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# The phylogenetic placement of *Eriosporella bambusicola* sp. nov. in *Capnodiales*

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**Abstract** – A new species of *Eriosporella, E. bambusicola*, is described from bamboo in Northern Thailand. *Eriosporella* is monotypic genus of coelomycetous fungi known from palms and bamboo and characterized by hyaline conidia which have a short basal cell and three slender divergent apical arms. Maximum-likelihood and maximum parsimony analyses of combined LSU and SSU rDNA sequence data set show *E. bambusicola* to belong to the *Capnodiales* where it forms a cluster with *Pseudoramichloridium*. Its relationships with other genera are unresolved and therefore considered as *Capnodiales incertae sedis.* The tree needs to be better populated with sequence data from more related species to clarify the familial placement of this genus.

**Asexual morphs / coelomycetous fungi / multi-gene analyses / taxonomy**

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## INTRODUCTION

Coelomycetous fungi are characterized by producing conidia inside the conidiomata *viz.* acervuli, pycnidia or stromata (Sutton, 1980; Nag Raj, 1993; Wijayawardene *et al.,* 2012b). Most of these described coelomycetous fungi have not been linked to sexual forms or placed in natural classification system (Wijayawardene *et al.,* 2012a). Recognition of mere co-occurrence of both morphs on same host material (Spooner & Kirk, 1982) and culture-based methods (Hyde *et al.,* 1996) were the most common practices used by taxonomists for establishing links of sexual and asexual states, before the introduction of molecular based methods (Hyde *et al.,* 2013a, b). Recent taxonomic studies of conidial fungi and their phylogenetic placements were entirely based on DNA sequence analyses (Boonmee *et al.,* 2011; Dai *et al.,* 2012; Zhang *et al.,* 2012; Wijayawardene *et al.,* 2013*,* 2014).

The genus *Eriosporella* was introduced by Höhnel (1916) with *E. calami* (≡ *Cryptosporium calami* Niessl.) as the type species. The genus is presently placed in *Pezizomycotina incertae sedis* (Kirk *et al.,* 2008). However, Wijayawardene *et al.* (2012a) stated that this genus might have a sexual state in *Laetinaevia* Nannf. (*Dermateaceae*, *Helotiales*). Currently gene sequences for this genus are lacking in GenBank hence its taxonomic placement is uncertain.

During studies on the diversity and taxonomy of microfungi occurring on bamboo (*Poaceae, Bambusoideae*) in Northern Thailand (Dai *et al.,* 2012), we have collected a coelomycetous species which has the main morphological features of *Eriosporella*. It is described as *Eriosporella bambusicola* on the basis of its morphology. Further, we have carried out maximum-likelihood (ML) and maximum-parsimony (MP) analyses of combined data set of LSU and SSU rDNA to show the ordinal placement of this genus.

## MATERIALS AND METHODS

**Collection and isolation of fungi:** Living bamboo leaves were collected from Chiang Rai Province, Thailand. The samples were placed in plastic zip lock bags and brought to laboratory. The specimens were incubated in a sterile moist chamber and examined at regular intervals until the resident fungi attained maturity and sporulated. The collection was isolated from single spores following the method of Chomnunti *et al.* (2011). Colonies were transferred to 1.5 ml. micro-centrifuge tubes with 2% potato-dextrose agar (PDA) and 2.0 ml screw cap microcentrifuge tubes with 10-15% glycerol for depositing at 4°C and –20°C respectively. Microscopic observation and photomicrographs were made as described in Liu *et al.* (2011) and Boonmee *et al.* (2011). Herbarium materials are deposited at MFLU herbarium of Mae Fah Luang University, Chiang Rai, Thailand (MFLU). The living cultures are maintained at Mae Fah Luang University Culture Collection (MFLUCC), Research Institute of Resource Insects, Chinese Academy of Forestry (IFRD), Landcare Research, New Zealand (ICPM) and Microbial diversity for science and industry, the latter under Material Transfer Agreement (No.C29/2011).

