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# Polyphasic characterisation of three new *Phyllosticta* spp.

Y.Y. Su<sup>1</sup>, L. Cai<sup>1</sup>

## Key words

molecular  
morphology  
phylogeny  
systematics  
taxonomy

**Abstract** Three new species of *Phyllosticta*, *P. hostae* on *Hosta plantaginea* (China), *P. schimae* on *Schima superba* (China), and *P. ilicis-aquifolii* on *Ilex aquifolium* (UK), are described and illustrated in this study. They are compared with morphologically similar and phylogenetically closely related species. A polyphasic approach using phylogeny, host association, disease symptoms, colony and morphological characteristics, is employed to justify the introduction of the new taxa. Phylogenetic relationships of the new species with other *Phyllosticta* species are revealed by DNA sequence analyses based on the nrDNA-internal transcribed spacer (ITS) regions and a combined multilocus alignment of the ITS, partial translation elongation factor 1-alpha (TEF1), actin (ACT), and glyceraldehyde 3-phosphate dehydrogenase (GPDH) gene regions.

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## INTRODUCTION

Many *Phyllosticta* (teleomorph *Guignardia*) species cause plant diseases such as leaf spots, leaf blotch, as well as black spots and lesions on fruits of various plants (van der Aa & Vanev 2002). These plant pathogenic fungi may cause serious damage to the host plant through reduced photosynthetic ability and premature leaf or fruit fall (Glienke-Blanco et al. 2002, Baldasari et al. 2008). *Phyllosticta* species have also been recorded as endophytes and saprobes on a wide range of host plants (Baayen et al. 2002, van der Aa & Vanev 2002, Okane et al. 2003, Wulandari et al. 2009, Glienke et al. 2011).

The generic circumscription of *Phyllosticta* as defined by van der Aa (1973) has been widely accepted (Bissett 1979, 1986, Yip 1989, Crous et al. 2006, Motohashi et al. 2008, 2009, Glienke et al. 2011, Wikee et al. 2011). The main characters are: pycnidial conidiomata, holoblastic conidiogenous cells with percurrent proliferation, conidia aseptate, surrounded by a mucilaginous sheath, and provided with an apical extracellular appendage, a *Guignardia* sexual state, and *Leptodothiorella* spermatial state (van der Aa 1973, van der Aa & Vanev 2002). According to these criteria, van der Aa & Vanev (2002) reconsidered 2 936 names in *Phyllosticta*, accepting 141 species based on original literature and a re-examination of herbarium specimens. About 50 % of the species were reclassified in *Phoma*, 20 % in *Asteromella*, 5 % in *Phomopsis* and c. 18 % in other coelomycetous genera or other taxonomic groups. Some *Phyllosticta* species have been linked to their teleomorph states, for example, *P. ampellicida* is the anamorph of *G. bidwellii* (van der Aa 1973), but most appear to be asexual. Recent changes to the rules that govern fungal nomenclature require that only one name for a single biological species should be used instead of different names for different morphs (Hawksworth et al. 2011, Wingfield et al. 2012). The earlier and well-known generic name *Phyllosticta* (Persoon 1818), thus has priority over *Guignardia* (Viala & Ravaz 1892), as followed by Glienke et al. (2011).

The systematics of *Phyllosticta* species has long been problematic because of the limited morphological characters and the

unreliable use of host-association based nomenclature. Polyphasic approaches combining morphological characters and phylogenetic relationships can resolve species relationships, based on which a natural classification could be established (Wulandari et al. 2009, Glienke et al. 2011). Although the rDNA-internal transcribed spacer (ITS) locus has some resolution at species level, it is insufficient for separating cryptic species in *Phyllosticta* (Wulandari et al. 2009, Glienke et al. 2011). Therefore, multilocus phylogenetic analyses have been increasingly used for species discrimination in this genus (Wulandari et al. 2009, Glienke et al. 2011, Wang et al. 2012). For example, it was shown that *G. mangiferae* is a distinct taxon from *P. capitalensis*, which is a species complex awaiting more detailed phylogenetic study (Glienke et al. 2011).

In the present study, three new species of *Phyllosticta* are described based on morphological characters and phylogenies derived from ITS and combined multilocus gene sequences.

## MATERIALS AND METHODS

### Isolates

*Phyllosticta* species were isolated from diseased leaves of ornamental or forest plant species from China and the United Kingdom. Infected leaves were incubated in moist chambers at room temperature to induce sporulation. Pure cultures were obtained by single spore isolation as described by Choi et al. (1999). Alternatively, 5 × 5 mm pieces of surface-sterilised tissue were taken from the margin of leaf lesions and were consecutively immersed in 70 % ethanol solution for 1 min, sodium hypochlorite solution with 3 % available chlorine for 2 min, rinsed in sterile distilled water, blotted dry in sterile paper towels and incubated on 2 % potato-dextrose agar (PDA) (Cai et al. 2009).

### Morphology

Cultures were grown on PDA for microscopic examination. Fungal structures were mounted on glass slides in clear lactic acid, and studied by means of a light microscope. Colony morphologies were assessed after 7 d growth on PDA, and colours rated according to the colour charts of Rayner (1970).

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### DNA extraction, PCR amplification and sequencing

Mycelial discs were taken from actively sporulating areas near the growing edge of 10 d old cultures and transferred to PDA. Genomic DNA was extracted with a Biospin Fungus Genomic DNA Extraction Kit (Bioer. Technology Co., Ltd., Hangzhou, P.R. China) according to the manufacturer's protocol. Quality and quantity of DNA were estimated visually by staining with GelRed after 1 % agarose gel electrophoresis. The ITS1 and ITS4 primer pair (White et al. 1990) was used to amplify the ITS region following the procedure described by White et al. (1990). The primers EF1-728F and EF1-986R (Carbone & Kohn 1999) were used to amplify a partial fragment of the translation elongation factor 1- $\alpha$  gene (TEF1); the primers ACT-512F and ACT-783R (Carbone & Kohn 1999) were used to amplify a partial fragment of the actin gene (ACT); the primers GDF1 (Guerber et al. 2003) and Gpd2-LM (Myllys et al. 2002) or GDR1 (Guerber et al. 2003) were used to amplify a partial fragment of the glyceraldehyde 3-phosphate dehydrogenase gene (GPDH). Amplification conditions followed Arzanlou et al. (2008). DNA sequencing was performed at the SinoGenoMax Company Limited, Beijing.

