", alt. 199.6 m, on branches and spines of *R. chinensis*, 5 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1881, cultures ROC 171, ROC 172, ROC 173, ROC 174).

Notes — The eight strains of *N. subepidermalis* in the present study form a well-supported independent clade distinct from known *Neopestalotiopsis* species (ML/MP/BI = 87/84/0.98). *Neopestalotiopsis subepidermalis* is most closely related to *N. camelliae-oleiferae*, *N. mesopotamica*, *N. rosae* and *N. vacciniicola* (Fig. 4), but differs from them in concatenated alignment. A comparison of the ITS region showed one nucleotide difference (453/454, 99.7 % with two gaps) with *N. camelliae-oleiferae*, three nucleotide differences (526/529, 99.4 % with a single gap) with *N. mesopotamica*, two nucleotide differences (524/526, 99.6 % with no gaps) with *N. rosae*, one nucleotide differences (519/520, 99.8 % with a single gap) with *N. vacciniicola*. Comparison of the *TEF* region revealed 15 bp differences (520/535, 97.1 % with no gaps) with *N. camelliae-oleiferae*, three bp differences (469/472, 99.5 % with no gaps) with *N. mesopotamica*, two bp differences (479/481, 99.5 % with no gaps) with *N. rosae*, 13 bp differences (462/475, 97.2 % with no gaps) with *N. vacciniicola*. Comparison of the *TUB* region revealed two bp differences (400/402, 99.5 % with no gaps) with *N. camelliae-oleiferae*, eight bp differences (723/731, 98.9 % with no gaps) with *N. mesopotamica*, 11 bp differences (736/747, 98.5 % with no gaps) with *N. rosae*, seven bp differences (412/419, 98.3 % with no gaps) with *N. vacciniicola*. *Neopestalotiopsis rosae* was also recorded from *Rosa*, but the morphological characteristics of *N. rosae*, in which the apical appendages do not arise from the apical crest are distinct from *N. subepidermalis* and other taxa in this genus (Maharachchikumbura et al. 2014). In addition, *N. subepidermalis* differs from the three other species in the dimensions of its conidia and apical appendages: the conidia of *N. subepidermalis* are shorter than *N. mesopotamica* (20–25 µm vs 26–32 µm), but longer than those of *N. vacciniicola* (20–25 µm vs 14.5–15.2 µm). Furthermore, the apical appendages of *N. subepidermalis* are significantly longer than those of *N. camelliae-oleiferae* (27–32.5 µm vs 15.5–18.5 µm) and *N. vacciniicola* (27–32.5 µm vs 4.3–24.3 µm).

Based on the phylogeny, *N. subepidermalis* is distinct from *N. clavispora*, *N. palmarum*, *N. rosicola* and *N. versicolor*, the four *Neopestalotiopsis* species associated with *Rosa* besides *N. rosae* (Liu et al. 2010, Feng et al. 2014, Jiang et al. 2018, Vu et al. 2019) (Fig. 4). Furthermore, *N. subepidermalis* differs from *N. clavispora* and *N. versicolor* in having the longer basal appendage (7–7.5 µm vs 3–5.5 µm and 7–7.5 µm vs 2.4–6.8 µm), while *N. subepidermalis* has longer apical appendages than *N. rosicola* and *N. palmarum* (27–32.5 µm vs 17–22.8 µm and 27–32.5 µm vs 11.8–18.9 µm).

Key to Neopestalotiopsis species on Rosa spp.

1. Conidial width less than 6 µm 2
1. Conidial width more than 6 µm 3
2. Conidia 14–18.5 × 4.5–5 µm, apical appendage 19–26 µm long . . . . . *N. concentrica*
2. Conidia 19–23.6 × 5.6–6.6 µm, apical appendage 11.8–18.9 µm long . . . . . *N. palmarum*
3. Basal appendages less than 5.5 µm 4
3. Basal appendages more than 5.5 µm 5
4. Conidia 20–24 × 6–8 µm, apical appendages 22–32 µm . . . . . *N. clavispora*
4. Conidia 21.2–28.3 × 7.1–8.3 µm, apical appendage 18.9–30.7 µm long . . . . . *N. versicolor*
5. Apical appendages do not arise from the apical crest . . . . . *N. rosae*
5. Apical appendages arise from the apical crest 6
6. Conidia 20.2–25.5 × 5.5–8.0 µm, apical appendages 17.0–22.8 µm . . . . . *N. rosicola*
6. Conidia 20–25 × 7.5–9 µm, apical appendages 27–32.5 µm . . . . . *N. subepidermalis*

Pestalotiopsis chamaeropis Maharachch. et al., Stud. Mycol. 79: 158. 2014 — Fig. 12

Sexual morph not observed. Asexual morph: *Acervular conidiomata* globose or irregular, superficial to semi-immersed, scattered or aggregated, visible as black acervuli on the host. *Conidiophores* septate, branched, subcylindrical, hyaline, verruculose. *Conidiogenous cells* discrete, cylindrical, hyaline, smooth-walled, collarette present and not flared, with prominent periclinal thickening, (5.5–)7–8.5(–10) × 2–4(–4.5) µm (av. = 7.6 ± 1.32 × 3.4 ± 0.66 µm). *Conidia* fusoid, ellipsoid, straight to slightly curved, 4-septate, (25–)26–27.5(–28) × 7–8.5(–9) µm (av. = 27 ± 0.54 × 7.9 ± 0.56 µm); basal cell obconic with a truncate base, hyaline, thin-walled, 4.5–5.5(–6) µm (av. = 5.1 ± 0.36 µm) long; three median cells doliiform to subcylindrical, (15–)16.5–17(–18) µm (av. = 16.7 ± 0.52 µm) long, wall verruculose, concolourous, but occasionally the two upper median cells are slightly darker than the lower median cell, brown, second cell from the base 3.5–6(–6.5) µm (av. = 5.2 ± 0.81 µm) long, third cell (3–)5–6(–6.5) µm (av. = 5.4 ± 0.35 µm) long, fourth cell (3.5–)5.5–6(–6.5) µm (av. = 5.7 ± 0.42 µm) long; apical cell 3.5–5(–6) µm (av. = 4.4 ± 0.57 µm) long, hyaline, subcylindrical, thin- and smooth walled; with 2–3 tubular apical appendages (mostly three), arising from the apical crest, unbranched, filiform, variable in size, 6–24(–24.5) µm (av. = 16.4 ± 3.66 µm) long; basal appendage single, tubular, unbranched, centric, 5.5–8(–8.5) µm (av. = 6.7 ± 1.07 µm) long.

Culture characteristics — Colony on PDA with fluffy mycelium, panniform, aerial mycelium white, reverse white or light yellow, being yellow at the centre and white at the edge. Colony 60–66 mm diam in 15 d at 28 °C. Conidiomata globose, irregularly distributed on the medium surface, exuding globose, dark brown to black conidial masses.

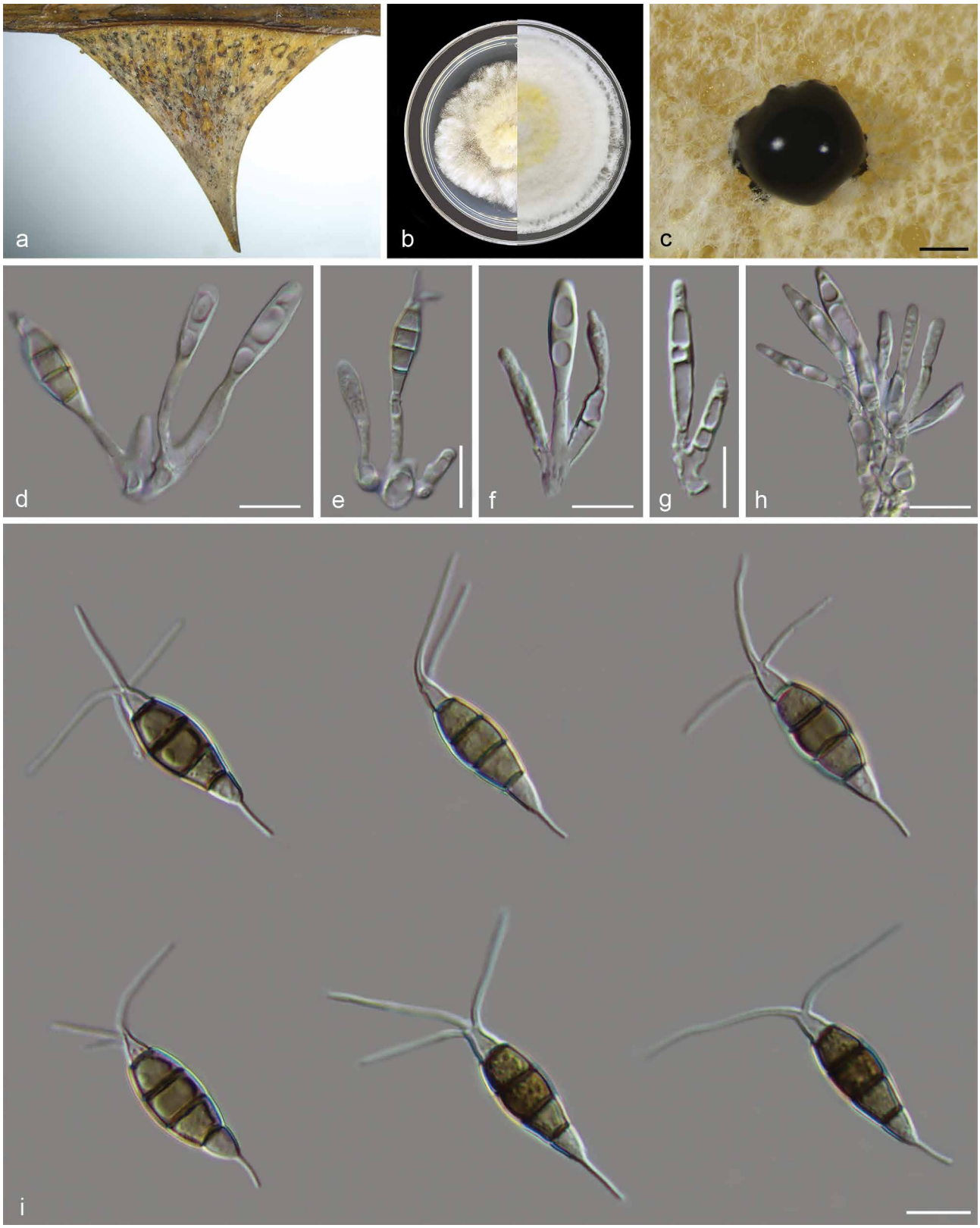

Fig. 12 *Pestalotiopsis chamaeropis* (BJFC-S1885). a. Appearance of conidiomata on host substrate; b. colonies on PDA at 3 d (left) and 15 d (right); c. conidiomata on PDA; d–i. conidiogenous cells with attached conidia; j. conidia. — Scale bars: c = 200 µm; d–i = 10 µm.

Materials examined. China, Gansu Province, Tianshui City, Maiji District, Maiji Mountain, N34°20'35" E106°0'22", alt. 1509 m, on spines of *R. chinensis*, 18 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1885, cultures CFCC 55156 = ROC 23-1, ROC 270, ROC 272, ROC 273, ROC 275); Gansu Province, Tianshui City, Maiji District, Maiji Mountain, N34°20'52" E106°0'16", alt. 1508 m, on spines of *R. chinensis*, 18 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1886, cultures CFCC 55157 = ROC 23-2, ROC 276, ROC 278, ROC 279, ROC 280); Gansu Province, Tianshui City, Maiji District, Maiji Mountain, N34°20'17" E106°0'36", alt. 1500 m, on spines of *R. chinensis*, 19 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1887, cultures ROC 281, ROC 282, ROC 283, ROC 286); ibid. (cultures ROC 289, ROC 290, ROC 292, ROC 293).

Notes — *Pestalotiopsis chamaeropis* was first described from leaves of *Chamaerops humilis* in Italy and subsequently reported on a wide range of hosts (e.g., *Camellia sinensis*, *Pieris japonica*, *Prostanthera rotundifolia*, *Vandopsis* spp. and *Vitis vinifera*) (Maharachchikumbura et al. 2014, Moslemi & Taylor 2015, Liu et al. 2017, Ran et al. 2017, Jayawardena

et al. 2018, Nozawa et al. 2019, Wang et al. 2019b). In this study, 18 isolates clustered together with the ex-type culture of *Pes. chamaeropis* (CBS 186.71) in the multi-locus phylogenetic tree (Fig. 5). This is the first report of this fungus on *R. chinensis*. Compared with the description of the ex-type isolate CBS 186.71, CFCC 55156 has smaller conidiogenous cells (7–8.5 × 2–4 µm vs 20–50 × 2–5 µm).

Pestalotiopsis rhodomyrtus Y. Song et al., Phytotaxa 126: 27. 2013 — Fig. 13

Sexual morph not observed. Asexual morph: *Acervular conidiomata* globose or irregular. superficial to semi-immersed, scattered or aggregated, visible as black acervuli on the host, 86–99 µm. *Conidiophores* branched, subcylindrical, hyaline. *Conidiogenous cells* discrete, cylindrical or ampulliform, hyaline, smooth-walled, collarette present and not flared, with prominent periclinal thickening, (5–)6.5–10(–11.5) × (1.5–)2–3 µm (av. = 8.4 ± 1.35 × 2.7 ± 0.67 µm). *Conidia* fusoid, ellipsoid, straight to slightly curved, 4-septate, (17.5–)19–26 × (5–)5.5–6.5(–7) µm (av. = 22.7 ± 1.21 × 5.9 ± 0.52 µm); basal cell obconic with a truncate base, hyaline, minutely verruculose and thin-walled, 3–5(–5.5) µm (av. = 4.2 ± 0.52 µm) long; three median cells doliiform to subcylindrical, (11–)12–18.5(–19.5) µm (av. = 14.9 ± 1.46 µm) long, wall verruculose, concolourous, pale brown, second cell from the base (3–)4.5–5.5 µm (av. = 4.8 ± 0.36 µm) long, third cell (3–)3.5–5(–5.5) µm (av. = 4.6 ± 0.54 µm), fourth cell 4–5.5(–6) µm (av. = 4.9 ± 0.38 µm); apical cell (3–)3.5–5.5 µm (av. = 4.4 ± 0.85 µm) long, hyaline, cylindrical to subcylindrical, thin and smooth walled; with 2–3 tubular apical appendages (mostly three), arising from the apical crest, unbranched, filiform, flexuous, (9–)11.5–20(–21.5) µm (av. = 15.7 ± 1.58 µm) long; one basal appendage, tubular, centric appendage tubular, branched or unbranched, (5.5–)6–7.5 µm (av. = 6.9 ± 1.74 µm) long.

Culture characteristics — Colonies on PDA flat with entire margin, aerial mycelium white, cottony, fluffy; reverse white in the centre and faint yellow margin, colony diam 59–63 mm

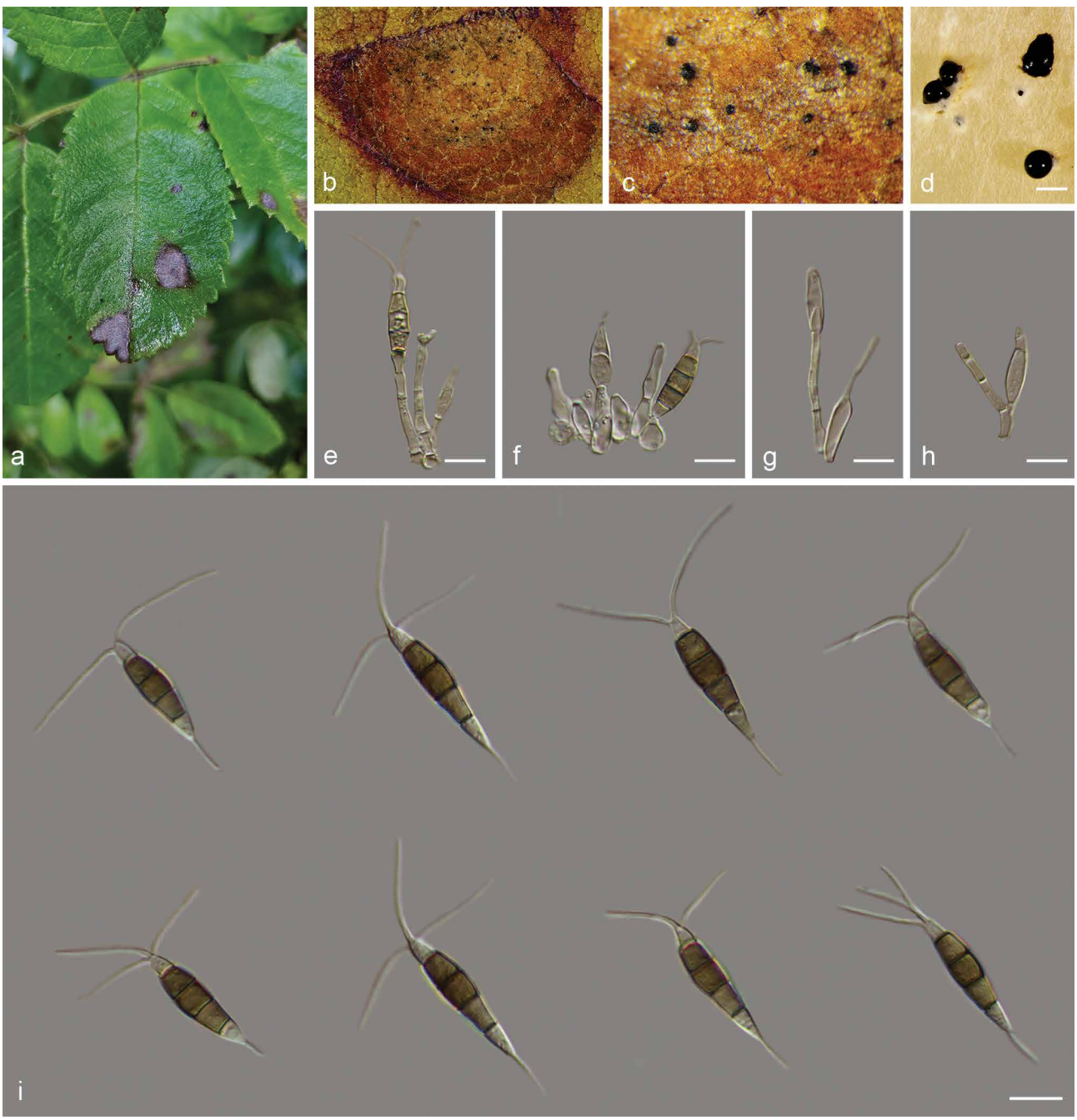

Fig. 13 *Pestalotiopsis rhodomyrtus* (BJFC-S1888). a. Disease symptoms; b–c. appearance of conidiomata on host substrate; d. conidiomata on PDA; d–h. conidiogenous cells with attached conidia; i. conidia. — Scale bars: d = 200 µm; e–i = 10 µm.

