

***Pestalotiopsis camelliae*, a new species associated with grey blight of *Camellia japonica* in China**

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We have been surveying diseases of ornamental plants in Yunnan Province, China and discovered a previously undescribed species of *Pestalotiopsis* causing grey blight disease on leaves of *Camellia japonica*. The associated causal agent of the disease is introduced as a new species, *Pestalotiopsis camelliae*, in this paper. The taxon can clearly be distinguished from all known species of *Pestalotiopsis* by its morphology and DNA (combined ITS, β -tubulin and *tef1* gene regions) phylogeny. Its most similar relative, *P. furcata* has conidia with more apical appendages (5–9) than in *P. camelliae* (3–6) and the appendages of *P. furcata* consistently divide into branches, that is rare in *P. camelliae*.

Keywords: asexual taxon, leaf spot, *Pestalotiopsis furcata* phylogeny, sp. nov.

During a survey of diseases of ornamental plants in Yunnan Province, China, we constantly observed grey blight of *Camellia japonica* L. (Japanese camellia) and primary identification found a *Pestalotiopsis* species associated with the disease symptom. *Pestalotiopsis* Steyaert is an appendage-bearing conidial asexual form (coelomycetes) in the family Amphispheeraceae (Barr 1975, 1990). Species of *Pestalotiopsis* are common in tropical and temperate ecosystems (Bate-Smith & Metcalfe 1957) and may cause plant disease (Das *et al.* 2010, Ko Ko *et al.* 2011, Zhang *et al.* 2012). They are also often isolated as endophytes (Wei *et al.* 2007, Xu *et al.* 2010), or occur as saprobes (Wu *et al.* 1982, Yanna *et al.* 2002).

The taxonomic status of species within the genus is confused and species identification using only molecular or morphological data is problem-

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atic (Hu *et al.* 2007, Maharachchikumbura *et al.* 2011, 2012 a, b). Therefore, distinct morphological characters as well as molecular data are needed to distinguish species in the genus (Maharachchikumbura *et al.* 2011). The aim of the current paper is to describe the distinct morphological and molecular characters of the new *Pestalotiopsis* species associated with *C. japonica* grey blight.

Materials and methods

Sample collection, isolation and identification

Fresh specimens of *Pestalotiopsis* sp. were obtained from leaf spots on living leaves of *Camellia japonica* in Shuangbai, Chuxiong, Yunnan Province, China. To induce sporulation, diseased leaves were placed in sterilized Petri dishes with moistened sterile filter paper. A single conidium culture technique was used to obtain pure colonies of the taxon following the method used by Chomnunti *et al.* (2011). Fungal mycelium and spores were observed under a light microscope (Nikon Ei800 and Leica DM3000) and photographed.

DNA extraction and PCR condition

Biospin Fungus Genomic DNA Extraction Kit (Produced Bioer Technology Co., Ltd. Hubei, China) was used to extract total genomic DNA from fresh fungal mycelia (500 mg) scraped from the margin of a colony on a PDA plate incubated at 25 °C for 7 to 10 days. The ITS and 5.8S region of rDNA molecule was amplified using primer pairs ITS4 and ITS5 (White *et al.* 1990), β -tubulin gene region was amplified with primer pairs BT2A and BT2B (Glass & Donaldson 1995, O'Donnell & Cigelnik 1997) and *tef1* was amplified using the primer pairs EF1-526F and EF1-1567R (Rehner 2001). PCR was performed under conditions used by Maharachchikumbura *et al.* (2012 a).

Phylogenetic analysis

Sequences were optimized manually to allow maximum alignment and maximum sequence similarity as detailed in Liu *et al.* (2011). A maximum parsimony analysis (MP) was performed using PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford 2002). Ambiguously aligned regions were excluded and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Maxtrees were set up to 10000, branches of zero length were collapsed and all multiple parsimonious trees were saved. Tree length [TL], consistency index [CI], retention index [RI], rescaled consistency index [RC], homoplasy index [HI], and log likelihood [-ln L] (HKY model) were calculated for trees generated under different optimality criteria. The robustness of the most parsimonious trees was evaluated by 100 bootstrap replications resulting from maximum parsimony analysis, each with ten replicates of random stepwise addition of taxa (Felsenstein 1985). The Kishino-

Hasegawa tests (Kishino & Hasegawa 1989) were performed in order to determine whether the trees inferred under different optimality criteria were significantly different. Trees were viewed in Treeview (Page 1996).