### Sequence alignment and phylogenetic analyses

Sequences from forward and reverse primers were aligned to obtain a consensus sequence. Sequences of our isolates, together with reference sequences obtained from GenBank (Table 1), were aligned using Clustal X (Thompson et al. 1997). The separate ITS and the combined multilocus alignments were manually optimised in BioEdit 7.0.9.0 for maximum alignment and minimum gaps (Hall 1999). Both these alignments were subjected to phylogenetic analyses.

Phylogenetic analyses were performed using PAUP v. 4.0b10 (Swofford 2003). Ambiguously aligned regions were excluded from all analyses. An unweighted parsimony (UP) analysis was performed. Trees were inferred using the heuristic search option with TBR branch swapping and 1 000 random sequence additions, branches of zero length were collapsed and all equally most parsimonious trees were saved. Descriptive tree statistics such as tree length [TL], consistency index [CI], retention index [RI], rescaled consistency index [RC], and homoplasy index [HI], were calculated for trees generated. Clade stability was assessed in a bootstrap analysis with 1 000 replicates, each with 10 replicates of random stepwise addition of taxa. A Shimodaira-Hasegawa test (SH test) (Shimodaira & Hasegawa 1999) was performed in order to determine whether trees were significantly different. Trees were visualised in TreeView v. 1.6.6 (Page 1996).

For the Bayesian analyses, the models of evolution were estimated by using MrModeltest v. 2.3 (Nylander 2004). Posterior probabilities (PP) (Rannala & Yang 1996, Zhaxybayeva & Gogarten 2002) were determined by Markov Chain Monte Carlo sampling (BMCMC) in MrBayes v. 3.0b4 (Huelsenbeck & Ronquist 2001), under the estimated model of evolution. Six simultaneous Markov chains were run for 1 000 000 generations and trees were sampled every 100th generation (resulting in 10 000 total trees). The first 2 000 trees, representing the burn-in phase of the analyses, were discarded and the remaining 8 000 trees were used for calculating posterior probabilities (PP) in the majority rule consensus tree. Novel sequence data were deposited in GenBank (Table 1), alignments in TreeBASE (www.treebase.org, submission no.: 12430), and taxonomic novelties in MycoBank (Crous et al. 2004).

**Table 1** Sources of isolates and GenBank accession numbers used in this study. The newly generated sequences in this study are shown in **bold**.

Species	Strain no. <sup>1</sup>	GenBank Accession number <sup>2</sup>			
		ITS	TEF1	ACT	GPDH
<i>Guignardia bidwellii</i>	<b>CBS 111645</b>	<b>JN692542</b>	<b>JN692530</b>	<b>JN692518</b>	–
<i>G. gautheriae</i>	<b>CBS 447.70</b>	<b>JN692543</b>	<b>JN692531</b>	<b>JN692519</b>	<b>JN692508</b>
<i>G. mangiferae</i>	IMI 260576	JF261459	JF261501	JF343641	JF343748
<i>G. sansevieriae</i>	CBS 120428	JN692544	JN692532	JN692520	JN692509
<i>Phyllosticta bifrenariae</i>	VIC 30556*	JF343565	JF343586	JF343649	JF343744
<i>P. brazilianiae</i>	LGMF 330*	JF343572	JF343593	JF343656	JF343758
	LGMF 334	JF343566	JF343587	JF343650	JF343752
<i>P. capitalensis</i>	CBS 123373	FJ538341	FJ538399	FJ538457	JF343703
	CBS 356.52; ATCC 11368	FJ538342	FJ538400	FJ538458	JF343721
	CPC 18848*	JF261465	JF261507	JF343647	JF343776
<i>P. citriasiana</i>	CBS 120486; PD 05/01969753*	FJ538360	FJ538418	FJ538476	JF343686
	CBS 123371; PD 05/03081053	FJ538356	FJ538414	FJ538472	JF343690
	<b>CBS 120488</b>	<b>JN692545</b>	<b>JN692533</b>	<b>JN692521</b>	–
<i>P. citribraziliensis</i>	CBS 100098*	FJ538352	FJ538410	FJ538468	JF343691
	LGMF08	JF261435	JF261477	JF343617	JF343692
<i>P. citricarpa</i>	CBS 122482	FJ538317	FJ538375	FJ538433	JF343677
	CBS 127454*	JF343583	JF343604	JF343667	JF343771
<i>P. cussonia</i>	CPC 14873	JF343578	JF343599	JF343662	JF343764
	CPC 14875	JF343579	JF343600	JF343663	JF343765
<i>P. hostae</i>	<b>CGMCC 3.14355*</b>	<b>JN692535</b>	<b>JN692523</b>	<b>JN692511</b>	<b>JN692503</b>
	<b>CGMCC 3.14356</b>	<b>JN692536</b>	<b>JN692524</b>	<b>JN692512</b>	<b>JN692504</b>
	<b>CGMCC 3.14357</b>	<b>JN692537</b>	<b>JN692525</b>	<b>JN692513</b>	<b>JN692505</b>
<i>P. hypoglossi</i>	CBS 101.72; IFO 32916	FJ538365	FJ538423	FJ538481	JF343694
	CBS 434.92	FJ538367	FJ538425	FJ538483	JF343695
<i>P. ilicis-aquifolii</i>	<b>CGMCC 3.14358*</b>	<b>JN692538</b>	<b>JN692526</b>	<b>JN692514</b>	–
	<b>CGMCC 3.14359</b>	<b>JN692539</b>	<b>JN692527</b>	<b>JN692515</b>	–
	<b>CGMCC 3.14360</b>	<b>JN692540</b>	<b>JN692528</b>	<b>JN692516</b>	–
<i>P. owaniana</i>	CBS 776.97	FJ538368	FJ538426	FJ538484	JF343767
<i>P. schimae</i>	<b>CGMCC 3.14354*</b>	<b>JN692534</b>	<b>JN692522</b>	<b>JN692510</b>	<b>JN692506</b>
<i>P. spinarium</i>	CBS 292.90	JF343585	JF343606	JF343669	JF343773
	CBS 937.70	FJ538350	FJ538408	FJ538466	JF411745
<i>P. yuccae</i>	<b>CBS 117136</b>	<b>JN692541</b>	<b>JN692529</b>	<b>JN692517</b>	<b>JN692507</b>

<sup>1</sup> ATCC: American Type Culture Collection, Virginia, USA; CBS: CBS Fungal Biodiversity Centre, Utrecht, The Netherlands; CGMCC: China General Microbial Culture Collection; CPC: Culture collection of P.W. Crous, housed at CBS; IFO: Institute for Fermentation, Osaka, Japan; IMI: International Mycological Institute, CABI-Bioscience, Egham, Basingstoke, UK; LGMF: Culture collection of Laboratory of Genetics of Microorganisms, Federal University of Parana, Curitiba, Brazil; PD: Plant Protection Service, Wageningen, The Netherlands; VIC: Culture collection of Federal University of Viçosa, Viçosa, Brazil.