**DNA extraction, PCR amplification and sequencing:** In our study, the fungal isolates were grown on PDA for 30 d at 27°C in dark. Genomic DNA was extracted from fresh mycelia, following the specification of Biospin Fungus Genomic

DNA Extraction Kit (BioFlux®). The primer pairs ITS5 (GGAAGTAAAAGTC GTAACAAGG) and ITS4 (TCCTCCGCTTATTGATATGC), and NS1 (GTAGTCATATGCTTGTCTC) and NS4 (CTTCCGTCAATTCCTTTAAG) (White *et al.,* 1990) and LROR (GTACCCGCTGAACTTAAGC) and LR5 (ATCCTGAGGGAAACTTC) (Vilgalys & Hester, 1990) were used to amplify the internal transcribed spacers (ITS) small subunit rDNA (SSU) and large subunit rDNA (LSU) respectively. Polymerase chain reaction (PCR) amplification was carried out following Phillips *et al.* (2008). Amplified PCR fragments were sequenced at Kunming Shuo Yang Technology Company (P.R. China).

**DNA sequence analyses:** Blast searches at GenBank were carried out both LSU and SSU rDNA sequences in order to reveal the closest relatives of our strain and their sequences were downloaded (Table 1). The downloaded sequences represent *Capnodiaceae*, *Cladosporiaceae* (*Davidiellaceae*)*, Dissoconiaceae, Mycosphaerellaceae, Schizothyriaceae a*nd *Teratosphaeriaceae*. Sequences were aligned by using Bioedit (Hall, 2001) and ClustalX (Kohli & Bachhawat, 2003). Alignments were checked and manual adjustments were made wherever necessary. Phylogenetic analyses were performed using PAUP v. 4.0b10 (Swofford, 2003) for maximum-parsimony (MP) and raxmlGUI v.0.9b2 (Silvestro & Michalak, 2010) for maximum-likelihood (ML). Trees were visualized with TreeView (Page, 1996). The whole ambiguously aligned regions within each dataset were excluded from the analyses (Begoude *et al.,* 2010). In the analyses, gaps were treated as missing data, and all characters were unordered and of equal weight (Liu *et al.,* 2011).

Maximum-parsimony analysis was performed using the heuristic search option with 1000 random taxa addition and tree bisection and reconnection (TBR) as the branch swapping algorithm. All characters were unordered and of equal weight and gaps were treated as missing data. Max trees were unlimited, branches of zero length were collapsed and all multiple, equally parsimonious trees were saved. Clade stability was assessed using a bootstrap (BT) analysis with 1000 replicates, each with 10 replicates of random stepwise addition of taxa (Hillis & Bull, 1993).

## RESULTS

### Phylogenetic analyses

Partial nucleotide sequences of the LSU and SSU ribosomal DNA (around 800 bp) were determined for the fresh isolate. LSU and SSU regions were used in the phylogenetic analyses for the species placement (Fig. 1). The ITS gene sequences are not included in the phylogenetic analyses of this study, but are deposited in GenBank (accession number KF548664) as it is preferred loci for use in fungal phylogenetics (Schoch *et al.,* 2011; Liu *et al.,* 2012).

The data set contained 33 sequences of 32 taxa including two outgroups (i.e. *Myriangium duriaei* and *M. hispanicum*). Of the 1821 characters used in the phylogenetic analyses, 329 were parsimony-informative, 88 variable and parsimony-uninformative and 1404 constant. Maximum-parsimony and maximum-likelihood analyses resulted in the same tree as shown in Fig. 1 with bootstrap support on the branches.