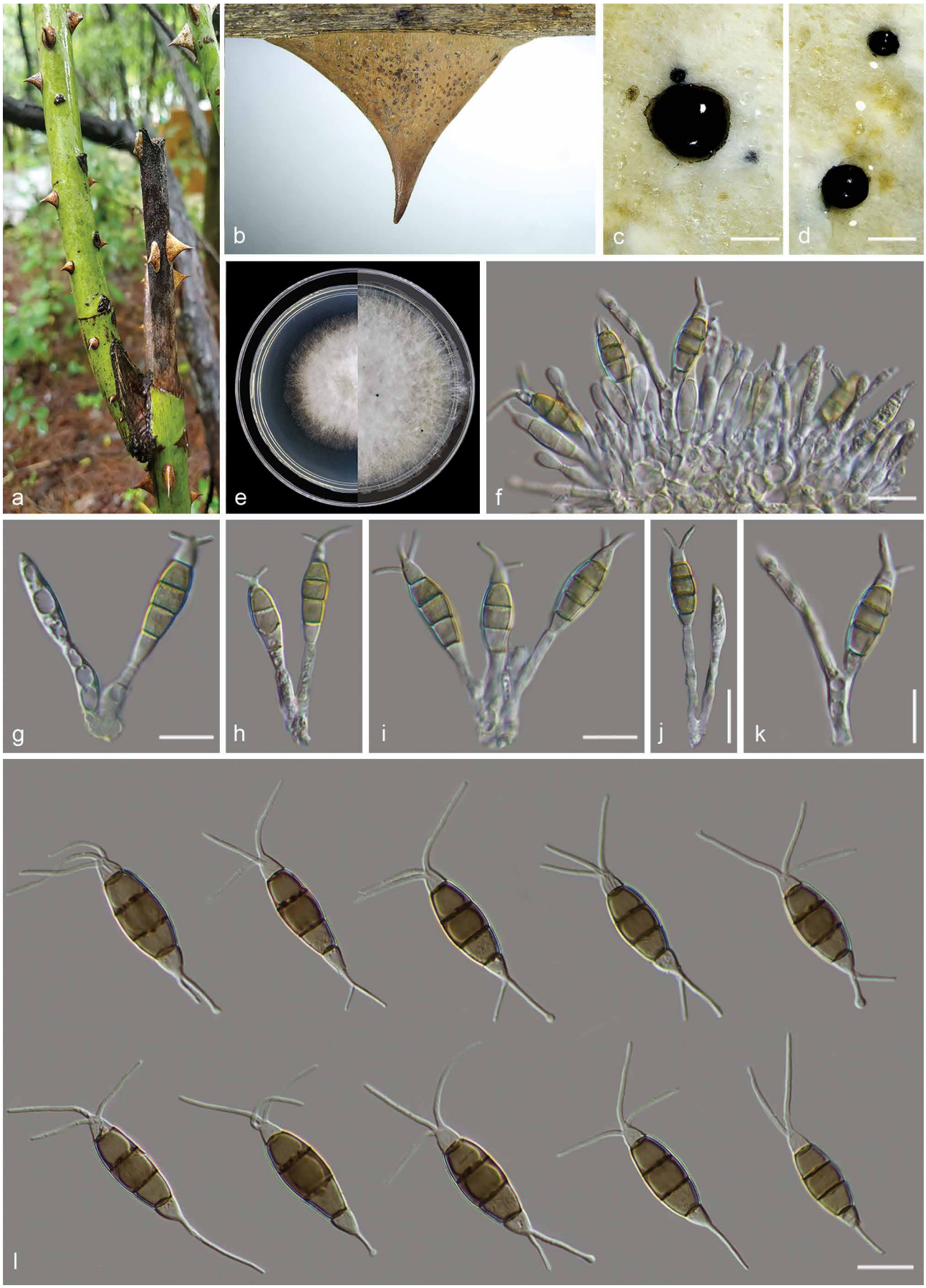

Fig. 14 *Pestalotiopsis tumida* (BJFC-S1891 holotype). a. Disease symptoms; b. appearance of conidiomata on host substrate; c–d. conidiomata on PDA; e. colonies on PDA at 3 d (left) and 15 d (right); f. conidiomata on *Rosa chinensis*; g–k. conidiogenous cells with attached conidia; l. conidia. — Scale bars: c–d = 200 µm; f–l = 10 µm.

diam in 15 d. Conidia in mass black. Conidiomata globose, irregularly distributed on the medium surface, exuding globose, black conidial masses.

Materials examined. China, Henan Province, Nanyang City, Neixiang county, Mahuang Village, N33°20'14" E114°52'1", alt. 266 m, on leaves of *R. rugosa*, 7 Aug. 2020, *Y.M. Liang* & *C. Peng* (BJFC-S1888, cultures ROC 056, ROC 057, ROC 058); ibid. (cultures ROC 059, ROC 060, ROC 061, ROC 062); Gansu Province, Gannan Tibetan Autonomous Prefecture, Lintan County, Yeliguan, N34°53'48" E103°35'2", alt. 2740 m, on spines of *R. multiflora*, 18 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1889, cultures ROC 303, ROC 304, ROC 305, ROC 306); ibid. (cultures ROC 307, ROC 309, ROC 311); Hunan Province, Changsha City, Changsha County, N28°58'52" E113°34'38", alt. 61 m, on branches of *R. chinensis*, 10 Nov. 2020, *C.M. Tian* & *N. Jiang* (BJFC-S1890, cultures ROC 356, ROC 357, ROC 358, ROC 359).

Notes — *Pestalotiopsis rhodomyrtus* was initially described from *Rhodomyrtus tomentosa* in Guangxi Province, China (Song et al. 2013). In addition, this species was discovered on *Camellia sinensis* (Liu et al. 2017, Wang et al. 2019a). In this study, 18 isolates were identified as belonging to this species (Fig. 5) and this is the first report of this fungus on the host genus *Rosa*.

Compared with the description of the ex-type isolate HGUP 4230, isolate ROC 056 has longer apical and basal appendages (11.5–20 µm vs 7.5–14.9 µm and 6–7.5 µm vs 2.8–4.9 µm).

Pestalotiopsis tumida C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843814; Fig. 14

Etymology. Name refers to the basal appendage that is occasionally swollen at the tip.

Typus. China, Gansu Province, Tianshui City, Maiji District, Maiji Mounta, N34°20'32" E106°0'29", alt. 1601 m, on spines of *R. chinensis*, 15 Aug. 2020, *C. Peng* & *S. Jia* (holotype BJFC-S1891, ex-type cultures CFCC 55158 = ROC 110, ROC 108, ROC 109).

Sexual morph not observed. Asexual morph: *Acervular conidiomata* globose or irregular. superficial to semi-immersed, scattered or aggregated, visible as black acervuli on the host. *Conidiophores* branched, subcylindrical, hyaline. *Conidiogenous cells* discrete, cylindrical or ampulliform, hyaline, smooth-walled, collarette present and not flared, with prominent periclinal thickening, (7–)8–11.5(–12) × (1.5–)2–4.5 µm (av. = 10.4 ± 2.23 × 2.9 ± 0.83 µm). *Conidia* fusoid, ellipsoid, straight to slightly curved, 4-septate, (19–)19.5–23.5(–24) × 6.5–7.5 µm (av. = 21.4 ± 1.33 × 6.9 ± 0.58 µm); basal cell obconic with a truncate base, hyaline, minutely verruculose and thin-walled, (2.5–)3–4.5 µm (av. = 3.9 ± 0.58 µm) long; three median cells doliiform to subcylindrical, (14–)14.5–18(–18.5) µm (av. = 16.6 ± 1.68 µm) long, wall verruculose, concolourous, light brown, second cell from the base (3.5–)4–5 µm (av. = 4.6 ± 0.36 µm) long, third cell (4–)4.5–6.5 µm (av. = 5.3 ± 0.68 µm), fourth cell (4.5–)5.5 µm (av. = 5.1 ± 0.34 µm); apical cell 4.5–6 µm (av. = 5.1 ± 0.49 µm) long, hyaline, cylindrical to subcylindrical, thin- and smooth walled; with 2–3 tubular apical appendages (mostly three), arising from the apical crest, unbranched, filiform, flexuous, (10–)10.5–15.5(–16) µm (av. = 13.1 ± 2.07 µm) long; 1–2 basal appendages, tubular, centric appendage tubular, branched or unbranched, occasionally swollen at the tip, (6.5–)7–19(–19.5) µm (av. = 10.9 ± 3.44 µm) long, excentric appendage tubular, 6.5–7.5(–8) µm (av. = 7.3 ± 0.26 µm) long.

Culture characteristics — Colonies on PDA with aerial mycelium white, fluffy, reverse yellow pigment accumulation in the centre, surrounded by amber, pure white at the colony margin. Colony 56–60 mm diam in 15 d at 28 °C. Conidiomata globose, irregularly distributed on the medium surface, exuding globose, black conidial masses.

Additional materials examined. China, Gansu Province, Tianshui City, Maiji District, Maiji Mounta, N34°20'36" E106°0'23", alt. 1557 m, on branches and spines of *R. chinensis*, 15 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1892, cultures CFCC 55159 = ROC 234, ROC 235, ROC 236, ROC 237); ibid. (cultures ROC 238, ROC 240).

Notes — *Pestalotiopsis tumida* formed a distinct clade (ML/MP/BI = 100/100/1) in the multi-locus analyses and is sister to *Pes. intermedia* and *Pes. linearis*. *Pestalotiopsis tumida* (Fig. 5) can be distinguished from *Pes. intermedia* and *Pes. linearis* in ITS (two different unique fixed alleles in *Pes. intermedia* (531/533, 99.5 % with a single gap) and two in *Pes. linearis* (536/538, 99.5 % with no gaps)), *TEF* loci (six different unique fixed alleles in *Pes. intermedia* (526/532, 98.6 % with no gaps) and four in *Pes. linearis* (528/532, 99.2 % with no gaps)) and *TUB* loci (10 different unique fixed alleles in *Pes. intermedia* (443/553, 97.7 % with four gaps) and 18 in *Pes. linearis* (415/433, 95.7 % with three gaps)). Moreover, the conidial morphology of *Pes. tumida* is significantly different from these two species. *Pestalotiopsis tumida* differs from *Pes. intermedia* and *Pes. linearis* by shorter conidia (*Pes. tumida*: 19.5–23.5 µm vs *Pes. intermedia*: 24–28 µm, *Pes. linearis*: 24–33 µm). In addition, it is different from *Pes. linearis* in bearing shorter apical appendages (10.5–15.5 µm vs 24–33 µm) and longer basal appendages (7–19 µm vs 4–7 µm).

There are 11 species of *Pestalotiopsis* that have been recorded from *Rosa*, namely *Pes. adusta*, *Pes. algeriensis*, *Pes. aquatica*, *Pes. lespedezae*, *Pes. longisetula*, *Pes. macrochaeta*, *Pes. maculans*, *Pes. oleandri*, *Pes. populi-nigrae*, *Pes. rosae* and *Pes. suffocata* (Riley 1960, Guba 1961, Mathur 1979, Rai 1990, Zhu et al. 1991, Nag Raj 1993, Mendes et al. 1998, Sameva 2004, Wei et al. 2005, Kobayashi 2007, Ge et al. 2009). *Pestalotiopsis tumida* can be easily distinguished from *Pes. adusta*, *Pes. algeriensis*, *Pes. aquatica*, *Pes. longisetula* and *Pes. oleandri* by the colour of its median conidial cells. The median conidial cells of these five species are versicolourous while the three median conidial cells of *Pes. tumida* are concolourous. *Pestalotiopsis tumida* can be distinguished from other *Rosa* associated species by the size of its conidia and length of appendages (Table 4). Furthermore, the basal appendage

Table 4 Synopsis of *Pestalotiopsis* species with concolourous median conidium cells from *Rosa.*

Species	Conidia length (µm)	Conidia width (µm)	Middle cells length (µm)	Length of apical appendages (µm)	Length of basal appendages (µm)	Host	Country	References
Pestalotiopsis lespedezae	20.2–25	7.5–8.8	13.8–17.5	15–27.5	5–6.3	*Rosa canina*	India	Mathur (1979)
Pes. macrochaeta	24.8–33	6.6–7.6	13.0–21.2	15.3–34.2	7.1–11.8	*Rosa* sp.	Brazil	Mendes al. (1998)
Pes. maculans	19–27.5	6–8	10–15.5	16–24	4.2–5	*Rosa* sp.	Bulgaria	Sameva ((2004)
Pes. populi-nigrae	21.2–28.3	7.1–8.3	14.2–16.5	21.2–31.9	2.4–7.1	*Rosa hybrida*	Japan	Kobayashi (2007)
Pes. rosae	20.5–28.8	5–6.3	11.8–16.3	10–25	4–5.3	*Rosa* sp.	China	Ge et al. (2009)
Pes. suffocata	20.8–28.6	5.8–7.1	13.6–18.8	15.6–35.1	1.3–3.5	*Rosa* sp.	China	Ge et al. (2009)
Pes. tumida	**19.5–23.5**	**6.5–7.5**	**14.5–18**	**10.5–15.5**	**7–19**	***Rosa chinensis***	**China**	**Present study**

* Newly described taxon is in **bold**.

of *Pes. tumida* is occasionally swollen at the tip, a unique morphological character that distinguishes it from other species that have been recorded from *Rosa*.

Key to Pestalotiopsis species on Rosa spp.

1. Median conidial cells versicolourous 2
1. Median conidial cells concolourous 6
2. Length of apical appendages less than 12 µm 3
2. Length of apical appendages more than 12 µm 5
3. Basal appendages less than 3.5 µm 4
3. Basal appendages more than 3.5 µm . . *Pes. algeriensis*
4. Conidia not or slightly constricted at the septa, 16–22 × 5–7 µm, apical appendages 5–12 µm . . . . *Pes. adusta*
4. Conidia constricted at the septa, 18.9–28.3 × 4.7–7.1 µm, apical appendages 16.5–28.3 µm . . . . . *Pes. oleandri*
5. Conidia 20.6–28.2 × 7.2–8.2 µm, apical appendages 12.8–23 µm, basal appendages 2–4 µm . . . . . *Pes. aquatica*
5. Conidia 20.6–25.7 × 6.4–7.7 µm, apical appendages 20.6–36 µm, basal appendages 5.1–7.7 µm . *Pes. longisetula*
6. Basal appendages less than 5 µm 7
6. Basal appendages more than 5 µm 9
7. Conidia 3–4-septate . . . . . *Pes. rosae*
7. Conidia 4-septate 8
8. Conidia 21.8–28.3 × 6.6–8.3 µm, apical appendages 21.2–31.9 µm, basal appendages 1.5–3 µm *Pes. populi-nigrae*
8. Conidia 19–27.5 × 6–8 µm, apical appendages 16–24 µm, basal appendages 4.2–5 µm . . . . . *Pes. maculans*
9. Conidial length less than 26 µm 10
9. Conidial length more than 26 µm 12
10. Basal appendages occasionally swollen at the tip . . . . . *Pes. tumida*
10. Basal appendages not occasionally swollen at the tip 11
11. Conidia 19.7–26.3 × 4.9–6.7 µm, apical appendages 7.5–14.9 µm, basal appendages 2.8–4.9 µm . . . . . *Pes. rhodomyrtus*
11. Conidia 20–25 × 7.5–8.5 µm, apical appendages 15–22.5 µm, basal appendages 3.7–7.5 µm *Pes. lespedezae*
12. Basal appendages less than 5.5 µm . . . . *Pes. suffocata*
12. Basal appendages more than 5.5 µm 13
13. On PDA, reverse of colonies cinnamon-rufous, conidia 24.8–33 × 6.6–7.6 µm, apical appendages 15.3–34.2 µm, basal appendages 7.1–11.8 µm . . . . . *Pes. macrochaeta*
13. On PDA, reverse of colonies white, conidia 26–27.5 × 7–8.5 µm, apical appendages 6–24 µm, basal appendages 5.5–8 µm . . . . . *Pes. chamaeropis*

Seimatosporium centrale C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843816; Fig. 15

Etymology. Name refers to conidiomata produced in the centre of the colonies on PDA.

Typus. China, Gansu Province, Tianshui City, Maiji District, Dongcha Town, N34°19'34" E106°34'27", alt. 1120 m, on spines of *R. chinensis*, 16 July 2019, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (holotype BJFC-S1893, ex-type cultures CFCC 55166 = ROC 003, ROC 001, ROC 002).

Sexual morph not observed. Asexual morph: *Acervular conidiomata* solitary to gregarious, immersed to semi-immersed, unilocular, subglobose, visible as black acervuli on the spines of *R. chinensis*. *Conidiophores* branched at the base, hyaline. *Conidiogenous cells* discrete or integrated, cylindrical, subcylindrical or irregular, hyaline, smooth, thick-walled, (6–)7.5–21.5(–23.5) × (2–)2.5–3(–3.5) µm (av. = 14.4 ± 3.23 × 2.7 ± 0.35 µm). *Conidia* straight or slightly curved, fusoid, cylindrical or subcylindrical, concolourous, 3-septate, mostly constricted at the septa, transverse septa fairly thick, smooth-walled, (18.5–)19.5–23.5(–24) × (5–)5.5–7 µm (av. = 20.9 ± 1.58 × 6.1 ± 0.52 µm); basal cell obconic with a truncate base, hyaline to pale brown, (4–)4.5–5.5(–6) µm (av. = 5.0 ± 0.64 µm) long; middle cells cylindrical, pale brown, second cell from base (4–)4.5–5.5 µm (av. = 5.0 ± 0.39 µm), third cell from base (4.5–)5–6(–6.5) µm (av. = 5.4 ± 0.58 µm), together (9.5–)10–11.5(–12) µm (av. = 10.7 ± 0.88 µm) long; apical cell conical, pale brown, (3.5–)4–5 µm (av. = 4.2 ± 0.32 µm); apical appendage single, unbranched, centric, occasionally excentric, 3.5–5.5(–7) µm (av. = 4.9 ± 0.67 µm) long; basal appendage single, unbranched, excentric, (3–)4.5–5(–6) µm (av. = 5.0 ± 0.27 µm) long; mean conidium length/width ratio = 3.40 : 1.

Culture characteristics — Colonies on PDA with aerial mycelium white, dense, reverse with tawny pigment accumulation, being darker at the centre and paler at the edge. Colony 56–58 mm diam in 15 d at 28 °C. Conidiomata are observed around 25 d and are mostly produced in the centre of the colony. Conidiomata globose, exuding black conidial masses.

Additional materials examined. China, Shaanxi Province, Baoji City, Fengxian County, Xinjia Mountain, N34°12'45" E106°36'25", alt. 1609 m, on spines of *R. chinensis*, 16 July 2019, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (BJFC-S1894, cultures CFCC 55169 = ROC 014, ROC 015, ROC 016); Gansu Province, Tianshui City, Maiji District, Maiji Mountain, N34°20'44" E106°0'22", alt. 1601 m, on spines of *R. chinensis*, 15 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1895, cultures ROC 145, ROC 146, ROC 147).

Notes — The nine isolates studied form a well-supported independent clade distinct from known *Seimatosporium* species (ML/MP/BI = 98/96/1). *Seimatosporium centrale* is most closely related to *Seim. botan*, *Seim. discosioides*, *Seim. gracile* sp. nov. and *Seim. nonappendiculatum* sp. nov. (Fig. 6). Among them, *Seim. discosioides* as pathogens occurring on some *Rosaceae* hosts, especially on *Rosa* spp. (Shoemaker 1964, Nag Raj 1993). A pairwise comparison of the ITS sequence showed seven nucleotide differences out of 557 nucleotides (98.7 % similarity, including two gaps) between *Seim. centrale* and *Seim. discosioides*, while LSU showed six nucleotide differences out of 794 nucleotides (99.2 % similarity, without gaps). Meanwhile, *Seim. discosioides* morphologically differs from our new species and other *Seimatosporium* species associated with *Rosa* by the absent of appendages. *Seimatosporium centrale* differs from *Seim. botan* in morphology, namely having wider conidia (5.5–7 µm vs 4–5 µm) and their mean conidium length/width ratio is quite distinct (3.4 : 1 in *Seim. centrale* vs 4.6 : 1 in *Seim. botan*). In addition, *Seim. botan* has two types of conidia (with only basal appendage and both apical and basal appendages) while *Seim. centrale* has only one conidial type (both apical and basal appendages). Furthermore, *Seim. centrale* can be distinguished from *Seim. gracile* by its extremely high mean conidium length/width ratio (3.40 : 1 vs 6.19 : 1) and from *Seim. nonappendiculatum* by the colour of its basal cell (pale brown vs hyaline).