\* indicates the ex-type cultures.

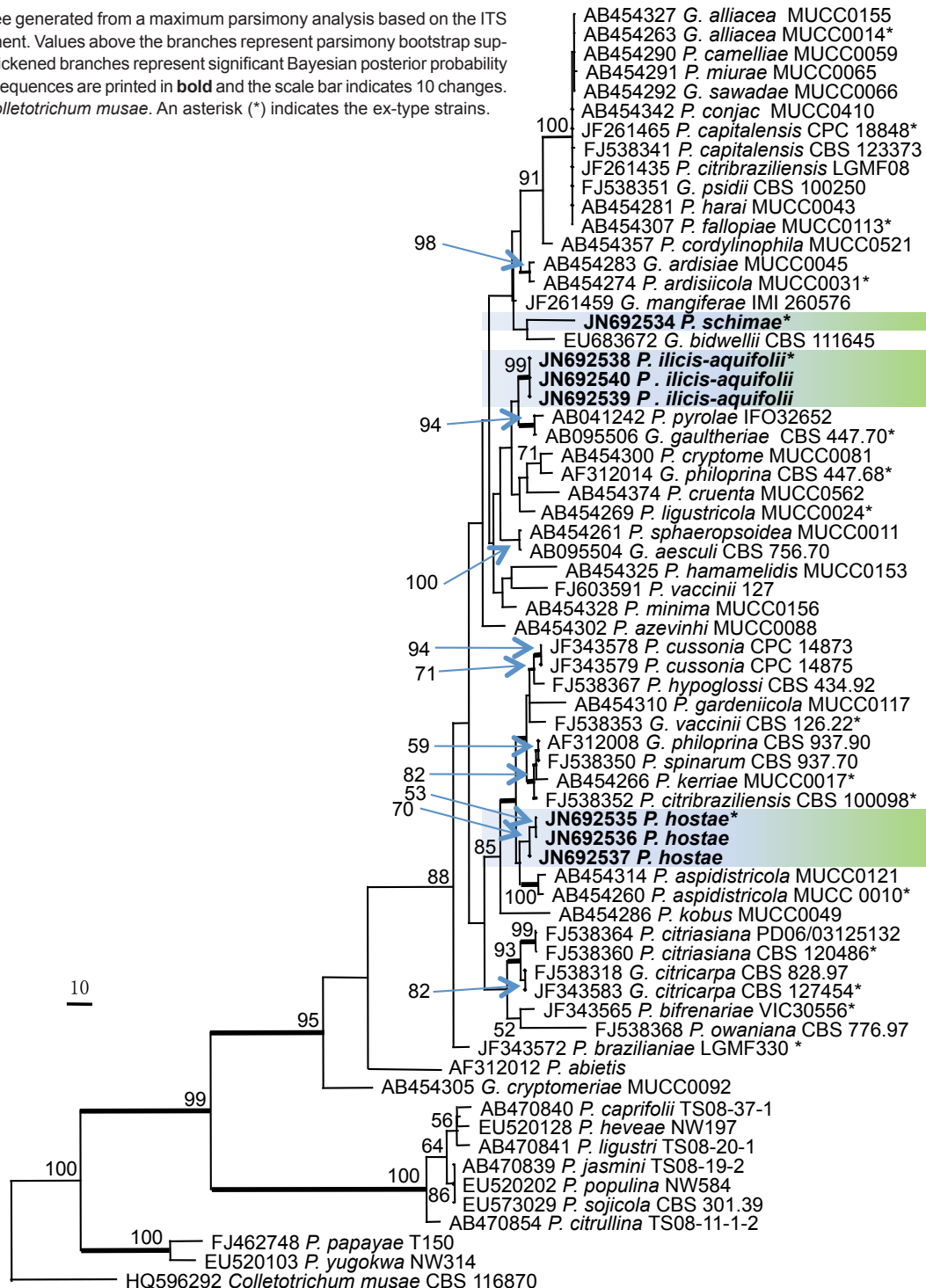
<sup>2</sup> ITS: Internal transcribed spacers 1 and 2 together with 5.8S rDNA; TEF1: partial translation elongation factor 1- $\alpha$  gene; ACT: partial actin gene; GPDH: partial glyceraldehyde-3-phosphate dehydrogenase gene.

## RESULTS

Phylogenetic relationships were inferred using the ITS alignment, and the combined ITS, TEF1, GPDH, and ACT sequence alignment. The 67 ITS sequence dataset from 52 taxa comprised 517 characters after alignment. Of these, 252 characters were parsimony informative, 47 were variable and parsimony-uninformative, and 218 were constant. Parsimony analysis generated two trees, and one of the equally most parsimonious trees with shorter tree length (TL = 935, CI = 0.539, RI = 0.827, RC = 0.446, HI = 0.461) was selected and shown in Fig. 1. For the Bayesian analyses, model (GTR+I+G) was selected in MrModeltest 2.3. The branches with significant Bayesian posterior probability ( $\geq 95\%$ ) were thickened in the phylogenetic tree. All three species described as new in this manuscript appear in distinct lineages (Fig. 1).