Table 1. The list of species used in this study

| *Species name* | *Source* | *GenBank accession numbers* | | |
|---|---|---|---|---|
| | | *LSU* | *SSU* | *ITS* |
| *Capnodium coartatum* | MFLUCC10-0069 | JN832614 | JN832599 | |
| *Capnodium coffeae* | CBS 147.52 | GU214400 | DQ247808 | |
| *Catenulostroma germanicum* | CBS 539.88 | EU019253 | GU214518 | |
| *Cladosporium bruhnei* | CBS 115683; ATCC66670 | GU214408 | AY251096 | |
| *Davidiella tassiana* | CBS 723.79; ATCC 201090 | GU214410 | HQ871897 | |
| *Devriesia staurophora* | CPC 3687; CBS 375.81 | GU214416 | EF137359 | |
| *Dissoconium aciculare* | CBS 204.89 | GU214419 | GU214522 | |
| *Dothidea insculpta* | CBS 189.58 | NG_027643 | DQ247810 | |
| *Dothidea sambuci* | DAOM 231303 | NG_027611 | AY544722 | |
| *Eriosporella bambusicola* | MFLUCC 11-0436 | KF548665 | KF548666 | KF548664 |
| *Graphiopsis chlorocephala* | CBS 121523; CPC 11969 | EU009458 | GU214534 | |
| *Leptoxyphium cacuminum* | MFLUCC10-0059 | JN832603 | JN832588 | |
| *Mycosphaerella graminicola* | CBS 110744 | EU019298 | AY251117 | |
| *Mycosphaerella punctiformis* | CBS 113265 | NG_027571 | AY490775 | |
| *Myriangium duriaei* | CBS 260.36 | NG_027579 | NG_013129 | |
| *Myriangium hispanicum* | CBS 247.33 | GU301854 | GU296180 | |
| *Passalora vaginae* | CBS 140.34; DSM 1148 | GQ852624 | GU214561 | |
| *Pleospora chenopodii* | CBS 344.78 | EU754132 | EU754033 | |
| *Pleospora herbarum* | CBS 191.86 | GU238160 | GU238232 | |
| *Pseudoramichloridium brasilianum* | CBS 283.92 | EU041854 | | |
| *Pseudoramichloridium henryi* | CBS:124775 | GQ303320 | | |
| *Ramichloridium apiculatum* | CPC 12310 | GU214687 | GU214687 | |
| *Ramularia nagornyi* | CBS 120253 | EU019257 | GU214579 | |
| *Schizothyrium pomi* | CBS 406.61 | EF134949 | EF134949 | |
| *Schizothyrium pomi* | CBS 486.50 | EF134948 | EF134948 | |
| *Teratosphaeria fibrillosa* | CBS 121707 | GU323213 | GU296199 | |
| *Teratosphaeria jonkershoekensis* | CBS 112224 | GU301874 | GU296200 | |
| *Toxicocladosporium irritans* | CBS 185.58 | EU040243 | GU214619 | |
| *Uwebraunia commune* | CBS:110747 | GU214420 | NG_016521 | |
| *Uwebraunia dekkeri* | CBS 110748; CMW14906 | GU214422 | GU214528 | |

Abbreviations of isolates and culture collections: ATCC: American Type Culture Collection, Virginia, USA; CBS: CBS Fungal Biodiversity Centre, Utrecht, The Netherlands; CPC: Culture collection of Pedro Crous, housed at CBS; CMW: Tree Pathology Co-operative Program, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa; DAOM: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada; DSM: Deutsche Sammlung von Mikrorrganismen und Zellkulturen GmbH, Braunschweig, Germany; MFUCC: Mae Fah Luang University Culture Collection, ChiangRai, Thailand.