Besides *Seim. discosioides*, four species of *Seimatosporium* have been recorded from *Rosa*, namely *Seim. caninum*, *Seim. pseudorosae*, *Seim. salicinum* and *Seim. rosae* (Nag Raj 1993, Kobayashi 2007, Mułenko et al. 2008, Norphanphoun et al. 2015, Hyde et al. 2016). *Seimatosporium centrale* has larger conidia than *Seim. pseudorosae* and *Seim. rosae* (19.5–23.5 × 5.5–7 µm vs 12–17.5 × 3–6 µm and 19.5–23.5 × 5.5–7 µm vs 10–16 × 3–4.5 µm). However, the apical appendages of *Seim. centrale* are noticeably shorter than those of the two species (3.5–5.5 µm vs 8–25 µm and 3.5–5.5 µm vs 1.5–15 µm). *Seimatosporium caninum* and *Seim. salicinum* can be distinguished from *Seim. centrale* based on the number of conidial septa. While *Seim. centrale* has 3-septate conidia, *Seim. salicinum* has 2–3-septate and *Seim. caninum* only has 2-septate conidia (Wanasinghe et al. 2018).

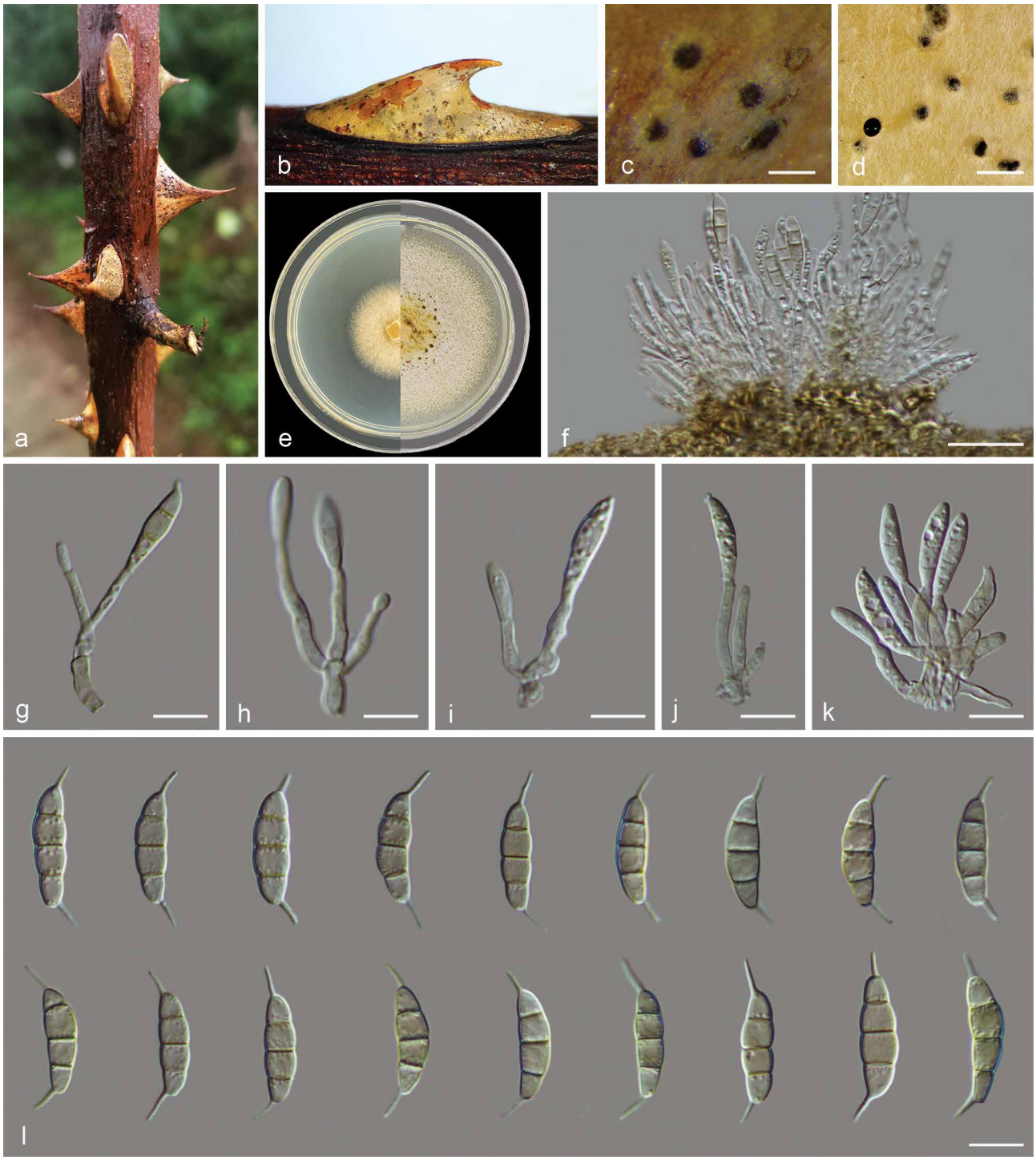

Fig. 15 *Seimatosporium centrale* (BJFC-S1893, holotype). a–b. Disease symptoms; c. appearance of conidiomata on host substrate; d. conidiomata on PDA; e. colonies on PDA at 3 d (left) and 15 d (right); f. longitudinal section through conidiomata; g–k. conidiogenous cells with attached conidia; l. conidia. — Scale bars: c–d = 200 µm; f = 20 µm; g–l = 10 µm.

Seimatosporium gracile C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843818; Fig. 16

Etymology. From Latin 'gracile' means slender/slim, which refers to the shape of the conidia.

Typus. China, Gansu Province, Tianshui City, Qingshui county, Shidong Mountain, N34°41'4" E106°21'34", alt. 1697 m, on spines of *R. xanthina*, 17 July 2019, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (holotype BJFC-S1896, ex-type cultures CFCC 55167 = ROC 004, ROC 005, ROC 006).

Sexual morph not observed. Asexual morph: *Acervular conidiomata* solitary to gregarious, immersed when immature, becoming erumpent at maturity, subglobose, up to 95–337 µm diam, 56–104 µm high, visible as black conidiomata on the spines. *Conidiophores* irregularly branched, mostly branched at the base, 1–3-septate, hyaline. *Conidiogenous cells* discrete or integrated, ampulliform, cylindrical or subcylindrical, hyaline, smooth, thick-walled, variable in size, (7–)8.5–21.5(–23) × 1.5–2(–3) µm (av. = 15.6 ± 3.23 × 1.6 ± 0.18 µm). *Conidia* straight or slightly curved, cymbiform or fusoid, concolourous, 3-septate, barely constricted at the septa, transverse septa dark brown and fairly thick, smooth-walled, (13.5–)14.5–19.5(–20) × 2.5–3(–3.5) µm (av. = 16.7 ± 1.82 × 2.7 ± 0.25 µm); basal cell obconic with or without a truncate base, pale brown to hyaline, (2.5–)3–4(–4.5) µm (av. = 3.6 ± 0.47 µm) long; middle cells cylindrical, pale brown, second cell from base (3–)3.5–4.5 µm (av. = 3.9 ± 0.37 µm), third cell from base 3.5–4(–4.5) µm (av. = 3.8 ± 0.27 µm), together 7–8(–9) µm (av. = 7.7 ± 0.43 µm) long; apical cell conical, pale brown, (2.5–)3–3.5(–4.5) µm

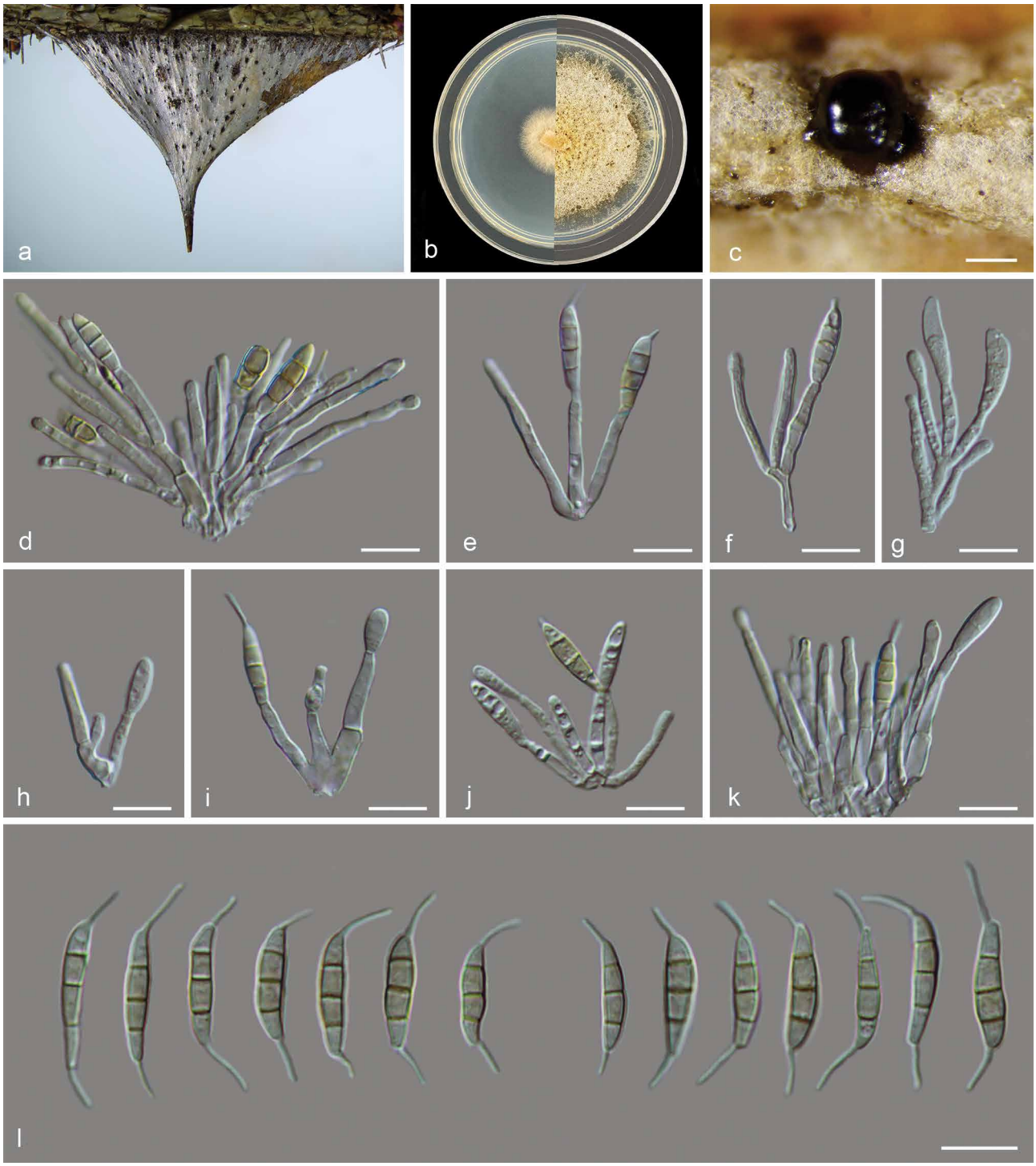

Fig. 16 *Seimatosporium gracile* (BJFC-S1896, holotype). a. Appearance of conidiomata on host substrate; b. colonies on PDA at 3 d (left) and 15 d (right); c. conidiomata formed on pine needles; d–k. conidiogenous cells with attached conidia; l. conidia. — Scale bars: c = 200 µm; d–l = 10 µm.

(av. = 3.2 ± 0.28 µm); apical appendage single, unbranched, centric, (3–)4–8(–8.5) µm (av. = 6.3 ± 1.58 µm) long; basal appendage single, unbranched, excentric, 4.5–8.5(–9) µm (av. = 6.1 ± 1.22 µm) long; mean conidium length/width ratio = 6.19 : 1.

Culture characteristics — Colonies on PDA flat with irregular margin, colony yellow or pale yellow in the centre with fluffy aerial mycelia and pale white margin; reverse tawny pigment accumulation formed in the shape of a concentric ring pattern. Colony 56–58 mm diam in 15 d at 28 °C. Conidiomata sparse, concentrically and irregularly distributed on the medium surface.

Additional materials examined. China, Gansu Province, Tianshui City, Qingshui county, Shidong mountain, N34°41'4" E106°21'35", alt. 1699 m, on spines of *R. xanthina*, 17 July 2019, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (BJFC-S1897, cultures ROC 007, ROC 008, ROC 009); ibid. (cultures ROC 010, ROC 011, ROC 012).

Notes — *Seimatosporium gracile* forms an independent clade (ML/MP/BI = 100/100/1) and is phylogenetically distinct from *Seim. nonappendiculatum* (described below) (Fig. 6). A comparison of the ITS region showed 0.35 % differences (two bp difference of 566 bp, with one single gap), 0.23 % bp differences (2 bp difference of 846 bp, with no gaps) in the LSU region, 2.1 % bp differences (7 bp difference of 326 bp, with no gaps) in *TEF*, 2.4 % bp differences (11 bp difference of 464 bp, with no gaps) in *TUB* and 0.38 % bp differences (4 bp difference of 1051 bp, with no gaps) in *RPB2*, which is evidence for new species rank. Moreover, the two species are morphologically distinct. *Seimatosporium gracile* differs from *Seim. nonappendiculatum* in the colour of its basal cell and presence or absence of appendages. While *Seim. gracile* has a pale brown basal cell with both apical and basal appendages, *Seim. nonappen-*

Fig. 17 *Seimatosporium nonappendiculatum* (BJFC-S1901, holotype). a–b. Disease symptoms; c. appearance of conidiomata on host substrate; d. conidiomata formed on PDA; e. longitudinal section through conidiomata; f–m. conidiogenous cells with attached conidia; n. conidia. — Scale bars: d = 200 µm; e = 20 µm; f–n = 10 µm.

diculatum has a hyaline basal cell with no appendages or only basal appendage. Furthermore, the typical characteristic of *Seim. gracile* is that the conidia are slender and has a markedly higher mean conidial length/width ratios (6.19 : 1) than other species that have been recorded from *Rosa* in this genus.

Seimatosporium nonappendiculatum C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843820; Fig. 17

Etymology. Referring to conidia lacking an apical appendage.

Typus. China, Ningxia Hui Autonomous Region, Guyuan City, Jingyuan County, N35°23'53" E106°22'33", alt. 1786 m, on fruits of *R. laevigata*, 29 Aug. 2020, *C. Peng* (holotype BJFC-S1901, ex-type cultures CFCC 55168 = ROC 377, ROC 378).

Symptoms are marked by slightly collapsed lesions, with regular margin, black dark brown, round spots on fruits (Fig. 19a–c). Sexual morph not observed. Asexual morph: *Acervular conidiomata* solitary to gregarious, subglobose, globose or irregular, up to 287–436 µm diam, 135–160 µm high. *Conidiophores* cylindrical, branched at the base, 1–3-septate, hyaline, smooth-walled. *Conidiogenous cells* discrete or integrated, ampulliform, cylindrical or subcylindrical, hyaline, smooth, thick-walled, variable in size, (5–)6.5–13.5(–16) × (1.5–)2–2.5(–3) µm (av. = 9.9 ± 2.21 × 2.3 ± 0.25 µm). *Conidia* straight or curved, fusoid or pyriform, 3-septate, distoseptate or euseptate, with or without constrictions at the septa, transverse septa dark brown and fairly thick, smooth-walled, (17–)18–23.5(–24) × (5–)5.5–7 µm (av. = 20.3 ± 1.47 × 6.4 ± 0.52 µm); basal cell obconic with a truncate base, hyaline or almost hyaline, (3–)3.5–4.5 µm (av. = 3.9 ± 0.39 µm) long; middle cells cylindrical, pale to medium brown, second cell from base 3–5(–5.5) µm (av. = 4.3 ± 0.32 µm), third cell from base (3.5–)4–4.5(–5) µm (av. = 4.3 ± 0.44 µm), together (7–)8–10(–11) µm (av. = 8.7 ± 0.32 µm) long; apical cell obtuse or conical, pale brown, (3–)4.5–5.5 µm (av. = 4.8 ± 0.31 µm); apical appendage absent; basal appendage lacking or, when present, single, unbranched, excentric, 1.5–4 µm (av. = 2.9 ± 0.93 µm) long; mean conidium length/width ratio = 3.17 : 1.

Culture characteristics — Colonies on PDA flat with entire margin, colony yellow or pale yellow in the centre with fluffy aerial mycelia and pale white margin; reverse with yellow pigment. Colony 50–52 mm diam in 15 d at 25 °C. Conidiomata sparse, concentrically and irregularly distributed on the medium surface.

Additional material examined. China, Ningxia Hui Autonomous Region, Guyuan City, Jingyuan County, N35°23'53" E106°22'36", alt. 1788 m, on fruits of *R. laevigata*, 29 Aug. 2020, *C. Peng* (BJFC-S1902, cultures ROC 379, ROC 380, ROC 381).

Notes — *Seimatosporium nonappendiculatum* forms an independent clade (ML/MP/BI = 89/93/1) and is phylogenetically distinct from *Seim. gracile* (Fig. 6). The differences between *Seim. nonappendiculatum* and *Seim. gracile* have been mentioned above (see *Seim. gracile*).

Seimatosporium nonappendiculatum is characterised by its fusoid to pyriform, 3-septate conidia with a hyaline basal cell, lacking an apical appendage or with an excentric basal appendage. These morphological characteristics can easily distinguish *Seim. nonappendiculatum* from other *Seimatosporium* species previously reported from *Rosa*. *Seimatosporium botan* which was collected from *Paeonia suffruticosa* in Japan also has two types of conidia (Hatakeyama & Harada 2004). *Seimatosporium botan* can produce conidia with only one basal appendage which morphologically resembles our new *Seimatosporium* species, but *Seim. botan* has longer basal appendages (4–8 µm vs 1.5–4 µm) and larger mean conidium length/width ratio (4.6 : 1 vs 3.17 : 1). The other conidial type of *Seim. botan* bears appendages at both ends, which is very different from the conidia of *Seim. nonappendiculatum*. Besides *Seim. botan*, *Seim. grammitum*, *Seim. hebeiense* and *Seim. hysterioides* produce conidia with only a basal appendage (Shoemaker 1964, Hatakeyama & Harada 2004). *Seimatosporium nonappendiculatum* can be distinguished from these three species by its larger conidia (18–23.5 × 5.5–7 µm vs 12–18.5 × 3.5–5.5 µm, 18–23.5 × 5.5–7 µm vs 13.5–17.6 × 4.5–6.5 µm and 18–23.5 × 5.5–7 µm vs 12–18 × 5.5–6.5 µm). *Seimatosporium pseudoglandigenum* produces conidia without appendages which morphologically resemble the other conidial type of *Seim. nonappendiculatum* (Wijayawardene et al. 2016a). However, the conidia of *Seim. pseudoglandigenum* only has one conidial type. Although *Seim. nonappendiculatum* is similar to *Seim. pseudoglandigenum* in conidial size (18–23.5 × 5.5–7 µm vs 15–23 × 5–8 µm), *Seim. pseudoglandigenum* can be distinguished from our new species based on the colour of its apical conidial cells. While *Seim. nonappendiculatum* has pale brown apical cells and the apical cell is heterochromatic to the basal cells, *Seim. pseudoglandigenum* has hyaline apical cells and the apical cell is concolourous to the basal cells (Wijayawardene et al. 2016a).