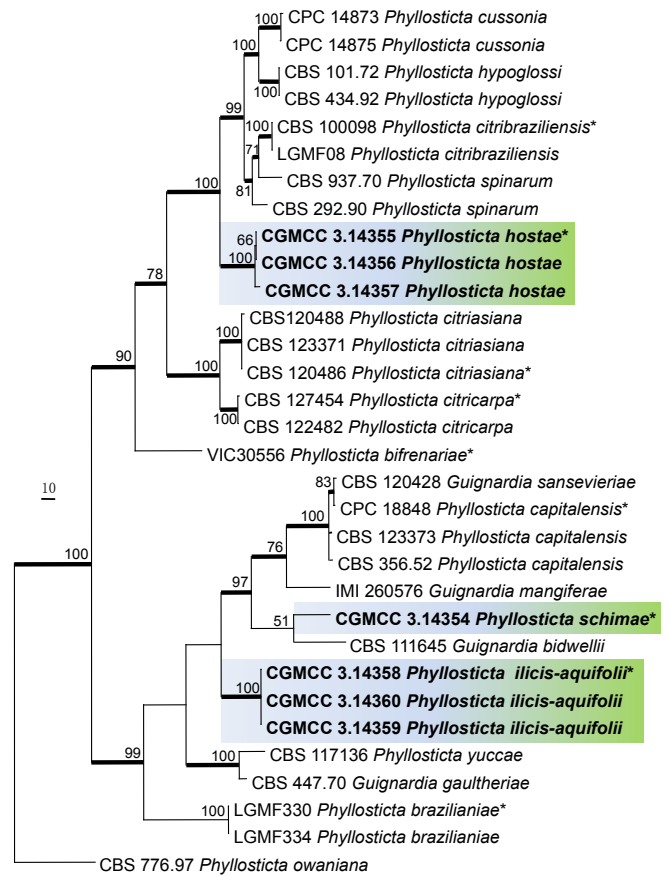
The combined datasets of ITS, TEF1, GPDH, and ACT contained 32 combined sequences from 18 taxa and comprised 1 791 characters after alignment. Of these, 407 characters were parsimony informative; 129 were variable and parsimony-uninformative, and 1 255 were constant. The parsimony analysis generated three equally most parsimonious trees and the tree with shortest tree length (TL = 1051, CI = 0.669, RI = 0.841, RC = 0.562, HI = 0.331) was selected and shown in Fig. 2. For the Bayesian analyses, the best-fit model (GTR+I+G) was selected in MrModeltest 2.3. The branches with significant Bayesian posterior probability ( $\geq 95\%$ ) were thickened in the phylogenetic tree. Similarly all three species appear in distinct lineages (Fig. 2).

**Fig. 1** Phylogenetic tree generated from a maximum parsimony analysis based on the ITS nrDNA sequence alignment. Values above the branches represent parsimony bootstrap support values ( $> 50\%$ ). Thickened branches represent significant Bayesian posterior probability values ( $\geq 95\%$ ). Novel sequences are printed in **bold** and the scale bar indicates 10 changes. The tree is rooted to *Colletotrichum musae*. An asterisk (\*) indicates the ex-type strains.



**Table 2** Synopsis of characters of *Phyllosticta* species from *Liliaceae*.

<i>Phyllosticta</i> species	Pycnidial size (µm)	Pycnidial wall	Conidiogenous cells (µm)	Conidia (µm)	Sheath diam (µm)	Appendage size (µm)	References
<i>P. aspidistricola</i>	61–118 × 86–110	–	7–12.5 × 1.2–2.5	9.5–12.5 × 8.5–10	–	17–24.5	Motohashi et al. (2008)
<i>P. cruenta</i>	80–200, mostly 120–160	1–4 cells, 7–20 µm thick	7–12 × 2–4	12–21 × 5–10, mostly 16–19 × 8–10	–	4–17 × 3	van der Aa (1973)
<i>P. crypta</i>	70–130 × 45–95	4–14 µm thick	5–12 × 2–3.5	5.4–8.9 × 3.8–6.2	0.3–1	3–8 × 0.5–1	Bissett (1979)
<i>P. cumminsii</i>	75–140	4–19 µm thick	3.5–14 × 3–6	9–19 × 6.7–10.5	1–2	5–20 × 1.6–4	Bissett (1979)
<i>P. hemerocallidis</i>	84–139	–	–	8–13 × 3–5 (av. 10 × 3.5)	–	3–10	van der Aa & Vanev (2002)
<i>P. hostae</i>	40–150	2–3 layers	7–22 × 2–5	8–15 × 5–9 (av. 10.9 × 7.6)	1–3	4–8 × 1–3	Present study
<i>P. hypoglossi</i>	120–250	2–4 cells, 12–30 µm thick	4–10 × 2–3.5	8–15(–18) × 6–10	–	10, up to 35	van der Aa (1973)
<i>P. subeffusa</i>	90–150 × 120–140	5–16 µm thick	5–8 × 3–4.5	7–13 × 7–10	–	5–7, up to 15	van der Aa (1973)
<i>P. uvulariae</i>	65–120 (usually 90–75)	5–12 µm thick	4–13 × 2.5–6	5–8.6 × 3.9–6.6 (av. 6.5–5.5)	less than 0.8	4–14 × 0.3–0.8	Bissett (1979)
<i>P. yuccae</i>	90–150	3–7 layers, 14–38 µm thick	5.4–9.8 × 2.7–6	7.5–15.4 × 6–9.5 (av. 10–7.3)	1	4–15	Bissett (1986)



**Fig. 2** Phylogenetic tree generated from a maximum parsimony analysis based on the combined ITS, EF, GPDH, and ACT sequence alignment, showing the phylogenetic relationships of the three new species. Values above the branches represent parsimony bootstrap support values (> 50 %). Thickened branches represent significant Bayesian posterior probability (≥ 95 %). Novel sequences are printed in **bold** and the scale bar indicates 10 changes. The tree is rooted to *Phyllosticta owaniiana*. An asterisk (\*) indicates the ex-type strains.