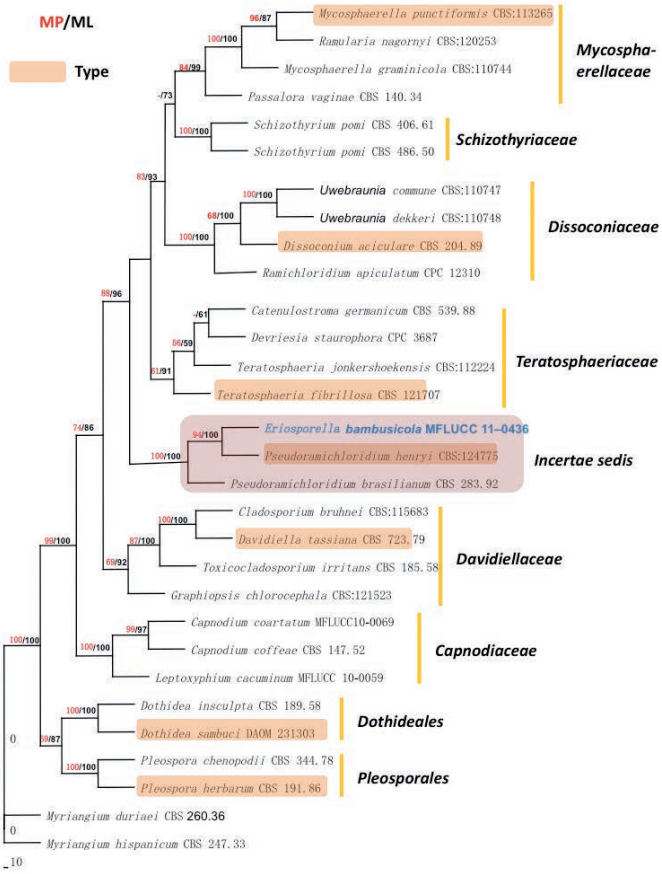


Fig. 1. RAxML tree based on a combined dataset of SSU and LSU sequences. Bootstrap support values for maximum likelihood (ML) and maximum parsimony (MP) greater than 50% are given above the nodes. The original culture numbers are given after the species names. The tree is rooted with *Myriangium duriaei* (CBS 260.36) and *M. hispanicum* (CBS 247.33).

Our *Eriosporella* species nested in a well-supported clade together with two species of *Pseudoramichloridium* (*P. henryi* (CBS: 124775) and *P. braziliensis* (CBS 283.92) (Cheewangkoon *et al.,* 2009) with 94/100% (MP/ML) bootstrap values.

## Taxonomy

***Eriosporella bambusicola*** D. Q. Dai, N.N. Wijayawardene & K.D. Hyde **sp. nov.**
Fig. 2

MycoBank: MB 805309
Holotype: MFLU 13-0107
Etymology: with reference to its occurrence on *Bambusa* sp.