Results

A phylogenetic tree was constructed using combined ITS, β -tubulin and *tef1* sequences of 18 isolates of *Pestalotiopsis*, with a *Seiridium* sp. as the outgroup (Tab. 1). The aligned data matrix consisted of 2006 characters (ITS = 543, β -tubulin = 460, *tef1* = 1003); 1454 characters were constant, 163 variable characters were parsimony-uninformative and 389 characters were parsimony-informative. The Kishino-Hasegawa (KH) test showed that the two trees generated from parsimonious analysis were not significantly different and one tree was selected as the best tree (length = 872 steps, CI = 0.826, RI = 0.916, HI = 0.174, RC = 0.756). In the phylogram the *Pestalotiopsis* strains separated into three major clades, named A, B and C, with high bootstrap support (Fig. 1). Clade A comprised species having pale brown or olivaceous concolorous median conidial cells. Clade B comprised species having versicolorous median conidial cells and Clade C species with dark concolorous median conidial cells, with knobbed apical appendages. We constructed phylogenetic trees separately for each gene region (results not shown) and the resolution increased from ITS, β -tubulin to *tef1*, respectively, but the best resolution was obtained when all three genes were combined.

Taxonomy

Pestalotiopsis camelliae Y. M. Zhang, S. S. N. Maharachchikumbura & K. D. Hyde, **sp. nov.** – Figs. 2–3.
MycoBank no.: MB 800980

Teleomorph. – Unknown.

Description. – Associated with grey blight on leaves of *Camellia japonica*, initially producing small, rounded, yellow-green spots on the leaves, spots becoming brown to grey, with concentric rings and producing black, scattered acervuli (Fig. 1). Acervuli grey to black, epidermal to subepidermal, separate or confluent, dehiscence irregular, 100–220 μm wide, 76 – 150 μm high, unilocular, glabrous; wall tissue (stroma and parietal cells) only a few cells thick, cell walls thick, outermost layer colourless, inner layers pale brown to brown, encrusted (Fig. 1). Conidiophores reduced to conidiogenous cells. Conidiogenous cells discrete, lageniform, smooth, thin-walled, colourless. Conidia 27–33 \times 7.5–9.3 μm (28.5 \times 8.5 μm), fusoid, straight to slightly curved, 4-septate, basal cell obconic, colourless, thin- and smooth-walled, 4–7 μm long (5.4 μm), with three median cells, doliiform to subcylindrical, with thick verruculose walls, slightly constricted at the septa, concolorous, olivaceous, septa and periclinal walls darker than the rest of the cell, wall rugose, together 19–22 μm long (20 μm) (second cell from base 5.6–

Tab. 1. Details of *Pestalotiopsis* isolates used in the phylogenetic study.