**TAXONOMY**

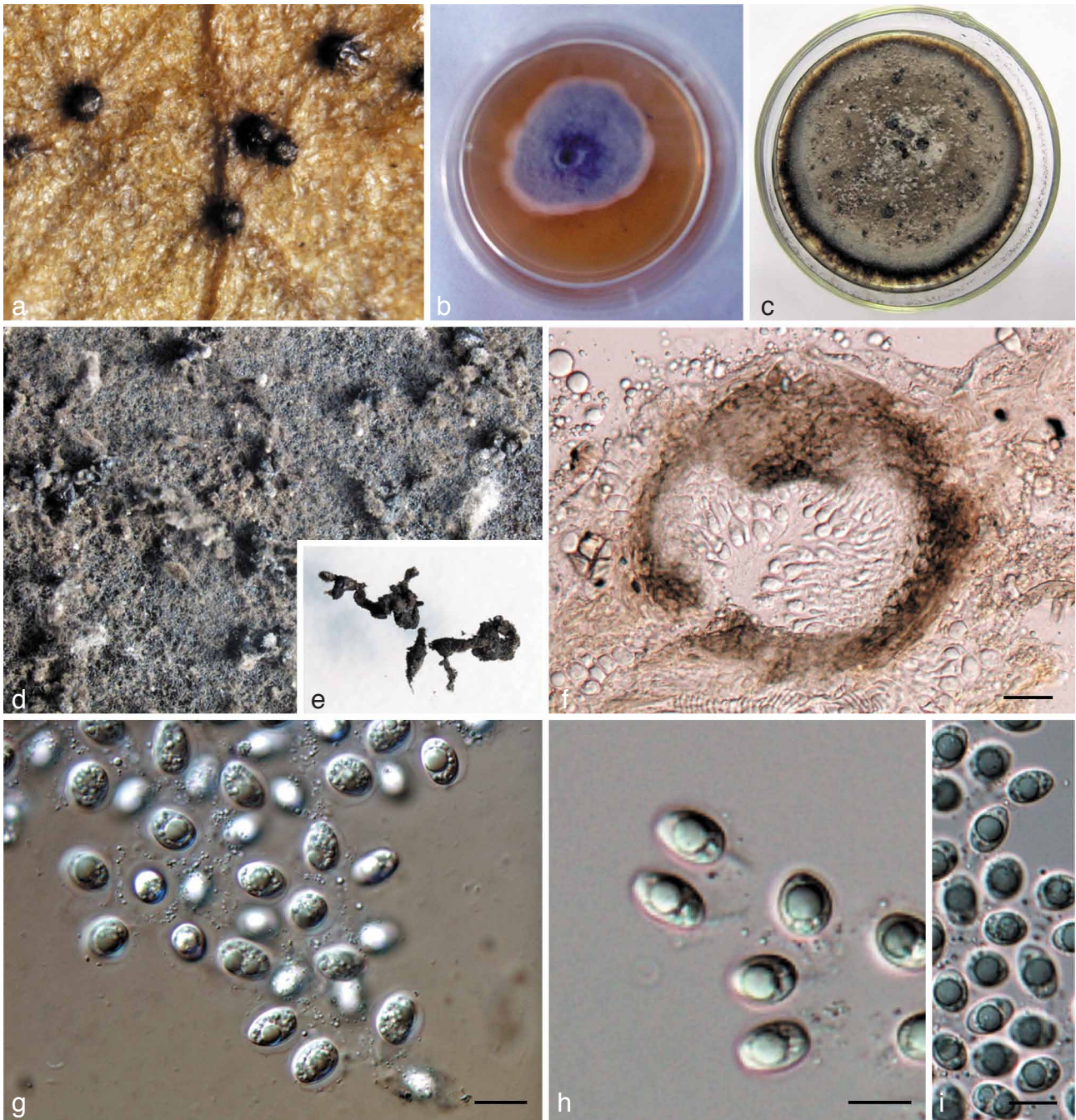
*Phyllosticta hostae* Y.Y. Su & L. Cai, *sp. nov.* — MycoBank MB564904; Fig. 3

*Etymology.* Named after its host, *Hosta plantaginea*.

*Leaf spots* ellipsoid or circular to somewhat irregular, yellow to pale brown, surrounded by dark brown border. *Pycnidia* black, subepidermal, globose, 40–150 µm diam. Pycnidial wall composed of depressed or irregular cells in 2–3 layers, brown to dark brown, darker around ostiole, hyaline or pale and flattened towards the inside. *Conidiogenous cells* 7–22 × 2–5 µm, holoblastic, phialidic, cylindrical, subcylindrical to ampulliform, hyaline, thin-walled, smooth. *Conidia* 8–15 × 5–9 µm ( $\bar{x}$  = 10.9 ± 1.4 × 7.6 ± 0.8, n = 30), unicellular, thin- and smooth-walled, ellipsoid, subglobose to obovoid, with a large central guttule, truncate at the base when young, later rounded at both ends, enclosed in a 1–3 µm thick mucilaginous sheath, and bearing a hyaline, mucoid apical appendage, 4–8 × 1–3 µm, straight to flexible, unbranched, tapering towards an acute tip.

*Culture characteristics* — Colonies on PDA flat, surface greenish grey in centre, white-grey at margin when young, becoming leaden-grey in centre, lavender-grey at margin after 2 wk.

*Specimens examined.* CHINA, Beijing, Botanical Garden, on leaf of *Hosta plantaginea*, 10 Sept. 2010, L. Cai, HMAS242924 (holotype); ex-type culture CGMCC3.14355; *ibid.* SYY572, culture CGMCC3.14356; *ibid.* SYY573, culture CGMCC3.14357.



**Fig. 3** *Phyllosticta hostae*. a. Appearance of conidiomata on host leaf surface; b. colony on PDA 7 d after inoculation; c. colony on PDA 1 mo after inoculation; d, e. pycnidia forming on PDA; f. vertical section of pycnidium in leaf tissue; g–i. conidia. — Scale bars: f = 20  $\mu$ m; g–i = 10  $\mu$ m.

**Notes** — *Phyllosticta hostae* was isolated from *Hosta plantaginea* (Liliaceae), which is grown as a common ornamental plant in China and many Asian countries. There are several reports of fungal pathogens isolated from *H. plantaginea*, e.g., *Alternaria asphodeli* (Zhang 1999), *Botrytis cinerea* (Zhang 2006), and *Colletotrichum omnivorum* (Cho & Shin 2004). To date, *P. hostae* is the only species of *Phyllosticta* described from the plant genus *Hosta*. However nine *Phyllosticta* species are currently known on Liliaceae, i.e. *P. aspidisticola*, *P. cruenta*, *P. crypta*, *P. cumminsii*, *P. hemerocallidis*, *P. hypoglossi*, *P. subeffusa*, *P. uvulariae*, and *P. yuccae* (van der Aa & Vanev 2002, Motohashi et al. 2008). A comparison of their morphological characters with *P. hostae* is given in Table 2.