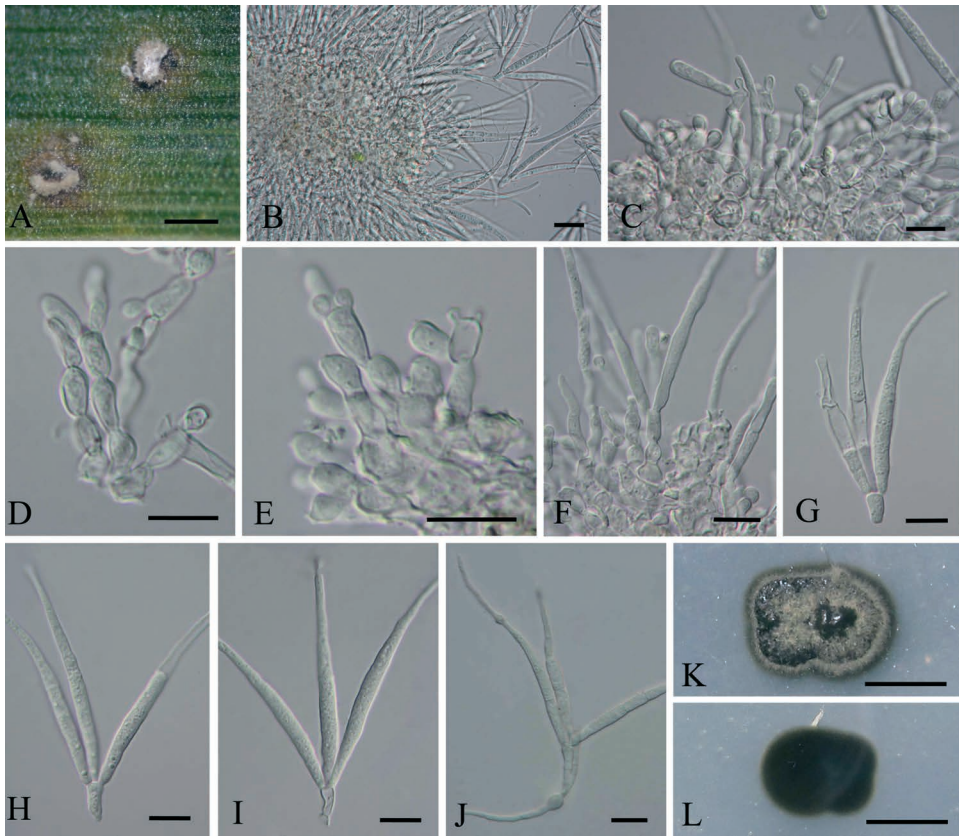


Fig. 2. ***Eriosporella bambusicola*** (holotype) **A.** Conidia group breaking through conidiomata. **B-F.** Conidiophores, conidiogenous cells and conidia. **G-I.** Hyaline conidium. **J.** Germinating conidium. **K.** Cultures on PDA from above after 15 days. **L.** Cultures on PDA from reverse after 15 days. Scale bars: A = 3 mm, B-J = 10 μm, K, L = 1 cm.

*Growing* on living bamboo leaves, forming brown to olive-green areas on leaf surface with conidial mass breaking through slightly raised areas. Sexual state: not observed. Asexual state: *Conidiomata* eustromatic, immersed, solitary, flattened to subglobose, with a concave base with loose, sub-hyaline, pseudoparenchymatous tissue. *Ostiole* not present. *Conidiophores* 10-13 × 4.5-7 μm ($\bar{x}$ = 11.6 × 6.2 μm, n = 20), arising from basal tissue in a palisade layer, hyaline, septate and branched at the base, smooth, cylindrical to irregular, formed from the inner cells of the locular wall. *Conidiogenous cells* 4-10.5 × 2.5-5 μm ($\bar{x}$ = 8.6 × 4.5 μm, n = 20), indeterminate, discrete, cylindrical to ellipsoidal, hyaline, smooth-walled, with several conidiogenous loci, phialidic, enteroblastic, polyblastic. *Conidia* complex, consisting of a short basal cell with 3 developing divergent arms; basal cell truncate to obtuse at the point of secession, sometimes carrying part of conidiogenous cell (Fig. 2, I) 4.5-8.5 × 2.5-5 μm ($\bar{x}$ = 6.6 × 3.9 μm, n = 20), aseptate, hyaline, smooth-walled; arms, cylindrical, tapering at the tip, constricted at the point of attachment to basal cell, 42.5-60 × 3-5 μm ($\bar{x}$ = 49.4 × 3.9 μm, n = 20), 0-3-septate, hyaline, smooth-walled.

Culture on PDA: Colonies slow growing, reaching 10 mm diam. after 15 d at 25-32°C, circular, with even margin, dark brown, viscous, with brown floccose on mucus surface. Dark brown from reverse.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, on living leaves of bamboo, 14 October 2011, Dong-Qin Dai, DDQ00214 (MFLU13-0107, holotype); ex-type living cultures = MFLUCC 11-0436 = IFRDCC 2582.