| Taxon | Isolates | Host/Location | GenBank accession number | | | Reference for sequence |
|--|----------------------|-------------------------------------|--------------------------|-----------|----------|---|
| | | | ITS | β-tubulin | tefl | |
| <i>P. cf. algeriensis</i> (Sacc. & Berl.) W. Wu | SD077 | <i>Camellia sinensis</i> / China | JQ683718 | JQ683702 | JQ683734 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. cf. disseminata</i> (Thüm.) Steyaert | SD034 | <i>C. sinensis</i> /China | JQ683716 | JQ683700 | JQ683732 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. cf. menezesiana</i> (Bres. & Torrend) Bissett | SG064 | <i>C. sinensis</i> /China | JQ683719 | JQ683703 | JQ683735 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. cf. menezesiana</i> | SD072 | <i>C. sinensis</i> /China | JQ683713 | JQ683697 | JQ683729 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. cf. microspora</i> (Speg.) G. C. Zhao & N. Li | SD056 | <i>C. sinensis</i> /China | JQ683722 | JQ683706 | JQ683738 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. cf. versicolor</i> (Speg.) Steyaert | SG100 | <i>C. sinensis</i> /China | JQ683712 | JQ683696 | JQ683728 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. cf. versicolor</i> | SD047 | <i>C. sinensis</i> /China | JQ683715 | JQ683699 | JQ683731 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. cf. versicolor</i> | SD091 | <i>C. sinensis</i> /China | JQ683714 | JQ683698 | JQ683730 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. camelliae</i> Y. M. Zhang, Maharachchikumbura & K. D. Hyde | OP111 | <i>C. japonica</i> /China | JX399010 | JX399041 | JX399074 | Maharachchikumbura <i>et al.</i> 2012 a |
| <i>P. camelliae</i> | OP131 | <i>C. japonica</i> /China | JX399011 | JX399042 | JX399075 | Maharachchikumbura <i>et al.</i> 2012 a |
| <i>P. cf. virgatula</i> (Kleb.) Steyaert | SD004 | <i>C. sinensis</i> /China | JQ683723 | JQ683707 | JQ683739 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. furcata</i> Maharachchikumbura & K. D. Hyde | MFL UCC12-0054/SS017 | <i>C. sinensis</i> / Thailand | JQ683724 | JQ683708 | JQ683740 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. theae</i> (Sawada) Steyaert | MFL UCC12-0055/SC027 | <i>C. sinensis</i> / Thailand | JQ683727 | JQ683711 | JQ683743 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. theae</i> | SC011 | <i>C. sinensis</i> / Thailand | JQ683726 | JQ683710 | JQ683742 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>P. trachycarpicola</i> Y. M. Zhang & K. D. Hyde | OP068 | <i>Trachycarpus fortunei</i> /China | JQ845947 | JQ845945 | JQ845946 | Zhang <i>et al.</i> 2012 |
| <i>Pestalotiopsis</i> sp. | SD012 | <i>C. sinensis</i> /China | JQ683720 | JQ683704 | JQ683736 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>Pestalotiopsis</i> sp. | SD072 | <i>C. sinensis</i> /China | JQ683713 | JQ683697 | JQ683729 | Maharachchikumbura <i>et al.</i> 2012 b |
| <i>Seiridium</i> sp. | SD096 | <i>C. reticulata</i> /China | JQ683725 | JQ683709 | JQ683741 | Maharachchikumbura <i>et al.</i> 2012 b |

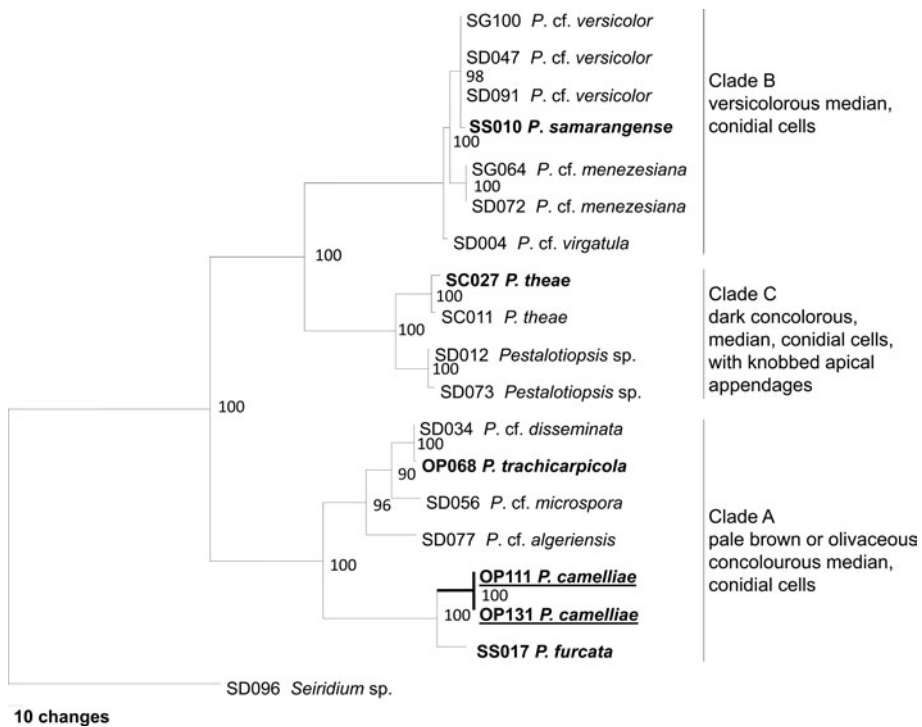


Fig. 1. Maximum parsimony phylogram generated from combine three genes (ITS, β -tubulin and *tef1*) analysis of species of *Pestalotiopsis*. Data were analyzed with random addition sequence, unweighted parsimony and treating gaps as missing data. *Seiridium* sp. was placed as outgroup, ex-type sequences are bold and the new species *P. camelliae* is underlined.