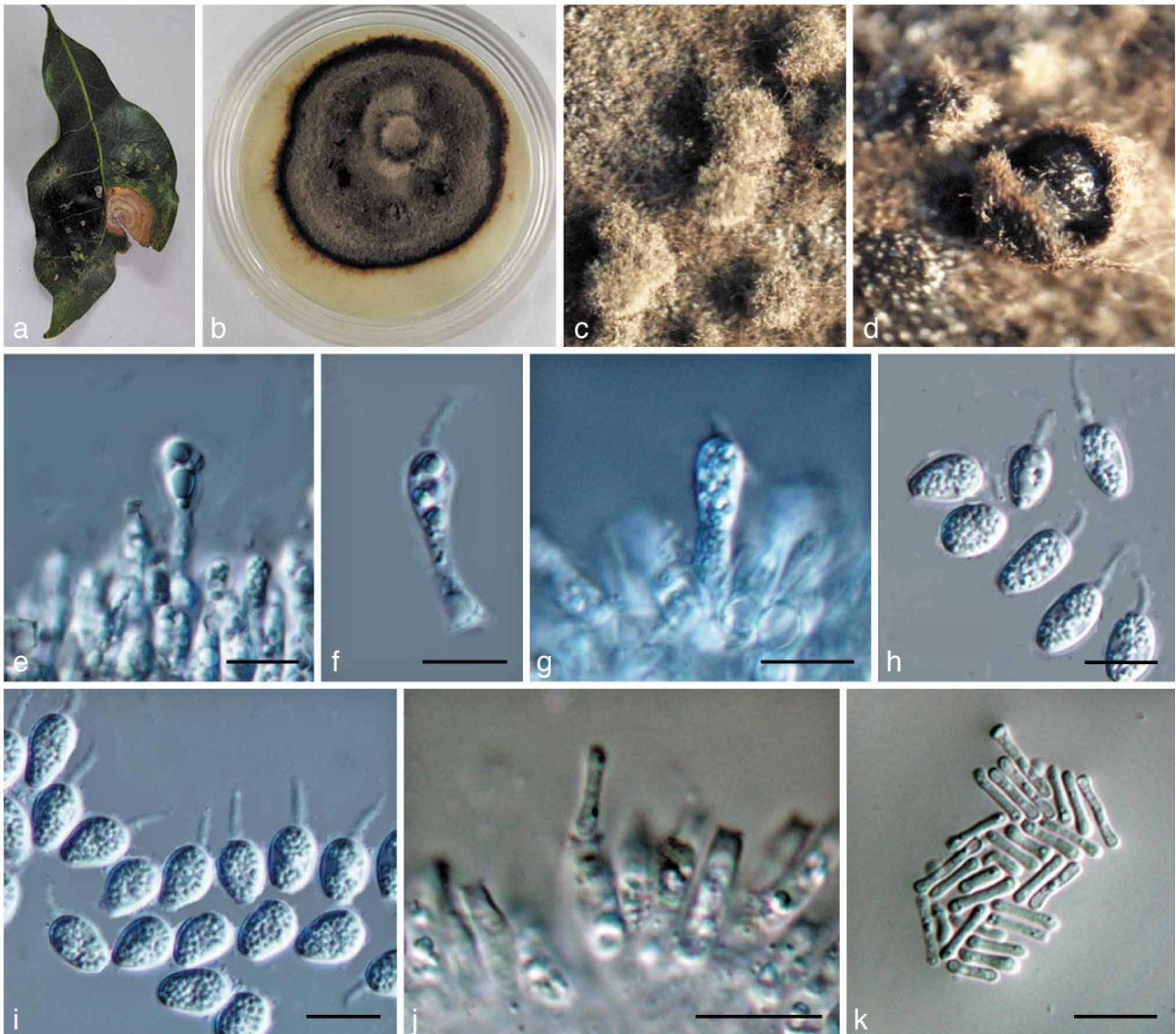
The phylogenetic tree generated from a multilocus sequence alignment showed that the three strains of *P. hostae* constituted a distinct lineage with 100 % bootstrap support (Fig. 2). DNA sequence analysis showed that *P. hostae* was most closely related to *P. citribraziliensis*, *P. cussonia*, *P. hypoglossi*, *P. spi-*

*narum*, and *P. vaccinii* (teleomorph *Guignardia vaccinii*). Of these species, *P. vaccinii* is morphologically most similar, but the ex-type strain (CBS 126.22) shares only 94 % identity to *P. hostae* in ITS sequence. *Phyllosticta vaccinii* was isolated from the leaves of *Vaccinium arboretum*. The pycnidia of *P. vaccinii* are larger (80–175  $\mu$ m vs 40–150  $\mu$ m) than that of *P. hostae*, and the conidia are slightly smaller (8–12  $\times$  5–8  $\mu$ m vs 8–15  $\times$  5–9  $\mu$ m). In addition, the appendages of *P. vaccinii* can be up to 17  $\mu$ m long, while that of *P. hostae* is less than 8  $\mu$ m (van der Aa 1973).

***Phyllosticta schimae*** Y.Y. Su & L. Cai, *sp. nov.* — MycoBank MB564905; Fig. 4

*Etymology.* Named after its host, *Schima superba*.

*Leaf spots* circular, somewhat irregular, yellow to pale brown, surrounded by dark brown borders, fruiting bodies not observed. *Pycnidia* on PDA grey to black, aggregated, superficial to



**Fig. 4** *Phyllosticta schimae*. a. Symptom on leaf of *Schima superba*; b. colony on PDA 1 mo after inoculation; c, d. pycnidia forming on PDA; e–g. conidiogenous cells giving rise to conidia; h, i. conidia; j. spermatogenous cells producing spermatia; k. spermatia. — Scale bars: e–k = 10 µm.

erumpent, globose to ampulliform, 150–200 µm diam. *Conidiogenous cells* 8–30 × 2–4 µm, holoblastic, phialidic, short cylindrical, subcylindrical to ampulliform, hyaline, thin-walled, smooth. *Conidia* 7–13 × 4–7 µm ( $\bar{x}$  = 9.5 ± 1.1 × 6.2 ± 0.4, n = 30), unicellular, thin- and smooth-walled, globose, ellipsoid to obovoid, truncate at the base when young, later rounded at both ends, enclosed in a mucilaginous sheath, and bearing a hyaline, mucoid apical appendage, 4–10 × 1–3 µm, straight to flexible, unbranched, tapering towards an acute tip. *Spermatogenous cells* subcylindrical to ampulliform, 11–25 × 2–4 µm. *Spermatia* aseptate, dumbbell-shaped, 7–11 × 1–2.5 µm ( $\bar{x}$  = 8.3 ± 1.4 × 1.4 ± 0.3, n = 30).