**Key to *Eriosporella* species**

1. Conidia with 2.5-5 µm wide basal cell, and 0-3 septate arms . . . . *E. bambusicola*
1. Conidia with 1.5-2 µm wide basal cell, and 3-5 septate arms . . . . . *E. calami*

## DISCUSSION

*Eriosporella* was introduced by Höhnel (1916) with one species, *E. calami* (≡ *Cryptosporium calami* Niessl.). This genus is characterized by immersed conidiomata with a thin lower wall and thick lateral wall, without an ostiole, hyaline, branched and septate conidiophores, blastic-type conidiogenesis, discrete conidiogenous cells and hyaline conidia with one basal cell (occasionally one septate) and three apical divergent, septate arms (Sutton, 1980). Sutton (1980) described the conidiogenesis in *Eriosporella* as enteroblastic and phialidic. Nag Raj & DiCosmo (1981) considered this genus has blastic and annelidic conidiogenesis. However, no annelations were observed in conidiogenesis of *Eriosporella bambusicola*.

*Eriosporella bambusicola* differs from *E. calami* in having wider basal cells (2.5-5 µm *versus* 1.5-2 µm respectively) and fewer septa in the arms (0-3 septa *versus* 3-5 septa respectively). *Eriosporella* is similar to *Suttoniella* Ahmad, typified by *S. gaubae* (Petr.) S. Ahmad, in having conidia with apical divergent arms. However, *Eriosporella* differs from *Suttoniella* in having multiseptate conidia with a short basal cell and three slender divergent arms developing from the tip of the basal cell. This character is not seen in *Suttoniella* which has one-celled, Y-shape conidia. *Eriosporella* are found on monocotyledons (Sutton, 1980), while *Suttoniella* are so far found on dicotyledons (Hoyo & Gomez-Bolea, 2004, Sutton, 1980). *Eriosporella* also can be compared with *Crucellisporium* Farr and *Belaina* Bat & Peres which has longer (more than 15 µm long) basal cells in the conidia (Nag Raj & DiCosmo, 1981; Sutton, 1980). In *Crucellisporium*, the conidia have 2-3 shorter conidial arms usually without septa (Nag Raj & DiCosmo, 1981). However, in *Belaina* the conidia have 2-4 conidial arms with one septum (Sutton, 1980).

The closest relative to *Eriosporella* (as deduced from our phylogenetic inferences) is the hyphomycetous *Pseudoramichloridium (*Fig. 1). Moreover, *Pseudoramichloridium* is characterized by unbranched conidiophores, polyblastic, pale brown conidiogenous cells and obovoid to ellipsoidal conidia without septa (Cheewangkoon *et al.,* 2009). For the time being, we place *Eriosporella* along with *Pseudoramichloridium* in *Capnodiales incertae sedis* (Cheewangkoon *et al.,* 2009).

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## REFERENCES

BEGOUDE B.A.D., SLIPPERS B., WINGFIELD M.J. & ROUX J., 2010 — *Botryosphaeriaceae* associated with *Terminalia* catappa in Cameroon, South Africa and Madagascar. *Mycological Progress* 9(1): 101-123.

BOONMEE S., ZHANG Y., CHOMNUNTI P., CHUKEATIROTE E., TSUI C.K.M., BAHKALI A.H. & HYDE K.D., 2011 — Revision of lignicolous *Tubeufiaceae* based on morphological re-examination and phylogenetic analysis. *Fungal Diversity* 51: 63-102.

CHEEWANGKOON R., GROENEWALD J., SUMMERELL B., HYDE K.D., TO-ANUN C. & CROUS P.W., 2009 — *Myrtaceae*, a cache of fungal biodiversity. *Persoonia* 23: 55-85.

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., 2011 — *Capnodiaceae*. *Fungal Diversity* 51: 103-134.

CROUS P.W., SCHOCH C., HYDE K.D., WOOD A., GUEIDAN C., DE HOOG G. & GROENEWALD J., 2009 — Phylogenetic lineages in the *Capnodiales*. *Studies in mycology* 64(1): 17-47.

CROUS P.W., SUMMERELL B., SHIVAS R., CARNEGIE A. & GROENEWALD J., 2012 — A re-appraisal of *Harknessia* (*Diaporthales*), and the introduction of *Harknessiaceae* fam. nov. *Persoonia* 28: 49-65.