7.4 μ m (6.1 μ m); third cell 5–8.3 μ m (6.7 μ m); fourth cell 6–8.3 μ m (7.2 μ m); apical cell colorless, conic to cylindrical 3–6.4 μ m long (4.7 μ m); 3–6 tubular apical appendages, rarely branched, arising from the upper portion of the apical cell, 13.5–34 μ m long (23.8 μ m); basal appendages absent.

Colonies relatively fast growing on PDA, reaching 7 cm after 7 days at 25 °C, edge entire, whitish, with dense, aerial mycelium on surface, conidiomata black, gregarious; reverse of culture white.

Etymology. – *camelliae*, in reference to the host genus *Camellia*.

Host plant. – on leaf spots of living leaves of *Camellia japonica*.

Distribution. – so far only known from the type locality Shuangbai, Chuxiong, Yunnan Province, China.

Holotype and further material examined. – CHINA, Yunnan Province, Chuxiong, Shuangbai, on leaf spots of living leaves of *Camellia japonica* L., July 2011, Y. M. Zhang OP111 (IFRD OP111; holotype) – ex-type culture MFLUCC = MFLUCC12-0277; *ibid.*, August 2011, Y. M. Zhang OP131 (IFRD OP131), MFLUCC = MFLUCC 12-0278.