**Culture characteristics** — Colonies on PDA flat, brown-black, with moderate aerial mycelium.

**Specimens examined.** CHINA, Zhejiang, Gutianshan Nature Reserve, on leaf of *Schima superba*, 18 Aug. 2010, Y.-Y. Su, HMAS242923 (holotype); ex-type culture CGMCC3.14354.

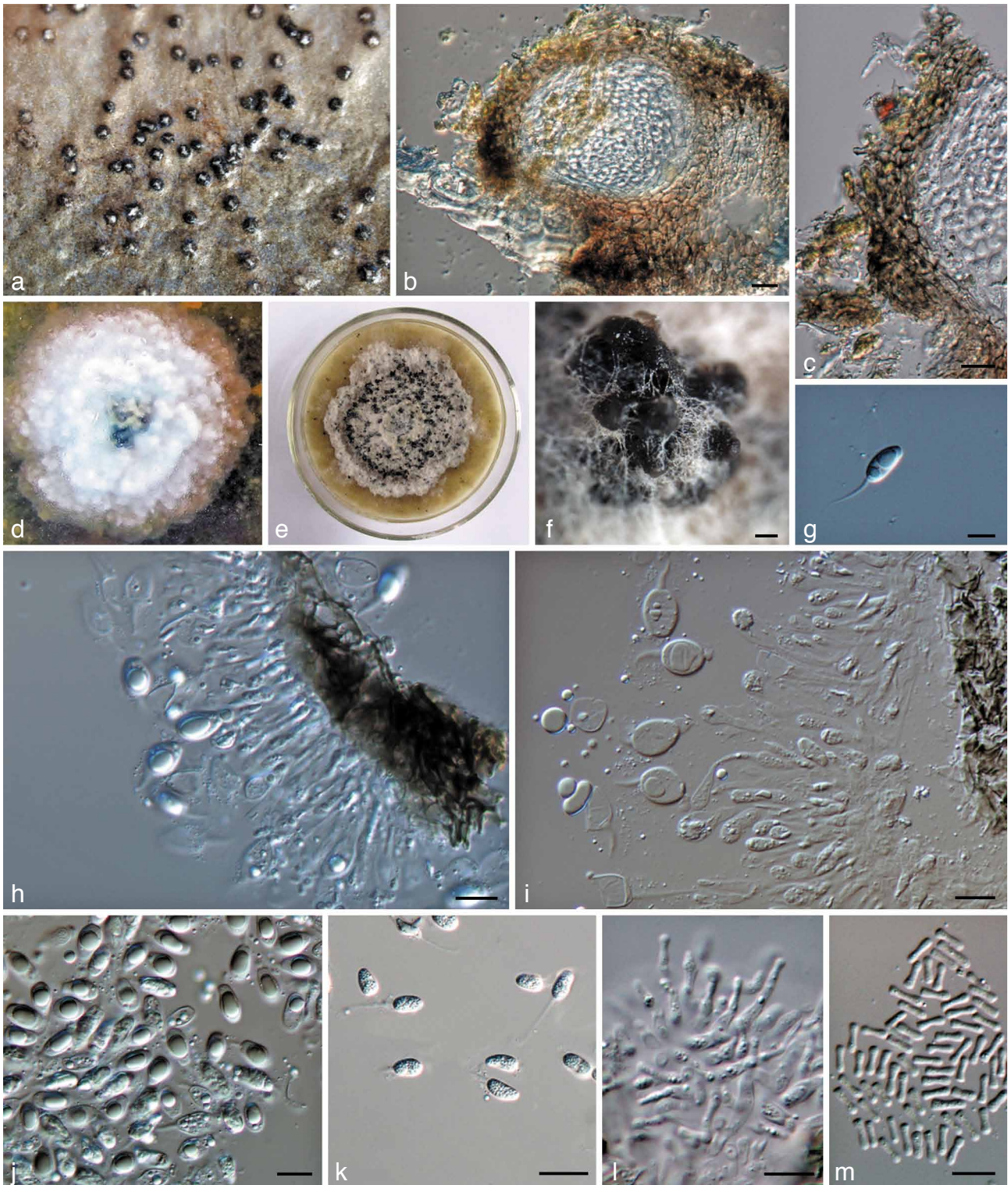
**Notes** — *Schima superba* is one of the dominant tree species in evergreen broad leaf subtropical forests in China. Currently there are only two unnamed *Phyllosticta* species reported from *Schima* (*Theaceae*) (Kobayashi 2007). Only two species, *P. plurivora* and *P. theacearum*, were recorded in the plant family *Theaceae* (van der Aa & Vanev 2002), and the former has been considered a synonym of *P. theacearum* (van der Aa & Vanev

2002). *Phyllosticta theacearum* produces shorter conidiogenous cells (4–6 µm vs 8–30 µm) than that of *P. schimae* (van der Aa 1973, van der Aa & Vanev 2002). *Phyllosticta schimae* appears closely related to *P. ampelicida* (teleomorph *G. bidwellii*) (92 % identity in ITS sequence) (Fig. 1, 2), which was isolated from the leaves of *Ampelopsis quinquefolia* (van der Aa 1973). Morphologically, *P. schimae* produces larger pycnidia (150–200 µm vs 70–180 µm), and longer conidiogenous cells (8–30 × 2–3 µm vs 6 × 3 µm) than *P. ampelicida* (van der Aa 1973).