DAI D.Q., BHAT D.J., LIU J.K., CHUKEATIROTE E., ZHAO R.L. & HYDE K.D., 2012 — *Bambusicola*, a new genus from bamboo with asexual and sexual morphs. *Cryptogamie Mycologie* 33(3): 363-379.

HALL T., 2001 — BioEdit version 5.0. 6. North Carolina State University, Department of Microbiology, Raleigh, North Carolina 192.

HILLIS D.M. & BULL J.J., 1993 — An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Systematic Biology* 42(2): 182-192.

HÖHNEL F. VON, 1916 — Fragmente zur Mykologie no. 944-1000. *Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften Math.-naturw. Klasse Abt. I.* 125: 27-138.

HOYO P. & GOMEZ-BOLEA A., 2004 — *Suttoniella arnaudii* sp. nov. (Coelomycetes) on dead leaves of *Buxus sempervirens*. *Mycotaxon* 89: 39-46.

HYDE K.D., ERIKSSON O.E. & YUE J.Z., 1996 — *Roussoëlla*, an ascomycete genus of uncertain relationships with a *Cytoplea* anamorph. *Mycological Research* 100: 1522-1528.

HYDE K.D., UDAYANGA D., MANAMGODA D.S., TEDERSOO L., LARSSON E., ABARENKOV K., BERTRAND Y.J.K., OXELMAN B., HARTMANN M., KAUSERUD H., RYBERG M., KRISTIANSSON E. & NILSSON R.H., 2013a — Incorporating molecular data in fungal systematics: a guide for aspiring researchers. *Current Research in Environmental & Applied Mycology* 3(1): 1-32.

HYDE K.D., JONES E.B.G., LIU J.K., ARIYAWANSA H., BOEHM E., BOONMEE S., BRAUN U., CHOMNUNTI P., CROUS P.W., DAI D.Q., DIEDERICH P., DISSANAYAKE A., DOILOM M., DOVERI F., HONGSANAN S., JAYAWARDENA R., LAWREY J.D., LI Y.M., LI, Y.X., LÜCKING R., MONKAI J., MUGGIA L., NELSEN M.P., PANG K.L., PHOOKAMSAK R., SENANAYAKE I., SHEARER C.A., SUETRONG S., TANAKA K., THAMBUGALA K.M., WIJAYAWARDENE N.N., WIKEE S., WU H.X., ZHANG Y., AGUIRRE-HUDSON B., ALIAS S.A., APTROOT A., BAHKALI A.H., BEZERRA J.L., BHAT, D.J., CAMPORESI E., CHUKEATIROTE E., GUEIDAN C., HAWKSWORTH D.L., HIRAYAMA K., HOOG S.D., KANG J.C., KNUDSEN K., LI W.J., LI X.H., LIU Z.Y., MAPOOK A., MCKENZIE E.H.C., MILLER A.N., MORTIMER P.E., PHILLIPS A.J.L., RAJA H.A., SCHEUER C., SCHUMM F., TAYLOR, J.E., TIAN Q., TIBPROMMA S., WANASINGHE D.N., WANG Y., XU J.C., YAN J.Y., YACHAROEN S. & ZHANG M., 2013 — Families of Dothideomycetes. *Fungal Diversity* 63: 1-313.

KENDRICK B., 2000 — The Fifth Kingdom. 3rd edn. Focus Publishing, Newbury. Massachsetts, USA.

KIRK P.M., CANNON P.F., MINTER D.W. & STALPERS J.A., 2008 — Dictionary of the Fungi, 10th edn. CABI, Wallingford.

KOHLI D.K. & BACHHAWAT A.K., 2003 — CLOURE: Clustal Output Reformatter, a program for reformatting ClustalX/ClustalW outputs for SNP analysis and molecular systematics. *Nucleic acids research 31*(13): 3501-3502.