Seimatosporium parvum C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843819; Fig. 18, 19

Etymology. From Latin parva 'small', referring to smaller conidia.

Typus. China, Qinghai Province, Huangnan Tibetan Autonomous Prefecture, Zeku County, N37°18'51" E101°56'34", alt. 2890 m, on spines of *R. spinosissima*, 12 July 2019, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (holotype BJFC-S1898, ex-type cultures CFCC 55164 = ROC 038, ROC 039, ROC 040).

Sexual morph: *Ascomata* 52–155 µm high × 102–254 µm diam, black, immersed, solitary or gregarious, fully or partly erumpent, globose, uniloculate. *Ostiole* 6.5–16.5 µm, single, dark grey to black. *Peridium* 22–68 µm wide, comprising 2 layers, outer most layer heavily pigmented, thick-walled, comprising dark brown cells of *textura angularis*, inner layer composed of hyaline, flattened cells of *textura angularis*. *Pseudoparaphyses* numerous, 1.6–2.7 µm wide, filamentous, branched. *Asci* (86.5–)91.5–99(–102.5) × (9–)10–11(–12.5) µm (av. = 96.7 ± 4.13 × 10.6 ± 1.16 µm), 8-spored, bitunicate, fissitunicate, clavate to cylindrical. *Ascospores* (21–)23.5–29(–30.5) × (3–)4.5–6(–7) µm (av. = 26.4 ± 2.21 × 5.4 ± 1.01 µm), overlapping biseriate, fusiform with narrow ends, mostly curved, 4–5-septate, constricted at the central septum, cells above central septum swollen, (3.5–)4.5–5.5(–6) × (4–)4.5–6 µm (av. = 5.1 ± 0.37 × 5.5 ± 1.02 µm). Asexual morph: *Acervuli conidiomata* solitary to gregarious, immersed when immature, becoming erumpent at maturity, unilocular, subglobose, up to 133–262 µm diam, 80–121 µm high, visible as black acervuli on the spines of *R. spinosissima*. *Conidiophores* cylindrical, branched at the base, smooth. *Conidiogenous cells* discrete or integrated, ampulliform, cylindrical or subcylindrical, hyaline, smooth, thick-walled, variable in size, (7–)9.5–24.5(–26.5) × (1–)1.5–2(–2.5) µm (av. = 16.5 ± 3.23 × 1.7 ± 0.97 µm). *Conidia* straight or slightly curved, cylindrical or subcylindrical, concolourous, 3-septate, without constrictions at the septa, transverse septa dark brown and fairly thick, smooth-walled, (10–)11–13.5(–14) × (2–)2.5–3.5(–4) µm (av. = 12.3 ± 0.51 × 2.9 ± 0.25 µm); basal cell obconic with a truncate base, pale brown to brown, (2–)2.5–3.5(–4) µm (av. = 2.6 ± 0.32 µm) long; middle cells cylindrical, pale brown to medium brown, second cell from base 2–3(–3.5) µm (av. = 2.7 ± 0.27 µm), third cell from base 2–3(–4) µm (av. = 2.4 ± 0.36 µm), together (5.5–)6–7(–8) µm (av. = 6.4 ± 0.41 µm) long; apical cell obtuse or conical, pale brown, (2–)2.5–3.5 µm (av. = 3.1 ± 0.31 µm); apical appendage single,

Fig. 18 Sexual morph of *Seimatosporium parvum* (BJFC-S1898, holotype). a. Disease symptoms; b. appearance of ascomata on host substrate; c–d. longitudinal section through ascomata; e. asci and pseudoparaphyses; f–g. asci; h–i. ascospores. — Scale bars: c–d = 50 µm; f–k = 10 µm.

unbranched, centric, (17–)19.5–22.5(–23) µm (av. = 21.3 ± 2.13 µm) long; basal appendage single, unbranched, excentric, (18–)19.5–28.5(–30) µm (av. = 25.8 ± 2.32 µm) long; mean conidium length/width ratio = 3.95 : 1.

Culture characteristics — Colonies on PDA flat with entire margin, colony yellow or pale yellow in the centre with fluffy aerial mycelia and pale white margin; reverse with yellow pigment. Colony 54–58 mm diam in 15 d at 28 °C. Conidiomata sparse, concentrically and irregularly distributed on the medium surface.

Additional materials examined. China, Qinghai Province, Huangnan Tibetan Autonomous Prefecture, Zeku County, N37°18'60" E101°56'43", alt. 2899 m, on spines of *R. spinosissima*, 12 July 2019, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (BJFC-S1899, cultures ROC 041, ROC 042, ROC 043); ibid., N37°18'56" E101°56'09", alt. 2910 m, on branches of *R. helenae*, 13 July 2019, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (BJFC-S1900, cultures CFCC 55165 = ROC 017, ROC 018, ROC 019, ROC 020).

Notes — *Seimatosporium parvum* is most closely related to *Seim. pseudorosae* which has also been reported from *Rosa* (Hyde et al. 2016) (Fig. 6). Pairwise comparison of the LSU sequence data reveals 7 bp difference from 668 (98.7 %, without gap region) between this species and *Seim. pseudorosae.* Moreover, morphological differences between *Seim. parvum* and *Seim. pseudorosae* are obvious, namely *Seim. parvum* have smaller conidia (11–13.5 × 2.5–3.5 µm vs 12–17.5 × 4–6 µm). Furthermore, the basal appendages of *Seim. parvum* are longer than those of *Seim. pseudorosae* (19.5–28.5 µm vs 6–15 µm).

In addition to *Seim. pseudorosae*, *Seim. parvum* is separated from *Seim. rosae* which has also been reported from *Rosa* based on phylogenetic analysis (Norphanphoun et al. 2015) (Fig. 6). Furthermore, *Seim. parvum* differs from other *Seimatosporium* species associated with *Rosa* in producing thinner conidia (*Seim. parvum*: 2.5–3.5 µm vs *Seim. salicinum*: 4–6 µm and *Seim. rosae*: 3–4.5 µm) and having longer apical appendage (*Seim. parvum*: 19.5–22.5 µm vs *Seim. salicinum*: 9–14 µm and *Seim. rosae*: 5–10 µm). Although *Seim. caninum* is similar to *Seim. parvum* in conidial dimensions (9.5–12 × 4–5 µm vs 11–13.5 × 2.5–3.5 µm), the conidia of this species only have two septa and lack appendages, which make *Seim. caninum* easily distinguishable from other species of *Seimatosporium* (Nag Raj 1993).

Fig. 19 Asexual morph of *Seimatosporium parvum* (BJFC-S1898, holotype). a. Appearance of conidiomata on host substrate; b. appearance of conidiomata on host substrate; c. conidiomata formed on pine needles; d. colonies on PDA at 3 d (left) and 15 d (right); e–l. conidiogenous cells with attached conidia; m. conidia. — Scale bars: c = 200 µm; e–m = 10 µm.

Key to Seimatosporium species on Rosa spp.

1. Conidia lacking appendages 2
1. Conidia with appendages at both ends 3
2. Conidia 2-septate . . . . . *Seim. caninum*
2. Conidia 3-septate . . . . . *Seim. discosioides*
3. Appendages less than 8 µm 4
3. Appendages more than 8 µm 7
4. Conidia with appendages at both ends 5
4. Conidia without apical appendage, with or without basal appendage . . . . . *Seim. nonappendiculatum*
5. Conidial length more than 15 µm 6
5. Conidial length less than 15 µm . . . . . *Seim. rosae*
6. Mean conidium length/width ratio = 3.40 : 1, conidia 19.5–23.5 × 5.5–7 µm . . . . . *Seim. centrale*
6. Mean conidium length/width ratio = 6.19 : 1, conidia 14.5–19.5 × 2.5–3 µm . . . . . *Seim. gracile*
7. Mean conidium length/width ratio less than 6 8
7. Mean conidium length/width ratio more than 6 . . . . . *Seim. parvum*
8. Conidia 3-septate, 12–17.5 × 3–6 µm *Seim. pseudorosae*
8. Conidia 2–3-septate, 11–17 × 4–6 µm . . . *Seim. salicinum*

Seiridium rosae C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843821; Fig. 20

Etymology. The epithet reflects the name of the host plant genus *Rosa.*

Typus. China, Ningxia Hui Autonomous Region, Guyuan City, Jingyuan County, N35°18'52" E106°21'53", alt. 2157 m, on branches of *R. rugosa*, 27 Aug. 2020, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (holotype BJFC-S1903, ex-type cultures CFCC55174 = ROC 208, ROC 209).

Symptoms appeared as elongate and ovoid, red or dark red, raised, dehiscent lesions on twigs or branches (Fig. 20a–c). Sexual morph not observed. Asexual morph: *Acervular conidiomata* irregularly scattered over the surface, solitary to gregarious, immersed when immature, erumpent from tissue at maturity, subglobose to globose and occasionally irregular. *Conidiophores* septate, cylindrical, irregularly branched, mostly branched at the base. *Conidiogenous cells* discrete, hyaline, subcylindrical to cylindrical, smooth- and thin-walled, the size varies tremendously, (8–)12–64.5(–70) × (1–)1.5–2(–3) µm (av. = 27.8 ± 15.43 × 1.7 ± 0.16 µm). *Conidia* fusoid, straight or slightly curved, 5-septate, not striate, distoseptate without pores, bearing one or two basal and one or more apical appendages, (29–)31–35(–36.5) × (7–)8–9.5 µm (av. = 32.6 ± 0.83 × 8.8 ± 0.47 µm); basal cell obconic, hyaline, smooth-walled, with marginal frill, (3–)3.5–4.5 µm (av. = 4.1 ± 0.63 µm); four median cells brown, smooth-walled, cylindrical to doliiform; second cell from base (4–)5.5–6.5(–7) µm (av. = 6.1 ± 0.21 µm); third cell (3–)4–5.5(–6) µm (av. = 4.9 ± 0.52 µm); fourth cell (3–)3.5–5.5(–6.5) µm (av. = 4.7 ± 0.68 µm), fifth cell (4–)6–7.5 µm (av. = 6.5 ± 0.48 µm), together (18–)20.5–24.5(–26) µm (av. = 22.8 ± 2.65 µm); apical cell conical, hyaline, smooth-walled, (3–)3.5–5.5(–7) µm (av. = 4.1 ± 1.05 µm) long; apical appendages single or multiple, centric, branched or unbranched, occasionally swollen at the tip, (27–)28.5–44.5(–46) µm (av. = 35.3 ± 4.68 µm); 1–2 basal appendages (mostly two), cylindrical, centric, occasionally excentric, unbranched or branched, (2–)3–4.5 µm (av. = 3.7 ± 0.55 µm).

Culture characteristics — Colony on PDA with flattened mycelium, white, smoke grey in the centre, reverse with pale yellow pigments formed in concentric pattern. Colony 36–40 mm diam in 15 d at 25 °C, with concentrically distributed conidiomata.

Additional materials examined. China, Ningxia Hui Autonomous Region, Guyuan City, Jingyuan County, N35°18'52" E106°21'55", alt. 2158 m, on branches of *R. rugosa*, 27 Aug. 2020, *C.M. Tian*, *Y.M. Liang* & *C. Peng* (cultures CFCC 55175 = ROC 267, ROC 268).

Notes — *Seiridium rosae* clustered in a well-supported independent clade (ML/MP/BI = 100/100/1) closely related to *Seir. aquaticum* and *Seir. venetum* (Fig. 7). *Seiridium rosae* can be distinguished from *Seir. venetum* in ITS (19 bp difference from 463 characters, with 95.8 % similarity, including 28 gaps) and *TUB* (7 bp difference from 365 characters, with 98.1 % similarity, including no gaps) sequences. Pairwise comparison of the ITS sequence data reveals 49 bp difference from 526 (90.6 % similarity, including 10 gaps) between our new species and the *Seir. aquaticum*. *Seiridium rosae* is distinct from *Seir. aquaticum* by its branched appendages, while *Seir. aquaticum* has conidia bearing single, short and unbranched appendage (Luo et al. 2019). Additionally, *Seir. rosae* has thinner conidia (8–9.5 µm vs 12–14 µm) and longer basal appendages (the basal appendages of *Seir. aquaticum* reduced to marginal frills) than *Seir. aquaticum* (Luo et al. 2019). *Seiridium venetum* can also produce conidia with branched apical appendages (Nag Raj 1985), but this species can be distinguished from *Seir. rosae* based on conidial dimensions (31–35 × 8–9.5 µm vs 20–30 × 6.5–8.5 µm).

Seiridium rosae morphologically resembles *Seir. pezizoides* (basionym: *Pestalotia pezizoides*) which was isolated from *Vitis* sp. in Italy and the USA having 5-distoseptate conidia with one or more, branched or unbranched apical appendages (Nag Raj 1985). However, *Seir. rosae* differs from *Seir. pezizoides* in having longer apical appendages (28.5–44.5 µm vs 8.5–27 µm) and shorter basal appendages (3–4.5 µm vs 5.5–14 µm). Besides, the conidia of *Seir. rosae* mostly bear two basal appendages while *Seir. pezizoides* only has one basal appendage (Nag Raj 1985, Marin-Felix et al. 2019). *Seiridium rosae* is also morphologically distinct from other *Seridium* species associated with *Rosa* (i.e., *Seir. marginatum* and *Seir. rosarum*) (Jaklitsch et al. 2016, Wanasinghe et al. 2018). *Seiridium rosae* differs from *Seir. marginatum* in having smaller conidia (31–35 × 8–9.5 µm vs 38–42 × 8.8–10.2 µm), and differs from *Seir. rosarum* in having larger conidia (31–35 × 8–9.5 µm vs 22–28 × 7–9 µm) and longer conidiogenous cell (12–64.5 µm vs 5–20 µm) (Jaklitsch et al. 2016, Wanasinghe et al. 2018).

Key to Seiridium species on Rosa spp.

1. Conidia with one or more, branched or unbranched apical appendages . . . . . *Seir. rosae*
1. Conidia with one unbranched apical appendage 2
2. Conidia 38.2–42 × 8.8–10.2 µm, appendages up to 52 µm long . . . . . *Seir. marginatum*
2. Conidia 22–28 × 7–9 µm, appendages up to 12 µm long . . . . . *Seir. rosarum*

Sporocadus brevis C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843822; Fig. 21

Etymology. The Latin 'brevis' meaning short, which refers to the conidial size.

Typus. China, Gansu Province, Gannan Tibetan Autonomous Prefecture, Lintan County, Yeliguan, N34°53'43" E103°35'2", alt. 2808 m, on spines of *R. spinosissima*, 21 Aug. 2020, *C. Peng* & *S. Jia* (holotype BJFC-S1904, ex-type cultures CFCC 55170 = ROC 091, ROC 092, ROC 093).

Sexual morph not observed. Asexual morph: *Acervular conidiomata* solitary to gregarious, mostly irregular or subglobose, erumpent through the surface of bark when mature, up to 187–251 µm diam, visible as black acervuli on the spines. *Conidiophores* septate, branched at base, smooth, hyaline, mostly reduced to conidiogenous cells. *Conidiogenous cells* discrete or integrated, lageniform, filiform or ampulliform, sometimes irregular, hyaline, smooth, without annellations, (2.5–)3.5–19(–21) × 1–2(–2.5) µm (av. = 8.2 ± 3.62 × 1.6 ± 0.24 µm). *Conidia* straight or slightly curved, fusoid or obovoid, pale brown, mostly 2-septate, rarely 3-septate, septa fairly thick-walled and darker than

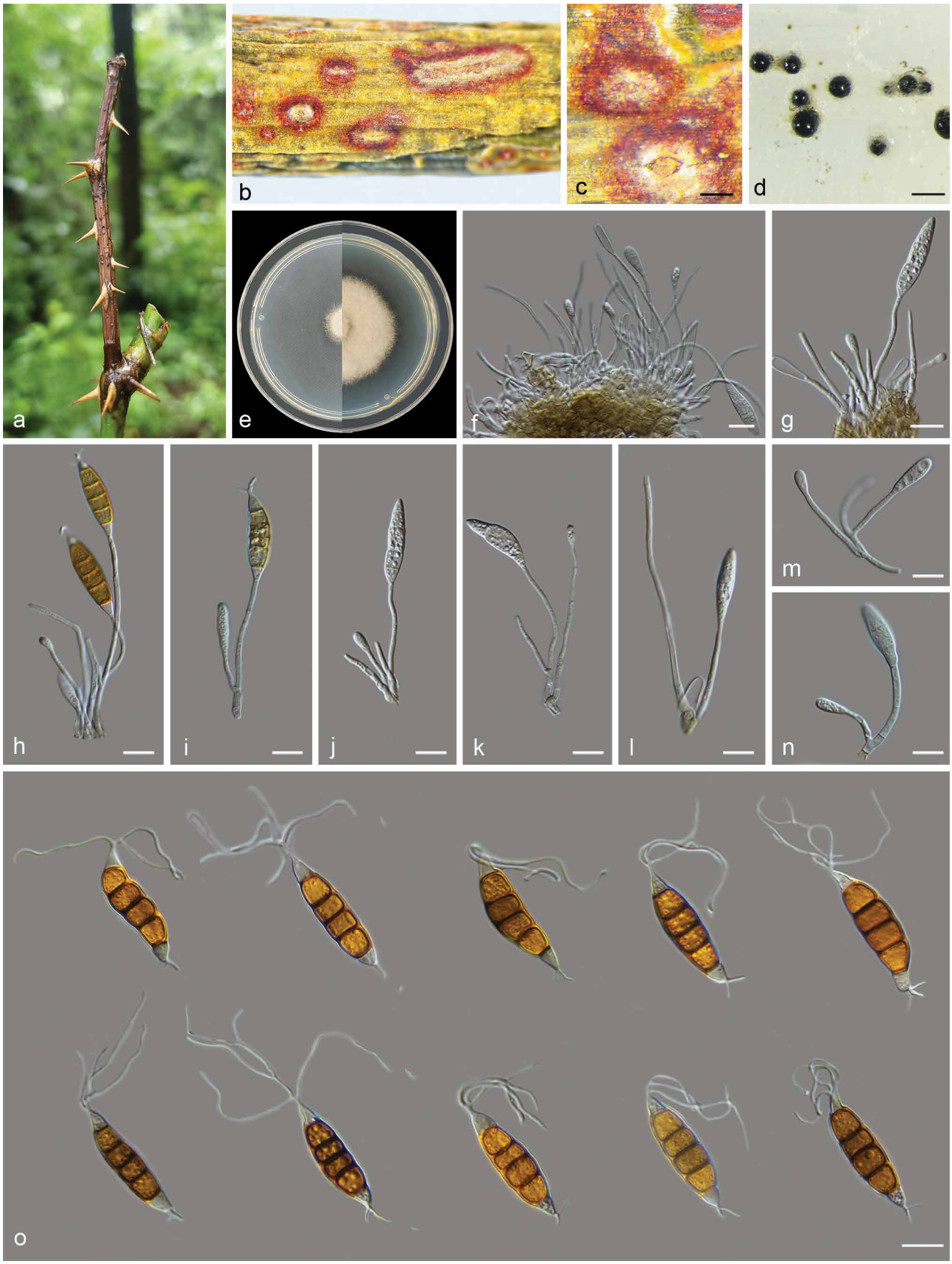

Fig. 20 *Seiridium rosae* (BJFC-S1903, holotype). a–b. Disease symptoms c. appearance of conidiomata on host substrate; d. conidiomata on PDA; e. colonies on PDA at 3 d (left) and 15 d (right); f–g. conidiomata on *Rosa rugosa*; h–n. conidiogenous cells with attached conidia; o. conidia. — Scale bars: c–d = 200 µm; h–o = 10 µm.