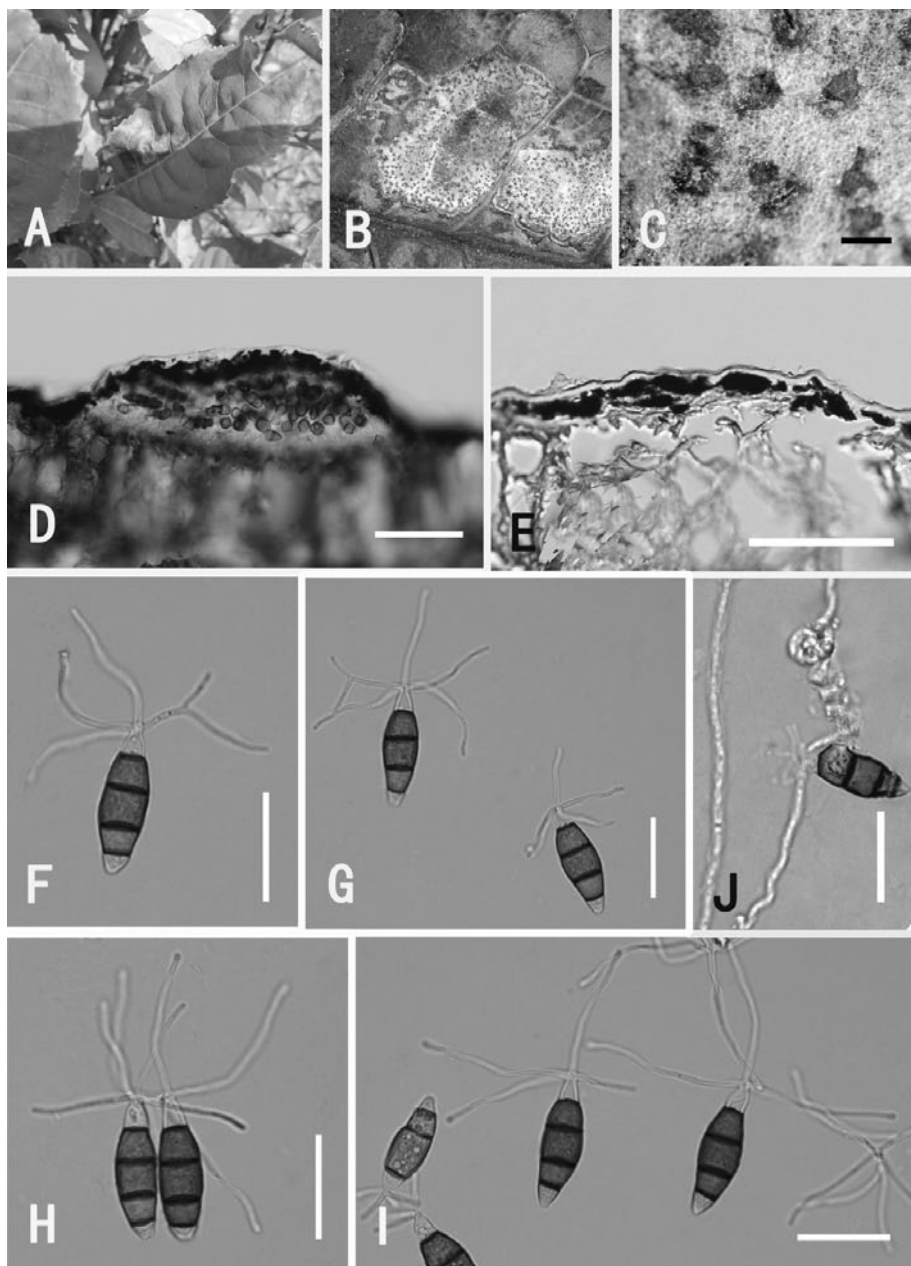


Fig. 2. *Pestalotiopsis camelliae* (holotype) from host. **A** Blight on leaf of *Camellia japonica*. **B, C** Conidiomata, splitting irregularly. **D** Section of conidiomata. **E** Conidiophores/ conidigenous cells. **F-I** Conidia with 3-6 appendages. **J** Germination of the conidia. Bars: **C** 200 µm; **D, E** 50 µm; **F-J** 20 µm.

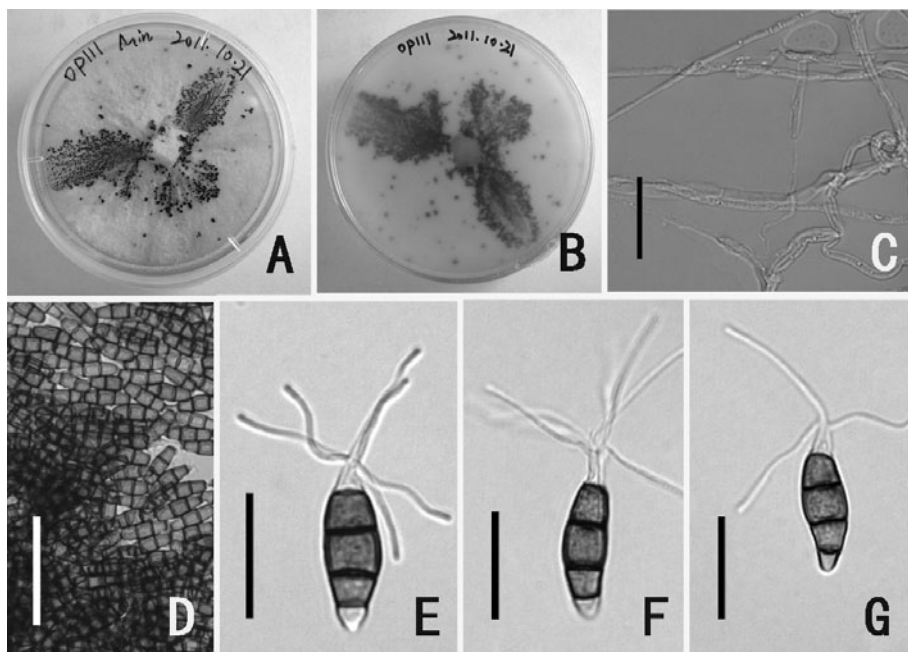


Fig. 3. *Pestalotiopsis camelliae* (holotype) from culture. **A, B** Colony on PDA, **A** from above, **B** from below. **C** Hyaline mycelium from colony. **D** Black slimy mass of conidia. **E–G** Conidia. Bars: **C–G** 20 µm; **D** 50 µm.

Discussion

Pestalotiopsis contains numerous species and several species are complexes within which species can only be distinguished by using multi-gene sequence data. This is true of many other plant pathogenic genera that have been recently studied (Cai *et al.* 2011, Summerell *et al.* 2011).