LIU J.K., PHOOKAMSAK R., DOILOM M., WIKEE S., LI Y.M., ARIYAWANSHA H., BOONMEE S., CHOMNUNTI P., DAI D.Q., BHAT J.D., ROMERO A.I., ZHUANG W.Y., MONKAI J., JONES E.B.G., CHUKEATIROTE E., KO-KO W.T., ZHAO Y.C., WANG Y. & HYDE K.D., 2012 — Towards a natural classification of *Botryosphaeriales*. *Fungal Diversity* 57: 149-210.

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., 2011 — *Astrosphaeriella* is polyphyletic, with species in *Fissuroma* gen. nov., and *Neoastrosphaeriella* gen. nov. *Fungal Diversity* 51: 135-154.

NAG RAJ T.R., 1974— Icones generum coelomycetum VI. University of Waterloo Biology Series 6: 1-41. ? not seen in the text.

NAG RAJ T.R., 1993 — Coelomycetous Anamorphs with Appendage-bearing Conidia. Mycologue Publications, Waterloo, Canada.

NAG RAJ T.R. & DICOSMO F., 1981 — Icones generum coelomycetum XII. University of Waterloo Biology Series 12: 1-41.

PAGE R.D.M., 1996 — TreeView. An application to display phylogenetic trees on personal computer. *Comp Computer Applications in the Biosciences* 12: 357-358.

PHILLIPS A.J.L., ALVES A., PENNYCOOK S.R., JOHNSTON P.R., RAMALEY A., AKULOV A. & CROUS P.W., 2008 — Resolving the phylogenetic and taxonomic status of dark-spored teleomorph genera in the *Botryosphaeriaceae*. *Persoonia* 21: 29-55.

SCHOCH C.L., SEIFERT K.A., HUHNDORF S., ROBERT V., SPOUGE J.L., LEVESQUE C.A., CHEN W., BOLCHACOVA E., VOIGT K. & CROUS, P.W., 2011 — Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Sciences* 109(16): 6241-6246.

SILVESTRO D. & MICHALAK I., 2010 — raxmlGUI: a graphical front-end for RAxML. *Organisms Diversity & Evolution* 12(4): 335-337.

SPOONER B.M. & KIRK P.M., 1982 — Taxonomic notes on *Excipularia* and *Scolicosporium*. *Transactions of the British Mycological Society* 78(2): 247-257.

STAMATAKIS A., 2006 — RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 22: 2688-2690.

SUTTON B.C., 1980 — The Coelomycetes-Fungi Imperfecti with Pycnidia, Acervuli and Stromata. Commonwealth Mycological Institute, Kew, UK.

SWOFFORD D.L., 2003 — PAUP*: phylogenetic analysis using parsimony, version 4.0 b10.

VILGALYS R. & HESTER M., 1990 — Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172(8): 4238-4246.

WHITE T., BRUNS T., LEE S. & TAYLOR J., 1990 — Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. Academic Press, San Diego, CA, USA. pp. 315-322.

WIJAYAWARDENE D.N.N., MCKENZIE E.H.C., CHUKEATIROTE E., WANG Y. & HYDE K.D., 2012a — Coelomycetes. *Cryptogamie Mycologie* 33(3): 215-244.

WIJAYAWARDENE D.N.N., MCKENZIE E.H.C. & HYDE K.D., 2012b — Towards incorporating anamorphic fungi in a natural classification – checklist and notes for 2011. *Mycosphere* 3(2): 157-228.

WIJAYAWARDENE D.N.N., SONG Y., BHAT D.J., MCKENZIE E.H.C., CHUKEATIROTE E., WANG Y. & HYDE K.D., 2013 — *Wojnowicia viburni* sp. nov. from China and its phylogenetic placement. *Sydowia* 65(1): 181-190.

WIJAYAWARDENE N.N., CAMPORESI E., BHAT D.J., SONG Y., CHETHANA K.W.T., CHUKEATIROTE E., WANG Y. & HYDE K.D., 2014 — *Macrodipodiopsis* in *Lophiostomataceae*, Pleosporales. *Phytotaxa* (accepted).