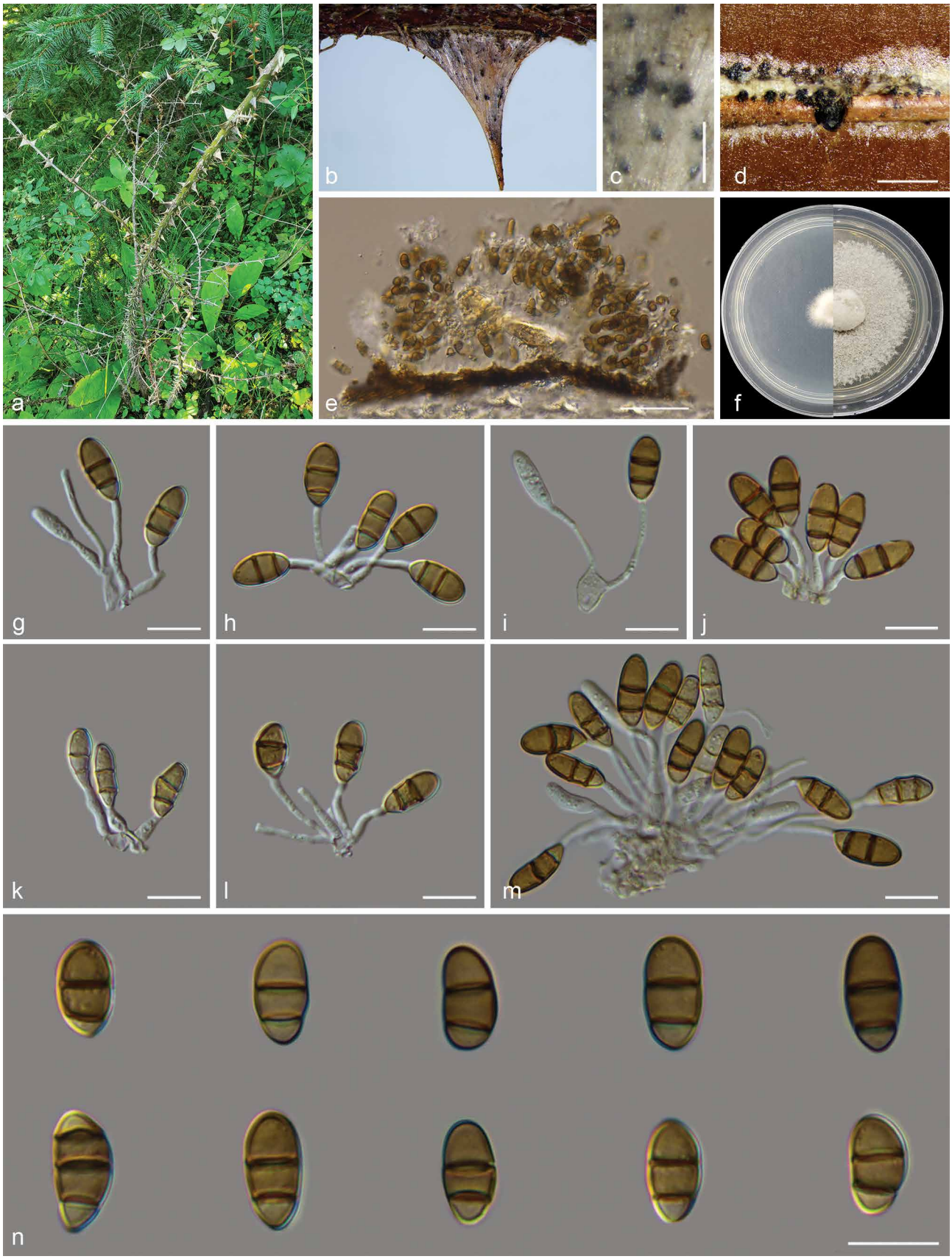

Fig. 21 *Sporocadus brevis* (BJFC-S1904, holotype). a. Disease symptoms; b–c. appearance of conidiomata on host substrate; d. conidiomata formed on pine needles; e. longitudinal section through conidiomata; f. colonies on PDA at 3 d (left) and 15 d (right); g–m. conidiogenous cells with attached conidia; n. conidia. — Scale bars: c–d = 200 µm; e = 50 µm; g–n = 10 µm.

the rest of the cell, wall smooth and occasionally slightly constricted at the septa, (9–)10–12(–12.5) × (6–)6.5–7(–7.5) µm (av. = 11.3 ± 0.74 × 6.4 ± 0.22 µm), lacking appendages; basal cell obconic with or without a truncate base, hyaline to pale brown, thick-walled, shorter than other cells, 1.5–3.5(–4) µm (av. = 2.4 ± 0.47 µm) long; median cells doliiform, each (2–)3–4.5(–5) µm (av. = 3.7 ± 0.43 µm) long, pale to mid-brown; apical cell (2.5–)3–5(–5.5) µm (av. = 4.2 ± 0.68 µm), short conic with a wide round apex, concolourous with the median cell in 2-septate conidia paler than median cells in 3-septate conidia; mean conidium length/width ratio = 1.76 : 1.

Culture characteristics — Cultures on PDA with aerial mycelium white, fluffy, reverse with a mottled tawny pigment. Colony 54–56 mm diam in 15 d at 28 °C. Conidiomata sparse and distributed irregularly on the medium surface.

Additional material examined. China, Gansu Province, Gannan Tibetan Autonomous Prefecture, Lintan County, Yeliguan, N34°53'48" E103°35'2", alt. 2806 m, on spines of *R. spinosissima*, 21 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1905, cultures ROC 094, ROC 095).

Notes — *Sporocadus brevis* is introduced based on multigene phylogenetic analysis, with five isolates clustering separately in a well-supported clade (ML/MP/BI = 100/100/1) (Fig. 8). *Sporocadus brevis* is most closely related to *Spo. trimorphus*, which was isolated from *R. canina* in Sweden (Liu et al. 2019), but distinguished based on ITS, *RPB2*, *TEF* and *TUB* loci from *Spo. trimorphus* by 34 bp in the concatenated alignment, in which 2 bp are distinct in the ITS region (from 506 characters, with 99.6 % sequence identity, including 1 gap), 5 bp in the *RPB2* region (from 832 characters, with 99.3 % sequence identity, no gaps), 11 bp in the *TEF* region (from 468 characters, with 97.6 % sequence identity, including 1 gap) and 16 bp in the *TUB* region (from 702 characters, with 97.7 % sequence identity, including 1 gap). Morphologically, *Spo. trimorphus* can produce conidia with appendages but the conidia of *Spo. brevis* lack appendages (Liu et al. 2019). Moreover, conidia of *Spo. brevis* are wider than those of *Spo. trimorphus* (6.5–7 µm vs 3–4.5 µm).

Fig. 22 *Sporocadus sorbi* (BJFC-S1906). a–b. Appearance of conidiomata on host substrate; c. conidiomata on PDA; d–g. conidiogenous cells with attached conidia; h. conidia. — Scale bars: c = 200 µm; d–h = 10 µm.

In addition to *Sporocadus trimorphus*, *Spo. lichenicola*, *Spo. rosarum* and *Spo. rosigena* are also associated with *Rosa* spp. (Wanasinghe et al. 2018, Liu et al. 2019). *Sporocadus brevis* can be easily distinguished from these species by the conidial length (10–12 µm in *Spo. brevis* vs 18–25 µm in *Spo. lichenicola*) and width (6.5–7 µm in *Spo. brevis* vs 4–6 µm in *Spo. rosarum*, 3.5–6.5 µm in *Spo. rosigena*). Furthermore, the mean conidium length/width ratio of *Spo. brevis* is smaller than these four species (*Spo. brevis*: 1.76 : 1 vs *Spo. lichenicola*: 3 : 1, *Spo. rosarum*: 2.24 : 1, *Spo. rosigena*: 2.4 : 1 and *Spo. trimorphus*: 3.4 : 1).

Sporocadus sorbi (Wijayaw. et al.) F. Liu et al., Stud. Mycol. 92: 404. 2019 — Fig. 22

Sexual morph not observed. Asexual morph: *Acervular conidiomata* solitary to gregarious, mostly subglobose, immersed to semi-immersed, up to 390–420 µm diam, 121–130 µm high, visible as black or dark red acervuli on the stems. *Conidiophores* septate, mostly branched at base, hyaline, smooth. *Conidiogenous cells* discrete or integrated, sub-cylindrical or lageniform, variable in size, hyaline, smooth, with annellations, (7–)12–43.5(–48) × 1.5–2(–2.5) µm (av. = 17.2 ± 9.78 × 1.9 ± 0.34 µm). *Conidia* fusoid or obovoid, straight, 3-septate, transverse septa brown to dark brown, slightly constricted at the septa, wall smooth, (9.5–)11–15.5(–17) × (3–)3.5–5.5(–6) µm (av. = 13.7 ± 1.54 × 4.3 ± 0.21 µm), lacking appendages; basal cell obconic with or without a truncate base, hyaline to pale grey, 2–3(–3.5) µm (av. = 2.7 ± 0.38 µm) long; median cells mostly two, cylindrical, fairly thick-walled and pale brown, each 3–4.5(–5) µm (av. = 4.1 ± 0.54 µm) long; apical cell conic, hyaline or concolourous with median cells, 2–3(–4) µm (av. = 2.6 ± 0.32 µm) long; mean conidium length/width ratio = 3.18 : 1.

Culture characteristics — Colony on PDA with fluffy aerial mycelium, panniform, aerial mycelium white to pale brown, reverse umber coloured, being darker at the centre and paler at the edge. Colony 36–42 mm diam in 15 d at 25 °C. Conidiomata black, distributed circularly at the colony margin on the medium surface.

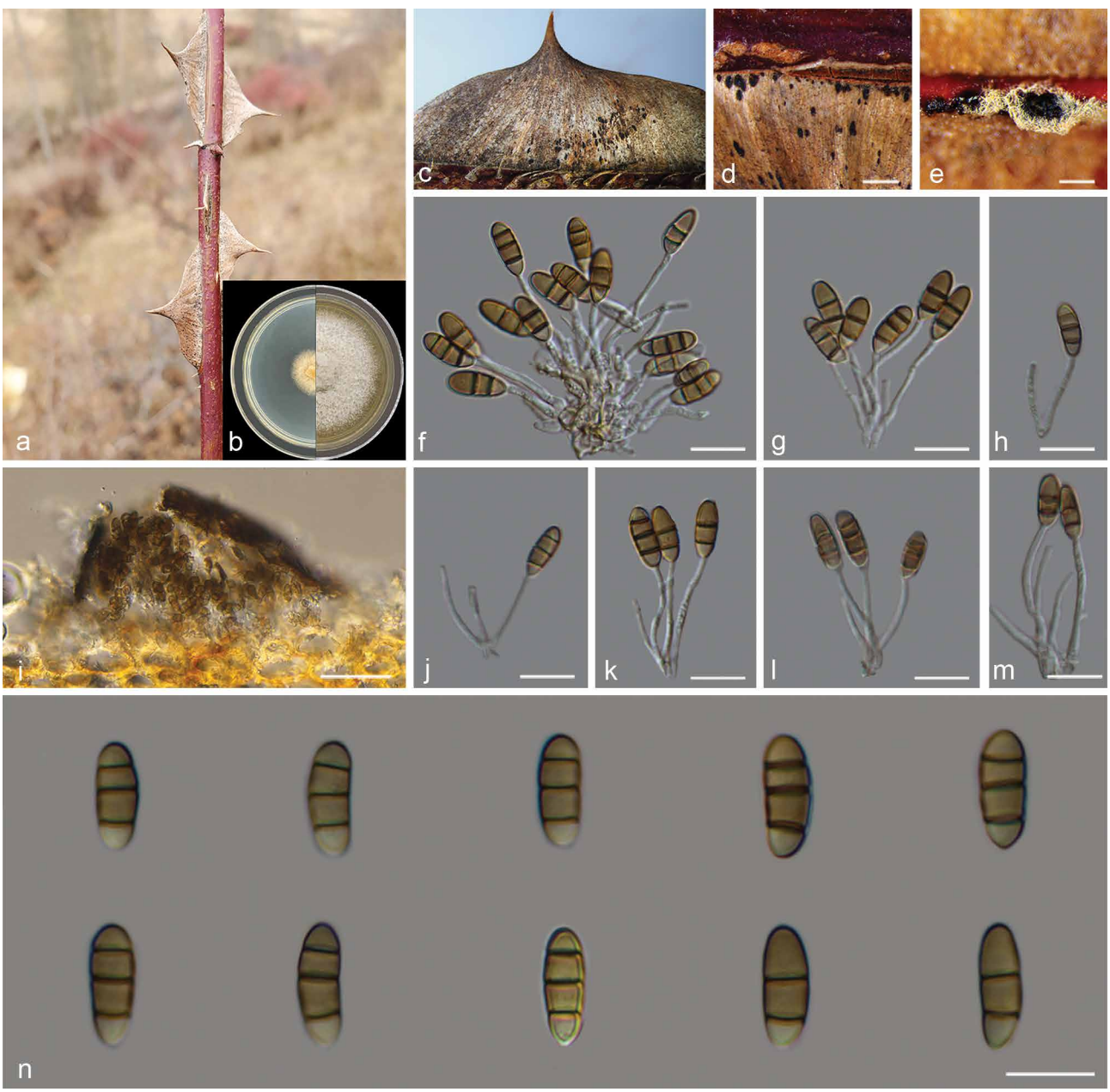

Fig. 23 *Sporocadus spiniger* (BJFC-S1908, holotype). a. Disease symptoms; b. colonies on PDA at 3 d (left) and 15 d (right); c–d. appearance of conidiomata on host substrate; e. conidiomata formed on pine needles; f–h, j–m. conidiogenous cells with attached conidia; i. longitudinal section through conidiomata; n. conidia. — Scale bars: e = 200 µm; f–h, j–m, n = 10 µm; i = 50 µm.

Materials examined. China, Gansu Province, Lanzhou City, Yuzhong County, Xinglong Mountain, N35°48'2" E104°3'57", alt. 2160 m, on branches of *R. xanthina*, 26 Aug. 2020, *C. Peng* (BJFC-S1906, cultures ROC 102, ROC 103, ROC 105); Gansu Province, Gannan Tibetan Autonomous Prefecture, Lintan County, Yeliguan, N34°53'45" E103°35'2", alt. 2806 m, on spines of *R. xanthina*, 21 Aug. 2020, *C. Peng* & *S. Jia* (BJFC-S1907, cultures ROC 159, ROC 160, ROC 161).

Notes — *Sporocadus sorbi* was first reported from a dead leaf of *Sorbus torminalis* in Italy (Lawrence et al. 2018). In this study, six isolates of *Sporocadus* were identified as belonging to this species, and this is the first report of this fungus on *Rosa* plants, and in China.

Conidia of the ex-type (MFLUCC 14-0469) of *Spo. sorbi* are slightly wider than those of isolate ROC 101 (5.5–7.5 µm vs 3.5–5.5 µm), and it has shorter conidiogenous cells (8–20 µm vs 12–43.5 µm).

Sporocadus spiniger C. Peng & C.M. Tian, *sp. nov.* — MycoBank MB 843823; Fig. 23

Etymology. Referring to the fact that this strain was isolated from spines.

Typus. China, Gansu Province, Lanzhou City, Yongdeng County, Dayou Town, N36°44'20" E102°49'27", alt. 2743 m, on spines of *R. omeiensis*, 25 Oct. 2020, *C. Peng* (holotype BJFC-S1908, ex-type cultures ROC 119, ROC 120, ROC 121).

Sexual morph not observed. Asexual morph: *Acervular conidiomata* solitary to gregarious, mostly irregular, occasionally subglobose, superficial to semi-immersed, up to 154–196 µm diam, 61–95 µm high, visible as black acervuli on the spines. *Conidiophores* septate, mostly branched at base, hyaline, smooth. *Conidiogenous cells* discrete, filiform or ampulliform, sometimes cylindrical and subcylindrical, hyaline, smooth, without annellations, (12–)14.5–30.5(–34) × 1–1.5 µm (av. = 23.8 ± 4.27 × 1.2 ± 0.18 µm). *Conidia* straight or slightly curved, clavate or subcylindrical, with round ends, pale brown, (2–)3-septate, septa darker than the rest of cell, wall smooth and slightly constricted at the septa, (12.5–)14.5–16.5(–17.5) × (4–)4.5–5(–5.5) µm (av. = 15.8 ± 0.54 × 4.9 ± 0.31 µm), lacking appendages; basal cell obconic with round base, hyaline to pale brown, paler than other cells, thick-walled, (2–)2.5–3.5(–4) µm (av. = 2.8 ± 0.21 µm) long; median cells doliiform, the second cell from base is slightly longer than the third cell in 3-septate conidia, 3.5–4.5 µm (av. = 4.2 ± 2.17 µm) vs 2.5–3 µm (av. = 2.7 ± 0.16 µm), pale to mid-brown; median cell 4.9–5.0 µm (av. = 5.0 ± 0.07 µm), pale brown in 2-septate conidia; apical cell in 2-septate conidia significantly longer than apical cell in 3-septate conidia, (5.5–)6–6.5 µm (av. = 6.2 ± 0.09 µm) vs (2–)2.5–3.5 µm (av. = 2.7 ± 0.31 µm), short conic with a wide round apex, concolourous with the median cells; mean conidium length/width ratio = 3.22 : 1.

Culture characteristics — Cultures on PDA with white aerial mycelium and regular margin, fluffy, reverse yellowish brown. Colony 48–52 mm diam in 15 d at 25 °C. Acervuli black, distributed irregularly at the colony margin on the medium surface.

Additional material examined. China, Lanzhou City, Yongdeng County, Dayou Town, N36°44'17" E102°49'25", alt. 2745 m, on spines of *R. omeiensis*, 25 Oct. 2020, *C. Peng* (BJFC-S1909, cultures ROC 122, ROC 123, ROC 124, ROC 125).

Notes — Based on the multi-locus phylogenetic analysis, the seven isolates cluster separately in a well-supported clade (ML/MP/BI = 100/100/1) (Fig. 8). *Sporocadus spiniger* is most closely related to *Spo. brevis* and *Spo. trimorphus*, differentiated from them in ITS (three different unique fixed alleles in *Spo. brevis* (521/524, 99.4 % with no gaps) and three in *Spo. trimorphus* (503/506, 99.4 % with no gaps)), LSU loci (four bp in *Spo. brevis* (884/888, 99.5 % with a single gap) and eight bp in *Spo. trimorphus* (876/884, 99.0 % with no gaps)), *RPB2* loci (35 bp in *Spo. brevis* (812/847, 95.8 % with no gaps) and 39 bp in *Spo. trimorphus* (793/832, 95.3 % with no gaps)), *TEF* loci (40 bp in *Spo. brevis* (433/473, 91.5 % with 11 gaps) and 45 bp in *Spo. trimorphus* (427/472, 91.5 % with 11 gaps)) and *TUB* loci (45 bp in *Spo. brevis* (663/708, 93.6 % with 10 gaps) and 41 bp in *Spo. trimorphus* (667/708, 94.2 % with 10 gaps)). Moreover, *Spo. spiniger* differs from *Spo. brevis* in having longer conidia (14.5–16.5 µm vs 10–12 µm) and conidiogenous cells (14.5–30.5 µm vs 3.5–19 µm). The conidia are also wider than those of *Spo. trimorphus* (4.5–5 µm vs 3–4.5 µm).