Some morphological characters of *Pestalotiopsis camelliae* and related species are synoptically compared in Tab. 2. *Pestalotiopsis camelliae* is similar to *P. furcata* Maharachchikumbura & K. D. Hyde but is a distinct species in terms of its characteristic morphology and DNA phylogeny. It has relatively small conidia ($26.8\text{--}33 \times 7.5\text{--}9.3$ µm), although these overlap in size with those of *P. furcata* ($29\text{--}39 \times 8.5\text{--}10.5$ µm). *Pestalotiopsis furcata* has more apical appendages (5–9) than *P. camelliae* (3–6). The apical appendages of *P. furcata* consistently divide into branches while this is a rare character in *P. camelliae*. In addition, *P. camelliae* separates from *P. furcata* with high bootstrap support (100%) (Fig. 1). The conidia of *P. camelliae* ($27\text{--}33 \times 7.5\text{--}9.3$ µm) lack basal appendages when comparing those of morphologically similar species such as *P. leucopogonis* Nag Raj ($27\text{--}32 \times 7.5\text{--}9.5$ µm), *P. macrospora* (Ces.) Steyaert ($30\text{--}40 \times 7\text{--}9$ µm) and *P. natrassi* Steyaert ($27\text{--}33 \times 8\text{--}9$ µm).

Tab. 2. Synopsis of *Pestalotiopsis camelliae* and related species.

| Species | <i>P. camelliae</i> | <i>P. furcata</i> | <i>P. natrassi</i> ^b | <i>P. leucopogonis</i> ^c | <i>P. hainanensi</i> A.R. Liu, T. Xu & L.D. Guo ^d |
|--------------------|----------------------------|----------------------------|---------------------------------|---------------------------------------|---|
| Conidia size (µm) | 27–33 × 7.5–9.3 | 29–39 × 8.5–10.5 | 27–33 × 8–9 | 27–32 × 7.5–9.5 | 19–22 × 5–6 |
| Median cells | concolorous, olivaceous | concolorous, olivaceous | concolorous, brown | concolorous, brown | concolorous, brown to olivaceous |
| Apical appendages: | 3–6 | 5–9 | 1–4 | 7–11 | 1–3 |
| Length (µm) | 13.5–33.7 | 20–35 | 25–44 | 12–19 | 1–10 |
| Branching | sometimes | branched | no | no | no |
| Position | apex | apex | apex | 3 rows (top, middle and bottom) | apex |
| Basal appendages | absent | absent | absent or present | absent or present | absent |

^a Maharachchikumbura *et al.* (2012 b), ^b Guba (1961), ^c Nag Raj (1993), ^d Liu (2007)

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References

Barr M. E. (1975) *Pestalospheeria*, a new genus in the Amphisphaeriaceae. *Mycologia* **67**: 187–194.
Barr M. E. (1990) Prodromus to nonlichenized, pyrenomycetous members of class Hymeniascomycetes. *Mycotaxon* **39**: 43–184.
Bate-Smith E. C., Metcalfe C. R. (1957) Leucanthocyanins. 3. The nature and systematic distribution of tannins in dicotyledonous plants. *Journal of the Linnean Society (Botany)* **55**: 669–705.
Cai L., Giraud T., Zhang N., Begerow D., Cai G., Shivas R. G. (2011) The evolution of species concepts and species recognition criteria in plant pathogenic fungi. *Fungal Diversity* **50**: 121–133.
Chomnunti P., Schoch C. L., Aguirre-Hudson B., Ko Ko T. W., Hongsanan S., Jones E. B. G., Kodsueb R., Phookamsak R., Chukeatirote E., Bahkali A. H., Hyde K. D. (2011) Capnodiaceae. *Fungal Diversity* **51**: 103–134.