***Phyllosticta ilicis-aquifolii*** Y.Y. Su & L. Cai, sp. nov. — MycoBank MB564906; Fig. 5

**Etymology.** Named after its host, *Ilex aquifolium*.

**Leaf spots** ellipsoid or circular to somewhat irregular, grey to pale brown, about 7 mm diam, surrounded by dark brown border. *Pycnidia* amphigenous, subepidermal, single, 70–230 µm diam. Pycnidial wall composed of depressed or irregular cells of 2–4 layers, brown to dark brown, darker around ostiole, hyaline or pale and flattened towards the inside. *Conidiogenous cells* (8–)12–17(–19) × (2–)3–4 µm, holoblastic, phialidic, cylindrical, subcylindrical to ampulliform, hyaline, thin-walled, smooth. *Conidia* 10–18 × 6–9 µm ( $\bar{x}$  = 13.4 ± 1.8 × 7 ± 0.7, n = 30), unicellular, thin- and smooth-walled, globose, ellipsoid



**Fig. 5** *Phyllosticta ilicis-aquifolii*. a. Appearance of conidiomata on host leaf surface; b. vertical section of pycnidium in leaf tissue; c. vertical section through the peridium; d. colony on PDA 7 d after inoculation; e. colony on PDA 1 mo after inoculation; f. pycnidia forming on PDA; g. conidium; h, i. conidiogenous cells giving rise to conidia; j, k. conidia; l. spermatogenous cells producing spermata; m. spermata. — Scale bars: b, c, k = 20  $\mu$ m, f = 50  $\mu$ m, g, h–j, l, m = 10  $\mu$ m.

to obovoid, with a large central guttule, truncate at the base when young, later rounded at both ends, enclosed in a thick mucilaginous sheath, 1–3  $\mu$ m thick, and bearing a hyaline, mucoid apical appendage, (9–)12–17(–30)  $\times$  2–3  $\mu$ m, straight to flexible, unbranched, tapering towards an acute tip. *Spermatogenous cells* subcylindrical to ampulliform, 5–17  $\times$  1–4  $\mu$ m. *Spermata* aseptate, dumbbell-shaped, 5–8  $\times$  1.5–2.5  $\mu$ m ( $\bar{x}$  = 6.7  $\pm$  0.7  $\times$  1.9  $\pm$  0.2, n = 30).

**Culture characteristics** — Colonies on PDA flat, with irregular margin, surface white-grey when young; leaden-grey in centre, and white-grey at margin after 2 wk.

**Specimens examined.** UK, England, London, on leaf of *Ilex aquifolium*, 15 Aug. 2010, L. Cai, HMAS242922 (holotype), ex-type culture CGMCC3.14358; ibid. SYY590, culture CGMCC3.14359; ibid. SYY591, culture CGMCC3.14360. Three duplicate strains were deposited in IMI.

**Notes** — *Phyllosticta ilicis-aquifolii* was isolated from the common ornamental and hedge plant *Ilex aquifolium*. It is characterised by its large conidia that have a long mucoid appendage, which is distinct from most *Phyllosticta* species. Other *Phyllosticta* species reported from *Aquifoliaceae* include *P. llimonae* and *P. concentrica* (van der Aa & Vanev 2002). *Phyllosticta ilicis-aquifolii* differs from *P. llimonae* in producing



shorter conidiogenous cells (12–17 vs 28–32 µm) (Bertault 1982), and from *P. concentrica* (teleomorph *Guignardia philo-prina*) in producing larger spermatia (6–15 × 1.5–3 µm vs 5–8 × 1.5–2.5 µm) (van der Aa 1973). In addition, the ex-type strains *Phyllosticta ilicis-aquifolii* and *G. philoprina* shared 94 % identity in ITS sequence and clustered in different clades in the ITS phylogenetic tree (Fig. 1). Although there are 26 synonyms listed under *P. concentrica* (<http://www.mycobank.org>), the conidial sizes in these species descriptions are all smaller (shorter than 12 µm) than that of *P. ilicis-aquifolii*, except for *Sphaeria taxi* (20–22 × 10 µm vs 10–18 × 6–9 µm in *P. ilicis-aquifolii*) and *Phoma ilicis* (12–15 × 3 µm vs 10–18 × 6–9 µm).

*Phyllosticta ilicis-aquifolii* appears most closely related to *P. gaultheriae* (teleomorph *G. gaultheriae*) (94 % identity in ITS sequence) and *P. pyrolae* (95 % identity in ITS sequence) (Fig. 1). Morphologically, *P. ilicis-aquifolii* can be distinguished from these species by its larger conidia (10–18 × 6–9 µm vs 4–9 × 4–7 µm in *P. gaultheriae* and 4.5–7.5 × 4–9 µm in *P. pyrolae*) (van der Aa 1973).

## DISCUSSION

In this paper we have described and named three new *Phyllosticta* species based on morphological and molecular characters. Each has morphological characters typical for *Phyllosticta*, i.e., stromatic conidiomata, holoblastic conidiogenesis, one-celled conidia provided with a surrounding mucoid layer and an apical appendage (van der Aa 1973, van der Aa & Vanev 2002).

Plant pathogenic *Phyllosticta* species are usually specific to host species or genera (van der Aa 1973, van der Aa & Vanev 2002, Motohashi et al. 2008, 2009, Wikee et al. 2011). Morphological comparisons of *Phyllosticta* spp. are often made with species reported from congeneric hosts (van der Aa & Vanev 2002, Motohashi et al. 2008, Wulandari et al. 2009, Glienke et al. 2011, Wang et al. 2012). In our study, the new species were compared with other species reported from the same host family and species that are morphologically and phylogenetically closely related. These results showed that the three species were distinct, representing novel taxa.

Jin (2011) reported that the conidial appendages of some *Phyllosticta* species might disappear with time or elongate when mounted in water. Therefore, fresh cultures were used for morphological observations, and the conidial appendages were not given undue significance in species delimitation. In this study, the morphological comparisons were made mainly based on other characters, e.g., the shape and size of conidia, pycnidia, and conidiogenous cells.

Although the generic concept of *Phyllosticta* as defined by van der Aa (1973) is extensively accepted, the identification of species is still difficult due to limited morphological characters that can be used for comparison. Recent molecular studies have revealed the ambiguity of taxonomy based on morphological characters and host associations (Wulandari et al. 2009, Glienke et al. 2011). Multilocus phylogenetic analysis has been shown to be more useful in predicting natural species relationships in the genus (Motohashi et al. 2009, Wulandari et al. 2009, Glienke et al. 2011). Traditionally applied phenotypic characters (host, symptom, colony characteristics, and morphology) should therefore be re-evaluated for their taxonomic usefulness in light of phylogenetic relationships (Hyde et al. 2010).

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