Other species of *Sporocadus* that have been recorded from *Rosa* can be distinguished from this new species based on the number of septa and presence or absence of appendages. While *Spo. spiniger* has mostly 3-septate conidia without appendages, *Spo. lichenicola* has 4–5-septate conidia and *Spo. rosarum* has conidia with one apical appendage (Liu et al. 2019). *Sporocadus rosigena* mostly has 3-septate conidia without appendages that are morphologically similar to those of *Spo. spiniger* (Liu et al. 2019), but these two species have a distinctly different mean conidium length/width ratio (*Spo. spiniger*: 3.22 : 1 vs *Spo. rosigena*: 2.4 : 1).

Sporocadus trimorphus F. Liu et al., Stud. Mycol. 92: 406. 2018 — Fig. 24

Sexual morph not observed. Asexual morph: *Acervular stromata* ostiolate, immersed or semi-immersed in plant tissues, slightly to strongly erumpent through the bark surface, sometimes delimited by a black or dark red marginal line, up to 207–269 µm diam, 82–144 µm high. *Conidiophores* septate, mostly branched at base, hyaline, smooth. *Conidiogenous cells* discrete or integrated, sub-cylindrical, lageniform or ampulliform, hyaline, smooth, with annellations, (11.5–)13–34(–38.5) × 1.5–2.5 µm (av. = 24.5 ± 6.43 × 2.0 ± 0.31 µm). *Conidia* fusoid or obovoid, straight, 3-septate, transverse septa fairly thick, wall smooth, (11–)12–16 × 4.5–5.5 µm (av. = 14.1 ± 1.22 × 4.8 ± 0.14 µm), bearing appendages; basal cell obconic with or without a truncate base, hyaline to pale brown, 2–3 µm (av. = 2.7 ± 0.41 µm) long; median cells mostly two, cylindrical, fairly thick-walled and pale brown, each (3–)3.5–4.5(–5) µm (av. = 4.1 ± 0.88 µm) long; apical cell conic, hyaline or concolourous with median cells, (1.5–)2–3.5(–4.5) µm (av. = 2.7 ± 0.28 µm) long; apical appendage lacking or, when present, single, unbranched, attenuated, tubular or flexuous, (6.5–)8–13.5 µm (av. = 11.3 ± 1.39 µm) long; basal appendage lacking or, when present, unbranched, tubular or flexuous, centric or excentric, (7–)9–12(–13.5) µm (av. = 10.4 ± 1.27 µm) long; mean conidium length/width ratio = 2.94 : 1.

Culture characteristics — On PDA, colonies initially white, irregular, lacking aerial mycelium, fast growing, reaching up to 60–62 mm diam in 15 d. Colonies pale white to pale grey after 15 d, lacking aerial mycelium. Conidiomata distributed sparsely over the medium surface.

Material examined. China, Gansu Province, Lanzhou City, Yuzhong County, Xinglong Mountain, N35°47'37" E104°3'53", alt. 2168 m, on branches of *R. xanthina*, 25 Aug. 2020, *C. Peng* (BJFC-S1910, cultures CFCC 55171 = ROC 112, ROC 113, ROC 114, ROC 115, ROC 116).

Notes — *Sporocadus trimorphus* was first described from *R. canina* in Sweden (Liu et al. 2019). In this study, five isolates were identified as belonging to this species and this species is also reported for the first time from China. *Sporocadus trimorphus* is characterised by three conidial types, i.e., non-appendaged, either apical or basal appendaged, and both apical and basal appendaged conidia (Liu et al. 2019).

Compared with the description of the ex-type isolate CBS 114203, isolate CFCC 55171 has shorter apical appendages (8–13.5 µm vs 2–20 µm), slightly wider conidia (4.5–5.5 µm vs 3–4.5 µm) and longer conidiogenous cells (13–34 µm vs 4.5–14 µm).

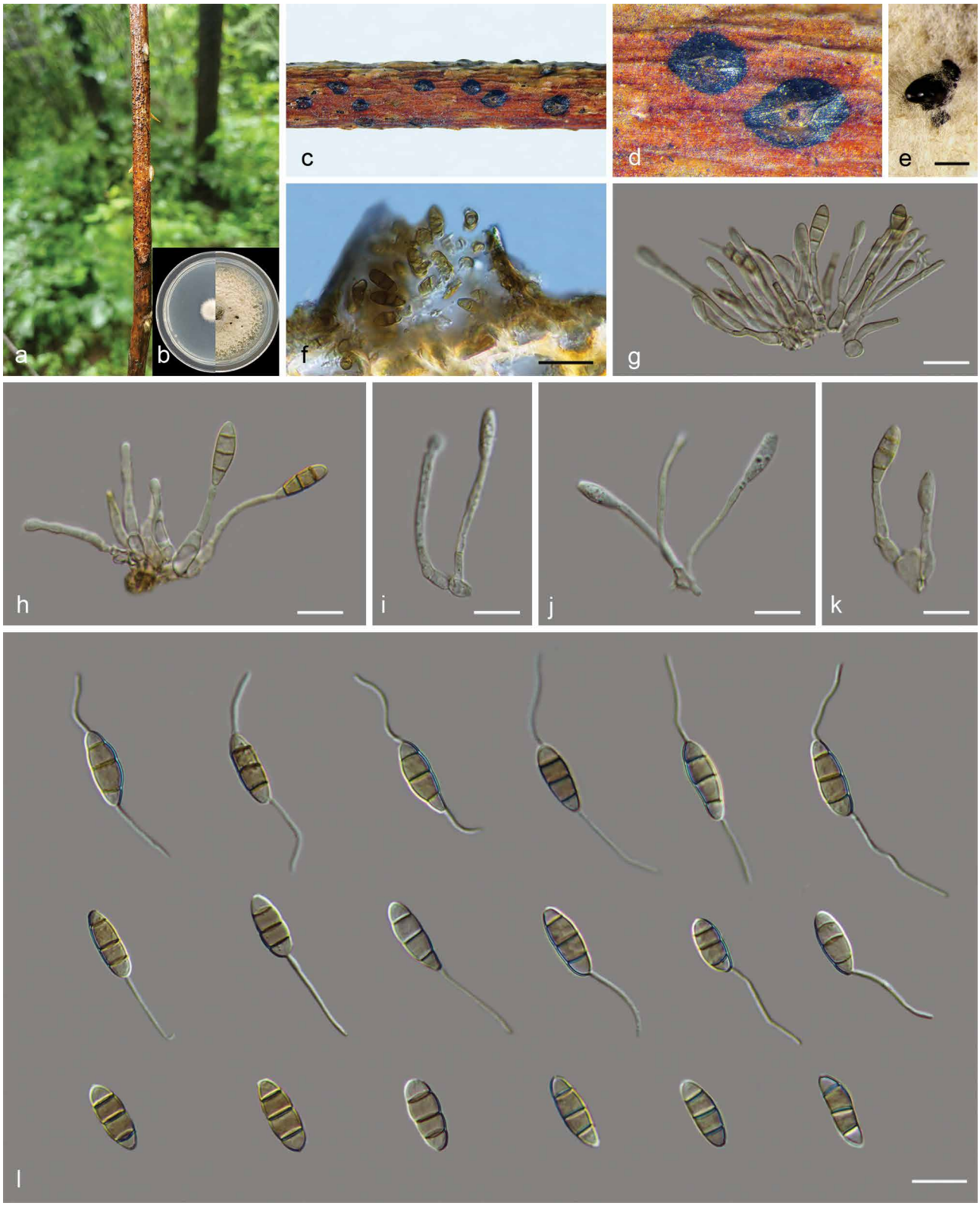

Fig. 24 *Sporocadus trimorphus* (BJFC-S1910). a. Disease symptoms; b. colonies on PDA at 3 d (left) and 15 d (right); c–d. appearance of conidiomata on host substrate; e. conidiomata on PDA; f. longitudinal section through conidiomata; g–k. conidiogenous cells with attached conidia; l. conidia. — Scale bars: e = 200 µm; f = 20 µm; g–l = 10 µm.

Key to Sporocadus species on Rosa spp.

1. Conidia with appendages 2
1. Conidia lacking appendages 6
2. Conidia 3–5-septate . . . . . *Spo. lichenicola*
2. Conidia 3-septate 3
3. Mean conidium length/width ratio less than 3 4
3. Mean conidium length/width ratio more than 3 5
4. Conidia 10–12 × 6.5–7 µm . . . . . *Spo. brevis*
4. Conidia 10–15 × 3.5–6.5 µm . . . . . *Spo. rosigena*
5. Conidia 11–15.5 × 3.5–5.5 µm, conidiogenous cells 11.0–28.5 × 1.0–1.7 µm . . . . . *Spo. sorbi*
5. Conidia 14.5–16.5 × 4.5–5 µm, conidiogenous cells 14.5–30.5 × 1.0–1.5 µm . . . . . *Spo. spiniger*
6. Conidia of two types, i.e., non-appendaged or only basal appendaged . . . . . *Spo. rosarum*
6. Conidia of three types, i.e., non-appendaged, either apical or basal appendaged, or both apical and basal appendaged conidia . . . . . *Spo. trimorphous*

Prevalence

Pestalotiopsis was the most prevalent genus (45 isolates, 35.2 % of the total isolates from *Rosa*), followed by *Seimatosporium* (33 isolates, 26.2 %) and *Sporocadus* (23 isolates, 18.3 %). The isolation rate of the other genera varied from 3.1 % to 13.5 % (Fig. 25). *Pestalotiopsis* was also the most abundant genus in all tissues investigated and had the highest isolation rate from all tissues. *Seiridium* was the genus with the lowest richness among all tissues, isolated only from branches (Fig. 26).

Fifteen species present in six genera (*Monochaetia*, *Neopestalotiopsis*, *Pestalotiopsis*, *Seimatosporium*, *Seiridium* and *Sporocadus*) were identified. *Pestalotiopsis chamaeropis* and *Pes. rhodomyrtus* (18 isolates, 14 % of the isolates from *Rosa*) were the two most prevalent species, followed by *Seim. parvum* (10 isolates, 8 %). *Neopestalotiopsis concentrica*, *Seim. centrale* and *Seim. gracile* have the same isolation rate of 7 %. In the current study, *N. concentrica*, *N. subepidermalis*, *Pes. rhodomyrtus* and *Seim. parvum* were isolated from spines/branches of two and three species of *Rosa*. Each of the remaining 11 species of *Sporocadaceae* was only isolated from one *Rosa* species (Fig. 29).

The isolation rate of *Seimatosporium* in fruits and *Pestalotiopsis* in leaves was 100 %. These data reveal low generic and species diversity in these plant organs. In contrast, the branches had the highest genus diversity among all organs in this study, except for *Seimatosporium*, the other five genera were isolated from branches. Although the generic diversity of spines was slightly lower than that of branches, the number of strains isolated from the spines and the species diversity of spines was the highest of all tissues and was much higher than that of any other tissues (Fig. 26, 27).

Analysis of the abundance of *Sporocadaceae* species on *Rosa* species revealed seven species from *R. chinensis*, four from *R. rugosa*, three from *R. xanthina* and two from *R. spinosissima*, respectively (Fig. 29), with only one species on the remaining *Rosa* species, namely *R. multiflora* (*Pes. rhodomyrtus*), *R. helenae* (*Seim. parvum*), *R. laevigata* (*Seim. nonappendiculatum*) and *R. omeiensis* (*Spo. spiniger*) (Fig. 29). These findings might be due to the smaller sampling size of *R. multiflora*, *R. helenae*, *R. laevigata* and *R. omeiensis* obtained, since symptomatic branches were far less commonly observed than for the other *Rosa* species.

DISCUSSION

In this study, many *Rosa* specimens were collected from six major rose production areas (Gansu, Henan, Hunan, Ningxia, Qinghai and Shaanxi) in China, and 126 pestalotioid strains were obtained elsewhere. Multi-locus phylogenetic and morphological analyses revealed 15 species belonging to six genera in *Sporocadaceae*, namely *Monochaetia*, *Neopestalotiopsis*, *Pestalotiopsis*, *Seimatosporium*, *Seiridium* and *Sporocadus*.

Seimatosporium species have been extensively studied on several hosts (Tanaka et al. 2011, Liu et al. 2019), but not yet on *Rosa* spp. Up to now, five species of *Seimatosporium* have been recorded from *Rosa*, namely *Seim. caninum* on *R. canina*, *Seim. pseudorosae* on *R. villosa*, *Seim. salicinum* on *R. multiflora* and *R. spinosissima*, *Seim. rosae* on *R. canina*, *R. kalmiussica*, *R. mucosa* and *R. pomifera*, *Seim. discosioides* on *R. blanda*, *R. heliophila*, *R. moschata*, *R. multiflora* and *R. rugosa* (Weiss 1950, Nag Raj 1993, Cho & Shin 2004, Kobayashi 2007, Li et al. 2016, Crous et al. 2018, Liu et al. 2019). Among them, *Seim. salicinum* has been recorded in China (Tai 1979). In this study, a total of four new *Seimatosporium* species were introduced from *Rosa* in China. *Seimatosporium* is the genus which has the most species found and has a relatively high isolation rate (26.2 %) (Fig. 25). *Seimatosporium* species from *Rosa* spp. in previous and present studies show quite a difference based on morphology and DNA sequence data. *Seimatosporium rosae* is distinguished from the four new species in this study based on DNA phylogenetic data (Fig. 6) and the number of conidial septa (3–6-septate vs 3-septate). Although *Seim. pseudorosae* is closely related to *Seim. parvum* in this study (Fig. 6), these two species can be clearly distinguished by the size of their conidia and the length of their appendages. There are no sequence data available for *Seim. caninum* and *Seim. salicinum* for comparison, but the morphological characteristics of *Seim. caninum* (appendages lacking, 2-septate conidia) clearly distinguish it from other *Seimatosporium* species (Nag Raj 1993). *Seimatosporium salicinum* also produces 2-septate conidia (Sutton 1975, Nag Raj 1993), and this morphological characteristic distinguishes it from our four new species. Except for *Seim. salicinum* (the main hosts are *Salix* spp. and *Rosaceae* plants) (Nag Raj 1993, Tanaka et al. 2011), the other species from *Rosa* spp. are rarely recorded on other hosts (Nag Raj 1993, Mułenko et al. 2008, Li et al. 2016, Bonthond et al. 2018). Currently, seven *Seimatosporium* species have been reported from China besides our new species and *Seim. salicinum*. However, none of them occur on *Rosa* spp., i.e., *Seim. botan*, *Seim. grammitum* and *Seim. hebeiensis* on *Paeonia suffruticosa*, *Seim. lonicerae* on *Pinus tabulaeformis*, *Seim. rhododendri* on *Rhododendron aureum*, *Seim. piceae* on *Picea jezoensis* and *Seim. maria* (Tai 1979, Wang 1985, Nag Raj 1993, Guo 2004, Duan et al. 2011). Among these species, *Seim. botan* can produce conidia with only basal appendages (Hatakeyama & Harada 2004), which is similar to *Seim. nonappendiculatum*, to which it formed a sister clade. *Seimatosporium grammitum* and *Seim. hebeiensis* produce conidia lacking appendages and are therefore similar to *Seim. nonappendiculatum*. However, they differ significantly in their conidial dimensions. Having conidia with only basal appendages or without appendages, makes *Seim. nonappendiculatum* unique in the *Sporocadaceae*, and phylogenetically it clustered closer *Sporocadus* (conidia lacking appendages) than other *Seimatosporium* species (Fig. 2). The most typical morphological characteristics of *Seim. piceae* is that the length of the appendages is longer than the conidia itself (Wang 1985), which is most similar to the new species *Seim. parvum* (Fig. 6), but the conidia and appendages of *Seim. parvum* are significantly shorter than *Seim. picea* (14.3–15 × 4.21–4.34 µm vs 18–23 × 5–7 µm). In addition, the conidial dimensions of the other two new species,

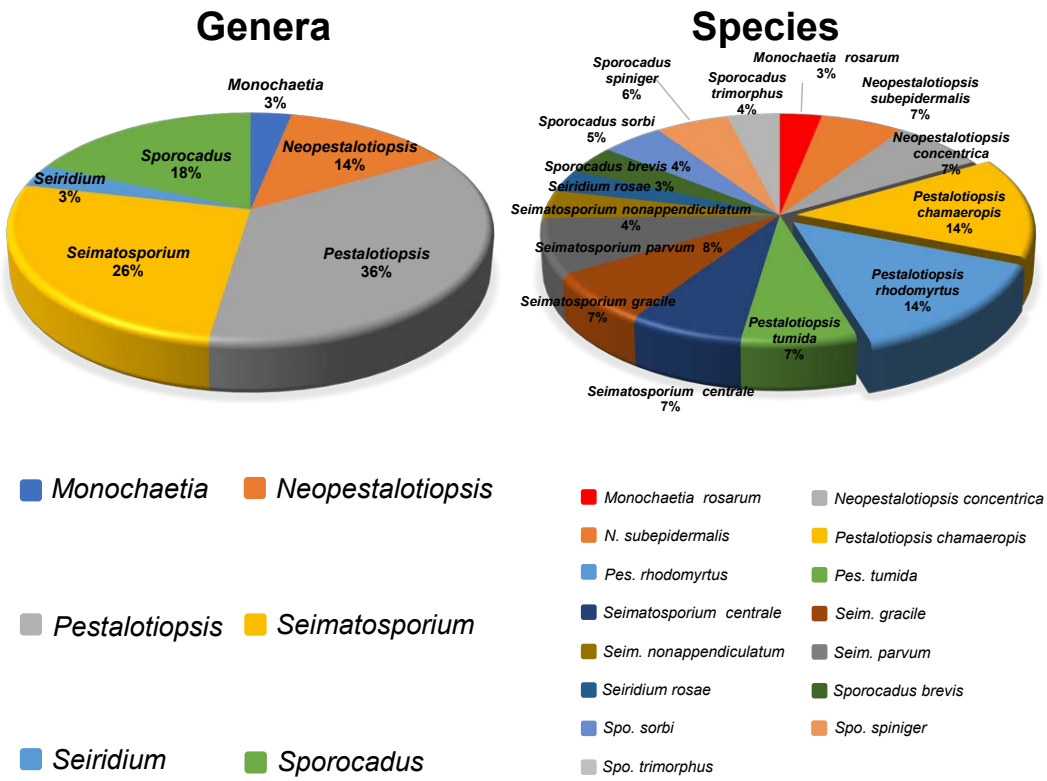

Fig. 25 Overall isolation rate (%) of *Sporocadaceae* genera and species.