- Das R., Chutia M., Das K., Jha D. K. (2010) Factors affecting sporulation of *Pestalotiopsis disseminata* causing grey blight disease of *Persea bombycina* Kost., the primary food plant of muga silkworm. *Crop Protection* **29**: 963–968.
- Felsenstein J. (1985) Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* **39**: 783–791.
- Glass N. L., Donaldson G. C. (1995) Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. *Applied and Environmental Microbiology* **61**: 1323–1330.
- Guba E. F. (1961) Monograph of *Pestalotia* and *Monochaetia*. Harvard University Press, Cambridge, Massachusetts, USA.
- Hu H. L., Jeewon R., Zhou D. Q., Zhou T. X., Hyde K. D. (2007) Phylogenetic diversity of endophytic *Pestalotiopsis* species in *Pinus armandii* and *Ribes* spp.: evidence from rDNA and β -tubulin gene phylogenies. *Fungal Diversity* **24**: 1–22.
- Kishino H., Hasegawa M. (1989) Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data. *Journal of Molecular Evolution* **29**: 170–179.
- Ko Ko T., Stephenson S. L., Bahkali A. H., Hyde K. D. (2011) From morphology to molecular biology: can we use sequence data to identify fungal endophytes? *Fungal Diversity* **50**: 113–120.
- Liu A. R., Xu T., Guo L. D. (2007) Molecular and morphological description of *Pestalotiopsis hainanensis* sp. nov., a new endophyte from a tropical region of China. *Fungal Diversity* **24**: 23–36.
- Liu J. K., Phookamsak R., Jones E. B. G., Zhang Y., Ko-Ko T. W., Hu H. L., Boonmee S., Doilom M., Chukeatirote E., Bahkali A. H., Wang Y., Hyde K. D. (2011) *Astrosphaeriella* is polyphyletic, with species in *Fissuroma* gen. nov., and *Neoastrorsphaeriella* gen. nov. *Fungal Diversity* **51**: 135–154.
- Maharachchikumbura S. S. N., Guo L. D., Chukeatirote E., Bahkali A. H., Hyde K. D. (2011) *Pestalotiopsis*-morphology, phylogeny, biochemistry and diversity. *Fungal Diversity* **50**: 167–187.
- Maharachchikumbura S. S. N., Guo L. D., Cai L., Chukeatirote E., Wu W. P., Sun X., Crous P. W., Bhat D. J., Hyde K. D. (2012 a) A multi-locus backbone tree for *Pestalotiopsis*, with a polyphasic characterization of 14 new species. *Fungal Diversity* **56**: 95–129.
- Maharachchikumbura S. S. N., Chukeatirote E., Guo L. D., Crous P. W., McKenzie E. H. C., Hyde K. D. (2012 b) *Pestalotiopsis* species associated with *Camellia sinensis* (tea). *Mycotaxon* (in press). 2012.
- Nag Rag T. R. (1993) Coelomycetous anamorphs with appendage bearing conidia. *Mycological*, Waterloo.
- O'Donnell K., Cigelnik E. (1997) Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* nonorthologous. *Molecular Phylogenetics and Evolution* **7**: 103–116.
- Page R. D. M. (1996) TREEVIEW: an application to display phylogenetic trees on personal computers. *Computer Applications in the Biosciences* **12**: 357–358.
- Rehner S. A. (2001) Primers for elongation factor 1- α (EF1- α). [http://ocid.nacse.org/research/deep hyphae/EF1primer.pdf](http://ocid.nacse.org/research/deep%20hyphae/EF1primer.pdf).
- Summerell, B. A., Leslie, J. F. (2011) Fifty years of *Fusarium*: how were nine species ever enough? *Fungal Diversity* **50**: 135–144.
- Swofford D. L. (2002) PAUP* 4.0: phylogenetic analysis using parsimony (* and other methods). Sinauer Associates, Sunderland.
- Wei J. G., Xu T., Guo L. D., Liu A. R., Zhang Y., Pan X. H. (2007) Endophytic *Pestalotiopsis* species associated with plants of *Podocarpaceae*, *Theaceae* and *Taxaceae* in southern China. *Fungal Diversity* **24**: 55–74.
- White T. J., Bruns T., Lee S., Taylor J. W. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: *PCR protocols: a guide to methods and applications* (eds. Innis M. A., Gelfand D. H., Sninsky J. J., White T. J.), Academic Press, New York: 315–322

- Wu C. G., Tseng H. Y., Chen Z. C. (1982) Fungi inhabiting on *Schoenoplectus triqueter* (L.) Palla (I). *Taiwania* **27**: 35–38.
- Xu J., Ebada S. S., Proksch P. (2010) *Pestalotiopsis* a highly creative genus: chemistry and bioactivity of secondary metabolites. *Fungal Diversity* **44**: 15–31.
- Yanna, Ho W. H., Hyde K. D. (2002) Fungal succession on fronds of *Phoenix hanceana* in Hong Kong. *Fungal Diversity* **10**: 185–211.
- Zhang Y., Maharachchikumbura S. S. N., McKenzie E. H. C., Hyde K. D. (2012) A novel species of *Pestalotiopsis* causing leaf spots of *Trachycarpus fortunei*. *Cryptogamie Mycologie* **33**: 1–8.

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