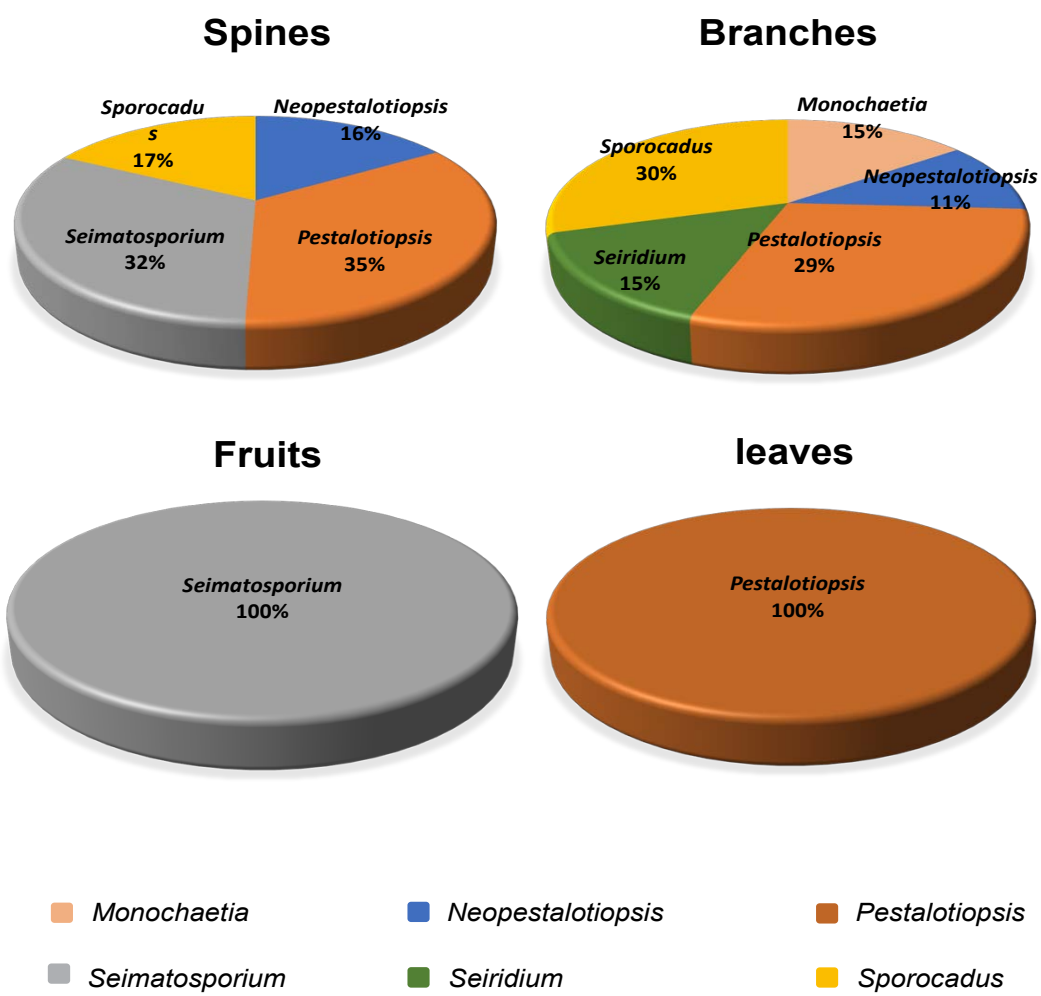

Fig. 26 Isolation rate (%) of *Sporocadaceae* genera from each *Rosa* organs.

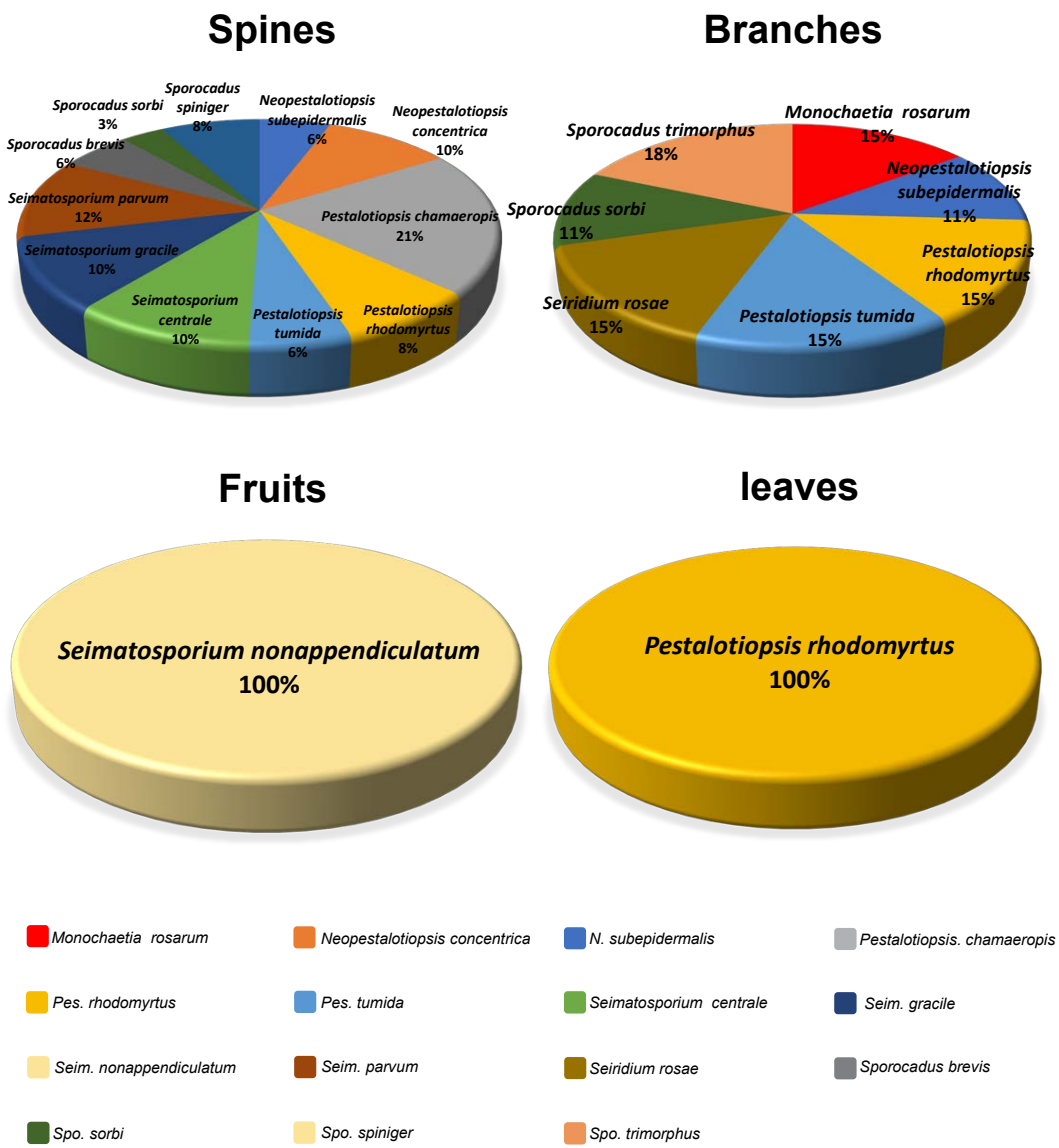

Fig. 27 Isolation rate (%) of *Sporocadaceae* species from each *Rosa* organs.

Seim. centrale and *Seim. gracile*, are significantly different from those species currently recorded in China.

Sporocadus is the type of *Sporocadaceae* and generally characterised by non-appendaged, 3-septate conidia (Liu et al. 2019). *Sporocadus* has long been assumed to be a synonym of *Seimatosporium* (Sutton 1975), but was confirmed to be a separate genus based on multigene phylogeny and conidial morphology (Brockmann 1976, Nag Raj 1993, Liu et al. 2019, Wijayawardene et al. 2020). However, in this study, although ITS-Blast is useful to locate species at the generic and family level, relatively weak in distinguishing *Seimatosporium* from *Sporocadus*, and even less so at the species level. Therefore, analysing these two genera at the family level is necessary to classify species into the correct genus (Fig. 2). Corresponding to the taxonomic classification determined by multi-locus phylogenetic analyses (Fig. 2), most *Sporocadus* species also exhibit characteristic morphological characters, including their non-appendaged and 3-septate conidia. In previous studies, most of these features have been used to delimit this genus (Brockmann 1976, Nag Raj 1993). It is worth to note that the presence or absence of conidial appendages is not a stable taxonomic character for the genus (Liu et al. 2019). For example, the conidia of *Seim. discosioides* and *Seim. germanicum* are also non-appendaged (Shoemaker 1964, Liu et al. 2019). Liu et al. (2019) introduced *Spo. trimorphus* and the conidia of this species have three types, i.e., non-appendaged which is the typical morphological characteristics of this genus; both apical and basal appendaged conidia which is the typical characteristics of *Seimatosporium* and either apical or basal appendaged conidia. This was also the first time that species with appendaged conidia were observed in *Sporocadus*, which renders morphology-based identifications more difficult, and underlines the necessity of molecular data for accurate identification. This study also found *Spo. trimorphus* on *R. xanthina*, which is also a first report from China. The other important morphological characteristic of this genus is 3-septate conidia (Nag Raj 1993). However, the number of conidial septa is far too unstable a feature to determine generic delineations. Liu et al. (2019) were the first to suggest that *Sporocadus* species could produce 2-septate conidia and introduced five species with this conidial type, namely *Spo. biseptatus*, *Spo. incanus*, *Spo. rosarum*, *Spo. rosigena* and *Spo. rotundatus*. Although the newly described species *Spo. brevis* can also produce conidia with two septa, this species is phylogenetically distinct from these five species (Fig. 8) and has significantly wider conidia (Table 5). To our knowledge, this study represents the first resolution of *Sporocadus* species in China based on multi-locus sequence data. A total of four species of *Sporocadus* were identified in this study, and the isolation rate is similar to that of *Seimatosporium* (Fig. 25). Besides *Spo. brevis* and

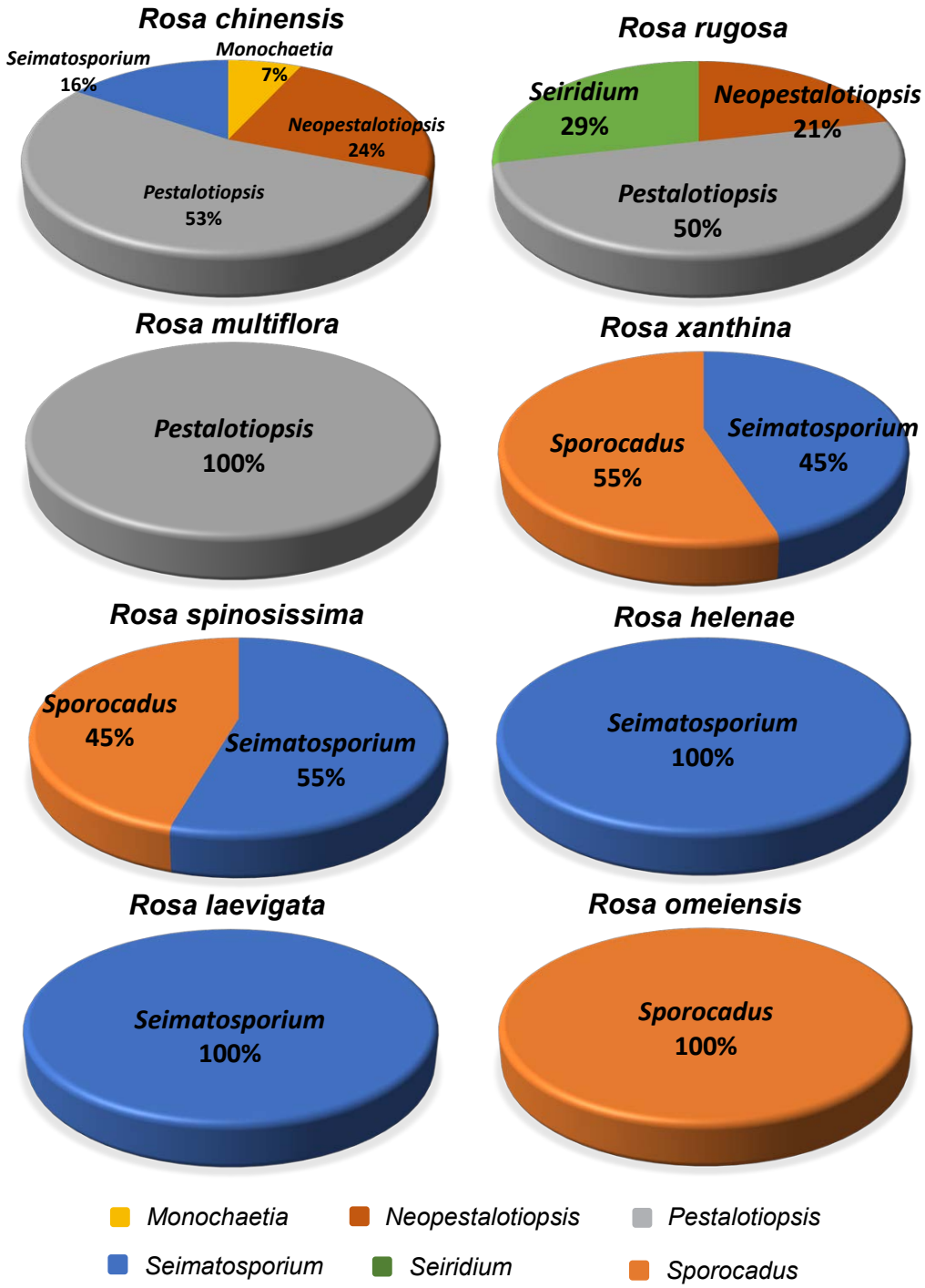

Fig. 28 Isolation rate (%) of *Sporocadaceae* genera from each *Rosa* sp.

Spo. trimorphus, this study also described a new species *Spo. spiniger*, and represents the first report of *Spo. sorbi* on *Rosa* globally. Currently, only one *Sporocadus* species has been reported from China, namely *Spo. lichenicola*, the type species of the genus (Tai 1979). The hosts of this species include many *Rosa* plants and can cause leaf spot or brown spot of *R. xanthina* in China (Tai 1979, Wu 1992, Chen 2003). Based on multigene phylogenetic analyses, *Spo. lichenicola* is also separated from the two new species (Fig. 8). Moreover, the conidia of *Spo. lichenicola* are 4–5-septate, which is also an important morphological characteristic distinguishing it from other species in *Sporocadus* (Norphanphoun et al. 2015). In addition to *Spo. lichenicola*, relatively little has been recorded about *Sporocadus* species associated with *Rosa*. Liu et al. (2019) transferred four *Seimatosporium* species associated with *Rosa* to *Sporocadus* based on molecular systematics and morphological characteristics, namely *Spo. rosarum* (synonyms: *Seim. rosarum*, *Seim. pseudorosarum* and *Seim. rosigenum*) and *Spo. rosigena* (basionym: *Seim. rosicola*). *Sporocadus rosarum* forms a large sister clade with the two new species and *Spo. trimorphus* (Fig. 8), but the conidia of *Spo. rosarum* have an apical appendage, which makes it easy to distinguish them from other species of *Sporocadus* (Wanasinghe et al. 2018, Liu et al. 2019). *Sporocadus rosigena* is separated from the two new species in this study based on DNA phylogeny (Fig. 8) and there are also differences in conidial dimensions. It is remarkable that *Seim. caninum* isolated from *R. chinensis* has the typical morphological characteristics of *Sporocadus*, that is, with conidia lacking appendages (Sutton 1975). The feature of 2-septate conidia distinguishes *Seim. caninum* from other species in *Seimatosporium* and most of the members in *Sporocadus*. As described above, six *Sporocadus* species

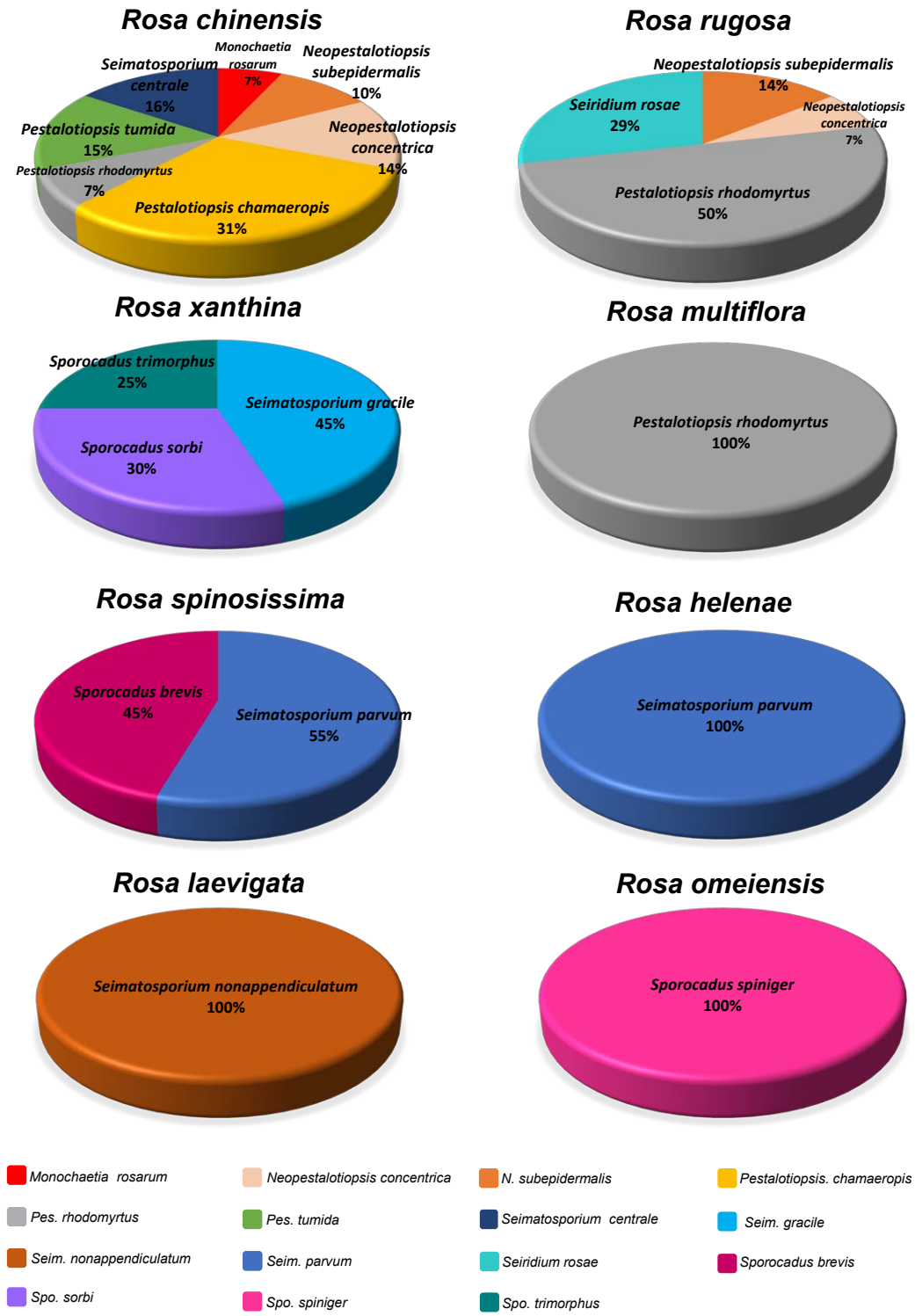

Fig. 29 Isolation rate (%) of *Sporocadaceae* species from each *Rosa* sp.

(including the new species described here) can produce 2-septate conidia similar to those of *Seim. caninum*, but the conidia of *Seim. caninum* are smaller than those of other species (Table 5). Therefore, since related sequence data of *Seim. caninum* are unavailable, further research is needed to resolve which genus it belongs to.

Pestalotiopsis is the genus with the highest isolation rate in this study, namely 29.6 % (Fig. 25), which is basically in line with expectations, because *Pestalotiopsis*, as an important plant pathogen, has many records and can parasitise more than 50 plant families in China (Tai 1979, Chen 2003, Ge et al. 2009). Cash crops such as palm, eucalypts, guava and tea trees have suffered serious damage due to species of *Pestalotiopsis* (Ge et al. 2009, Maharachchikumbura et al. 2013a, Wang et al. 2019a, b). This genus also has many records on *Rosa* plants. In China, five species of *Pestalotiopsis* have been recorded from *Rosa*, namely *Pes. rosae* and *Pes. suffocata* that are parasitic on *R. chinensis*, *Pes. oleandri* that is parasitic on *R. laevigata*, *Pes. longisetula* that is parasitic on *R. henryi* and *Pes. aquatica* that is saprophytic on *R. chinensis* (Zhu et al. 1991, Wei et al. 2005, Ge et al. 2009). Beyond that, there are six species of *Pestalotiopsis* recorded from *Rosa* in different countries (Riley 1960, Guba 1961, Mathur 1979, Rai 1990, Nag Raj 1993, Mendes et al. 1998, Sameva 2004, Kobayashi 2007). In this study, *Pes. chamaeropis* and *Pes. rhodomyrtus* are newly reported from *Rosa*. For the newly described species, *Pes. tumida* isolated from *R. chinensis*, morphological differences distinguish this species and other known species

Table 5 Synopsis of *Seimatosporium caninum* and species with 2-septate conidia in *Sporocadus*.

Species	Length of conidia (µm)	Width of conidia (µm)	Host	Country	References
Seimatosporium caninum	9.5–12	4.5–5.5	*Quercus incana*	India	Sutton (1975)
Sporocadus biseptatus	12.5–19.5	4.5–9	Unknown	Unknown	Liu et al. (2019)
Spo. brevis	**10–12**	**6.5–7**	***Rosa spinosissima***	**China**	**Present study**
Spo. incanus	11.5–20	4.5–6.5	*Prunus dulcis*	Spain	Liu et al. (2019)
Spo. rosarum	9.0–14.0	4.0–6.0	*Rosa canina*	Europe	Liu et al. (2019)
Spo. rosigena	10.0–15.0	3.5–6.5	*Vitis vinifera*	Iran	Liu et al. (2019)
			Rosa canina	Italy	Liu et al. (2019)
			Rhododendron sp.	Latvia	Liu et al. (2019)
			Rubus fruticosus	Netherlands	Liu et al. (2019)
Spo. rotundatus	9.0–16.5	4.5–7.5	*Arceuthobium pussilum*	Canada	Liu et al. (2019)

* Newly described taxon is in **bold**.

recorded on *Rosa*, especially in terms of the conidial dimensions and length of the appendages, as well as shape of basal appendages. The results of our study suggest that the species diversity of *Pestalotiopsis* on *Rosa* in China may be higher than what was previously expected.

Neopestalotiopsis was separated from *Pestalotiopsis* based on its versicolourous median conidium cells and indistinct conidiophores (Maharachchikumbura et al. 2014, Liu et al. 2017, 2019). In this study, two new species of *Neopestalotiopsis* were introduced from *Rosa* based on the phylogenetic analyses and morphological characteristics, namely *N. concentrica* and *N. subepidermalis*. Five *Neopestalotiopsis* species associated with *Rosa* have been recorded, namely *N. clavispora*, *N. palmarum*, *N. rosae*, *N. rosicola* and *N. versicolor* (Liu et al. 2010, Feng et al. 2014, Maharachchikumbura et al. 2014, Jiang et al. 2018, Vu et al. 2019). For these five species, *N. clavispora*, *N. palmarum*, *N. rosicola* and *N. versicolor* have been reported in China and cause leaf blotch, stem canker of *R. chinensis* and leaf spot disease of many other hosts (Ge et al. 2009, Feng et al. 2014, Jiang et al. 2018), but these four species are phylogenetically separated from our new species (Fig. 4) and there are also differences in their conidial morphology. *Neopestalotiopsis rosae* is morphologically quite distinct from other taxa in the genus (has appendages which do not arise from the apical crest, but at different regions in the upper half of the apical cell; Maharachchikumbura et al. 2014). With the increase of collections and DNA data, *N. clavispora*, *N. palmarum*, *N. rosae* and *N. versicolor* appear to be widely distributed in different countries where they cause severe diseases on different hosts, e.g., *N. rosae* causes dieback, crown rot, fruit rot and root rot of many economically important plants including *Eucalyptus*, *Fragaria*, *Paeonia* and *Vitis* (Maharachchikumbura et al. 2014, Rebollar-Alviter et al. 2020, Santos et al. 2020, Cosseboom & Hu 2021), and *N. clavispora* can infect more than 50 plant species belonging to 27 families in China and about 17 other countries, resulting in severe leaf diseases (Qiu et al. 2020). For this reason, the two new species isolated from *Rosa* may present dangerous pathogens for other hosts, and further work is needed to better understand the role and distribution of these two new *Neopestalotiopsis* species. For other pestalotiopsis-like species associated with *Rosa*, as mentioned above, some *Pestalotiopsis* spp. on *Rosa* (*Pes. adusta*, *Pes. algeriensis*, *Pes. aquatica*, *Pes. longisetula* and *Pes. oleandri*) have the typical morphological characteristics of *Neopestalotiopsis*, namely versicolourous median conidium cells (Guba 1961, Mordue & Holliday 1971, Zhu et al. 1991, Wei et al. 2005, Ge et al. 2009, Cardoso et al. 2017). However, due to the lack of related DNA sequence data, their taxonomy still needs to be resolved. However, our two new *Neopestalotiopsis* species can be distinguished from these five *Pestalotiopsis* species based on their conidial and appendage morphology (Table 6). This study also encountered the same problem as previous studies on *Neopetalotiopsis* compared to other genera, namely the short branch length and low support rate of the current phylogenetic tree based on ITS, *TEF* and *TUB* (Liu et al. 2017, Norphanphoun et al. 2019). More gene regions will have to be introduced in future studies to provide better support for species in the genus.

Many species of *Pestalotiopsis* and *Neopestalotiopsis* have overlapping morphological characteristics, and it is difficult to identify them solely based on morphology (Maharachchikumbura et al. 2014, Liu et al. 2017). Some morphological characteristics are unstable and vary with host range, culture and other environmental conditions (Maharachchikumbura et al. 2011, Norphanphoun et al. 2019). But at the same time, conidial morphology can still provide a good reference for species distinction of pestalotioid fungi (Crous et al. 2012). Therefore, the combination of morphology and molecular systematics based on sequence data has become an important means to solve the classification of pestalotiopsis-like and support the introduction

Table 6 Synopsis of two new *Neopestalotiopsis* species and species with versicolourous median conidium cells in *Pestalotiopsis*.

Species	Length of conidia (µm)	Width of conidia (µm)	Length of apical appendages (µm)	Length of basal appendages (µm)	Host	Country	References
Neopestalotiopsis concentrica	**14–18.5**	**4.5–5**	**19–26**	**3.5–5.5**	***Rosa rugosa***	**China**	**Present study**
N. subepidermalis	**20–25**	**7.5–9**	**27–32.5**	**7–7.5**	***Rosa rugosa***	**China**	**Present study**
Pestalotiopsis adusta	16–22.4	4.7–6.6	5–12	3.5	*Rosa indica*	India	Rai (1990)
Pes. algeriensis	20.5–31.3	6.3–8.0	13.3–17.8	3–6.3	*Rosa sempervirens*	Algeria	Nag Raj (1993)
Pes. aquatica	20.6–28.2	7.2–8.2	12.8–23	2–4	*Rosa* sp.	China	Ge et al. (2009)
Pes. longisetula	20.6–25.7	6.4–7.7	20.6–36	5.1–7.7	*Rosa henryi*	China	Ge et al. (2009)
					Rosa sp.	China	Ge et al. (2009)
Pes. oleandri	15–22.6	5–7.5	14–16.5	6.1–11.5	*Rosa laevigata*	China	Ge et al. (2009)
					Rosa sp.	China	Zhu et al. (1991)

* Newly described taxa are in **bold**.

Table 7 *Monochaetia* species that have been recorded in China in previous studies.

Species	Host	Location	Collector	References
Monochaetia caryotae	*Caryota ochlandra*	Guangxi, China	Y.X. Chen & G. Wei	Chen et al. (2002)
M. castaneae	*Castanea mollissima*	Sichuan, China	N. Jiang	Jiang et al. (2021)
M. celaeocarpi	*Elaeocarpus serratus*	Hainan, China	Z.W. Wang & G. Wei	Chen et al. (2002)
M. concentrica	*Rosa xanthina*	Jilin, China	P.K. Qi	Tai (1979)
M. cycadis	*Cycas revoluta*	Guangxi, China	G. Wei	Chen et al. (2002)
M. diospyri	*Diospyros lotus*	–	–	Chen et al. (2002)
M. garciniae	*Garcinia tinctoria*	Hainan, China	Z.W. Wang & G. Wei	Chen et al. (2002)
M. hirta	*Castanopsis fabri*	Hainan, China	Z.W. Wang & G. Wei	Chen et al. (2002)
M. kansensis	*Castanea mollissima*	–	–	Chen et al. (2002)
	Quercus dentata	Henan, China	M.Q, Wang	Tai (1979)
	Q. dentata	Gansu, China	Y.R. Meng	Meng (2003)
M. monochaeta	*Q. dentata*	Gansu, China	Y.R. Meng	Meng et al. (2003)
	Q. variabilis	Jiangsu, China	–	Teng (1963)
	Q. variabilis	Jiangsu, China	Q.Y. Shen	Tai (1979)
M. nattrassii	*Camellia sinensis*	Hong Kong	–	Sutton et al. (1980)
M. nodosporella	*Castanopsis delavayi*	Yunnan, China	Zhao & Li	Zhao & Li (1994)
M. sabinae	*Sabina chinensis*	Guangxi, China	G. Wei	Chen et al. (2002)
M. saccardoi	*Q. variabilis*	Jiangsu, China	–	Teng (1963)
M. salaccae	*Salacca secunda*	Yunnan, China	G. Wei	Chen et al. (2002)
M. seiridioides	*R. xanthina*	Henan, China	M.Q, Wang	Tai (1979)
M. turgida	*Pyrus communis*	Guangdong, China	Z. Tu	Tai (1979)

of new species (Crous et al. 2012, Maharachchikumbura et al. 2014, Liu et al. 2019).

Monochaetia has undergone a lot of changes since it was introduced, and many species have been transferred to other genera, such as *Diploceras*, *Monochaetinula*, *Sarcostroma*, *Seimatosporium* and *Seiridium* (De Silva et al. 2018, Liu et al. 2019). However, species of *Monochaetia* are morphologically conserved at present and the typical morphological characteristic of this genus is that conidia have a single centric apical and basal appendage (if present) (De Silva et al. 2018, Liu et al. 2019). Previous reports on the hosts of *Monochaetia* were mainly concentrated on *Fagaceae* (especially *Castanea* and *Quercus* spp.) (De Silva et al. 2018, Liu et al. 2019). In this study one new species, *M. rosarum,* was isolated from *Rosa* and can be distinguished from other phylogenetically allied species based on conidial dimensions. In addition, there are currently four species of *Monochaetia* that have been recorded from *Rosa*, namely *M. concentrica*, *M. rosae-caninae*, *M. seiridioides* and *M. turgida* (Guba 1961, Tai 1979, Chen 2003). Except for *M. rosae-caninae*, three other species have also been recorded in China (Tai 1979, Chen 2003). The species associated with *Rosa* have relatively wide host ranges mainly concentrated in the *Rosaceae*, excluding the *Fagaceae* (Weiss 1950, Sutton 1980, Nag Raj 1993), and the choice of host may also be affected by the geographical environment. For example, *M. turgida*, has been recorded on *Rosa* spp. in India, on *Crataegus* spp. in the USA, and on *Pyrus* spp in China (Mathur 1979, Tai 1979, Nag Raj 1993). Besides the three species on *Rosa* mentioned above (*M. concentrica*, *M. seiridioides* and *M. turgida*), 16 species of *Monochaetia* have been recorded from China (Table 7). Among them, Chen et al. (2002) introduced seven *Monochaetia* species based on morphology and host, i.e., *M. caryotae* on *Caryota ochlandra*, *M. cycadis* on *Cycas revoluta*, *M. elaeocarpi* on *Elaeocarpus serratus*, *M. garciniae* on *Garcinia tinctoria*, *M. hirta* on *Castanopsis fabri*, *M. sabinae* on *Sabina chinensis* and *M. salaccae* on *Salacca secanda*, and all these species are endemic to China. Although sequence data for these species are not available and reliance only on morphology and host data in *Monochaetia* taxonomy is far from perfect, the ongoing discovery of this genus from other hosts except for *Fagaceae* in China will deepen our understanding of the species in this genus. It is worth mentioning that Zhao & Li (1994) have described a species *M. nodosporella*, the hosts of which include also *Castanopsis* spp. Characteristics of this species are quite different from morphological characters of *Monochaetia*, including 4-celled distoseptate conidia with two olivaceous-brown median cells, lacking appendages. Considering the limited sampling and the lack of sequence data, the taxonomy of *M. nodosporella* remains unresolved and will be treated once DNA sequence data have been obtained. Aside from the species associated with *Rosa* and the Chinese endemic species mentioned above, the remaining species recorded in China have a relatively small range of host plants mainly on *Castanea* and *Quercus*, and are geographically widespread (Tai 1979, Zhao & Li 1994, Chen et al. 2002). For example, *M. monochaeta* and *M. kansensis* have also been recorded in many countries besides China, but the hosts are basically *Quercus* and *Castanea* (Ellis & Everhart 1893, Weiss 1950, Guba 1961, Nag Raj 1993, Cho & Shin 2004, Kobayashi 2007). Therefore, for the new species *M. rosarum* described in this study, many specimens still need to be collected to improve our understanding of its host range and distribution.

Seiridium generally produces 5-septate conidia with a single centric apical and single excentric basal appendage (Bonthond et al. 2018, Liu et al. 2019). Nees (1817) established *Seiridium* based on *Seir. marginatum* which was collected from rose stems in Germany, and this is also the earliest record of pestalotioid fungi on the *Rosa* plants. Presently, besides the type species *Seir. marginatum*, only one *Seiridium* species has been recorded from *Rosa*, namely *Seir. rosarum*, which is distributed in Europe and Australia (Sutton 1980, Nag Raj 1993, Jaklitsch et al. 2016). In this study, a new species *Seir. rosae* was introduced from *R. multiflora* in China. The newly described species can be distinguished from most *Seiridium* species by its numerous appendages, which are branched, while in *Seiridium* appendages are fewer and generally unbranched (Maharachchikumbura et al. 2014). However, conidial appendages are branched, which is not unique to *Seir. rosae* in *Seiridium* and is also typical for

Table 8 Synopsis of species with branched appendages in *Seiridium.*

Species	Length of conidia (µm)	Width of conidia (µm)	Length of apical appendages (µm)	Length of basal appendages (µm)	Host	Country	References
Seiridium indicum	22–30.8	7.7–8.8	4.4–11	1–1.8	*Spirea micrantha*	India	Nag Raj (1993)
Seir. pezizoides	28–33.5	7–8	8.5–27	5.5–14	*Vitis vinifera*	Italy	Marin-Felix et al. (2019)
Seir. rosae	**31–35**	**8–9.5**	**28.5–44.5**	**3–4.5**	***Rosa rugosa***	**China**	**Present study**
Seir. venetum	20–30	6.5–8.5	10–35	2–5	*Cornus sanguinea*	Italy	Nag Raj (1993)

* Newly described taxa is in **bold**.

Table 9 *Seiridium* species that have been recorded in China in previous studies.

Species	Host	Location	Collector	References
Seiridium camelliae	*Camellia reticulata*	Yunnan, China	Y.M. Zhang	Maharachchikumbura et al. (2015)
Seir. ceratosporum	*Vitis vinifera*	Yunnan, China	–	Bonthond et al. (2018)
Seir. chinense	*Trachycarpus fortunei*	Shaanxi, China	N. Jiang & C.M. Tian	Jiang et al. (2018)
Seir. cupressi	*Vitis* sp.	Zhejiang, China	–	Teng (1996)
Seir. eriobotryae	*Eriobotrya japonica*	Guangxi, China	G. Wei	Chen et al. (2002)
Seir. manilkarae	*Manilkara zapota*	Yunnan, China	G. Wei	Chen et al. (2002)
Seir. pezizoides	*Camellia oleifera*	Hunan, China	J.X. Yu	Yu et al. (2018)
Seir. unicorne	*Eriobotrya japonica*	Jiangsu, China	F.L. Tai	Tai (1979)
	Malus mandshurica	Jilin, China	Miura	Tai (1979)
	M. prunifolia	Jilin, China	P.K. Qi	Tai (1979)
	M. pumila	Yunnan, China	L.D. Lin	Tai (1979)
	Pyrus ussuriensis	Jilin, China	P.K. Qi	Tai (1979)
	Sorbus alnifolia	Jilin, China	Miura	Tai (1979)
	V. vinifera	Jiangsu, China	L. Ling	Tai (1979)
Seir. venetum	*Cornus* sp.	Yunnan, China	–	Tai (1979)

Seir. indicum, *Seir. pezizoides* and *Seir. venetum* (Pavgi & Singh 1970, Maharachchikumbura et al. 2015, Marin-Felix et al. 2019). *Seiridium rosae* is easily distinguishable from these three species based on conidial morphology (Table 8). It is worth mentioning that *Seiridium* is the most important pathogen group in *Sporocadaceae* (Bonthond et al. 2018). *Seiridium* is the main pathogen of cypress canker and causes huge economic losses worldwide (Boesewinkel 1983, Graniti 1986, 1993, 1998, Barnes et al. 2001, Tsopelas et al. 2007). There are currently nine species of *Seiridium* recorded in China, with diverse hosts (Table 9). However, thus far China still has no record of *Seiridium* spp. on *Cupressaceae*.

In this study, the species diversity of *Sporocadaceae* on the stems and spines of *Rosa* was significantly higher than that on the leaves and fruits. Nevertheless, a new species *Seim. non-appendiculatum* was isolated from the fruits of *Rosa laevigata* and *Pes. rhodomyrtus,* that was first reported on *Rosa*, was isolated from leaves of *Rosa rugosa*. Therefore, the leaves and fruits of *Rosa* plants might harbour many more species of pestalotioid fungi yet unknown to science. This study represents the first systematic investigation, morphological and molecular characterisation of *Sporocadaceae* on *Rosa*. The findings of this study reveal taxonomic, morphological and biological diversity of *Sporocadaceae* associated with different *Rosa* spp. in China. Other than expanding our knowledge of the genetic diversity and hosts of *Sporocadaceae* on *Rosa*, it provides crucially important information to understand the ecology of the *Sporocadaceae* associated with *Rosa*. Further study is needed to test the pathogenicity of these species and understand their biological and epidemiological characteristics to contribute towards better disease management.

Acknowledgements This study is financed by National Natural Science Foundation of China (Project No.: 31670647).

Declaration on conflict of interest The authors declare that there is no conflict of interest.

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Supplementary material

Fig. S1 Phylogenetic tree of *Monochaetia* resulting from maximum likelihood (ML) analysis of the ITS sequence alignment. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Isolates collected in this study are in **bold** and blue.

Fig. S2 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Neopestalotiopsis*. a. ITS region; b. *TEF* gene region; c. *TUB* gene region. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Isolates collected in this study are in **bold** and blue.

Fig. S3 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Pestalotiopsis*. a. ITS region; b. *TEF* gene region; c. *TUB* gene region. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Isolates collected in this study are in **bold** and blue.

Fig. S4 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Seimatosporium*. a. ITS region; b. LSU gene region. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Isolates collected in this study are in **bold** and blue.

Fig. S5 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Seiridium*. a. ITS region; b. *RPB2* gene region; c. *TEF* gene region; d. *TUB* gene region. Nodes are labelled with bootstrap values from RaxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Isolates collected in this study are in **bold** and blue.

Fig. S6 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Sporocadus*. a. ITS region; b. LSU gene region; c. *RPB2* gene region; d. *TEF* gene region; e. *TUB* gene region. Nodes are labelled with bootstrap values from RAxML/Parsimony bootstrap/Bayesian posterior probabilities values. Nodes receiving below 50 bootstrap values and 0.5 probability values are not labelled. The scale bar represents the expected number of changes per site. Isolates collected in this study are in **bold** and blue.