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Additions to brown spored coelomycetous taxa in Massarinae, Pleosporales: introducing *Phragmocamarosporium* gen. nov. and *Suttonomyces* gen. nov.

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Abstract − Three collections of coelomycetes producing brown spores have been subjected to morphological and molecular data analyses. Two of them have phragmosporous conidia and are morphologically similar to *Camarosporium hederae* which has the distinct morphology of *Camarosporium sensu stricto*. The other collection with muriform conidia is morphologically similar to *Camarosporium sensu stricto* but has paraphyses. Based on morphology and molecular data analyses of combined LSU and SSU rDNA sequences, two new genera are introduced *viz*. *Phragmocamarosporium* (in Lentitheciaceae) and *Suttonomyces* (in Massarinaceae).

Coelomycetous fungi / Molecular data / Morphology / Muriform / Phragmospore / Phylogeny

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INTRODUCTION

Traditional studies of asexual fungi were entirely based on morphological characteristics such as shapes and types of conidiomata, types of conidiophores, and nature of conidiogenous cells (Hughes, 1953; Sutton, 1980; Nag Raj, 1993; Seifert *et al.*, 2011). Furthermore, the shape, septation, ornamentation, and colour of conidia and presence of appendages were also considered as important characters for delimitation of genera and species (Guba, 1961; Sutton, 1980; Nag Raj, 1993).

During a re-collecting programme of coelomycetes with brown spores, we collected three interesting taxa from China and Europe. Two of them have similar morphology (i.e. only transverse septa, brown) as *Camarosporium hederae* which is characterized by brown, phragmosporous conidia (Ellis & Everhart, 1900). The other taxon is characterized by muriform conidia which is similar to *Camarosporium sensu stricto*. We subjected our collections to morphological and molecular studies. Maximum likelihood (ML) and maximum parsimony (MP) analyses of combined dataset of LSU and SSU gene regions showed that taxa with phragmospores grouped into Lentitheciaceae, Pleosporales, while the other taxon with muriform conidia (camarosporium-like) clustered in Massarinaceae.

MATERIALS AND METHODOLOGY

Collection. − Decaying plant materials, including aerial litter, were collected in China and Europe. Collected materials were placed in paper bags, and then brought to the laboratory. All the materials were observed first under a stereoscope to reveal fungal taxa.

Morphological studies and isolation. − Squash mounts (Sutton, 1980) and thin hand sections of conidioma were made using a razor blade to examine the shape of conidiomata, orientation of conidiophores, type of conidiogenous cells and conidia. All micro-morphological characters were examined under a compound microscope (Nikon Eclipse E600 DIC microscope and a Nikon DS-U2 camera or a Nikon Eclipse 80i compound microscope fitted with a Canon 450D digital camera) and the conidial characters were determined.

Single conidial isolation was carried out using the method of Chomnunti *et al.* (2014) and germinating conidia were transferred aseptically to potato dextrose agar (PDA) plates and grown at 18°C. Colonial colour and other characters were assessed after 1 to 2 weeks. The specimens are deposited in the Mae Fah Luang University Herbarium (MFLU), Chiang Rai, Thailand and Herbarium of the Department of Plant Pathology, Agricultural College, Guizhou University (HGUP). Culture Collection at Mae Fah Luang University (MFLUCC) and Department of Plant Pathology, Agriculture College, Guizhou University, China (GUCC).

DNA extraction, PCR amplification and sequencing. − Colonies generated from single conidia were grown on PDA for 14 days at 18°C. Fresh fungal mycelia were scraped from PDA to extract genomic DNA by using a BIOMIGA Fungus Genomic DNA Extraction Kit (GD2416). The amplification of rDNA regions of the internal transcribed spacers (ITS), small subunit rDNA (SSU) and large subunit (LSU) genes

was carried out by using ITS5 and ITS4, NS1 and NS4 and LROR and LR5 (Vilgalys & Hester, 1990; White *et al.,* 1990) primers. Optimum conditions for amplification of ITS and LSU regions are as described in Alves *et al.* (2004, 2005) and for SSU region as described in Phillips *et al.* (2008). Amplified PCR fragments were checked on 1% agarose electrophoresis gels stained with ethidium bromide. Purified PCR products (by minicolumns, purification resin and buffer according to the manufacturer's protocols Amersham product code: 27-9602-01) were sent to SinoGenoMax Co., Beijing, China for DNA sequencing. The nucleotide sequence data obtained are deposited in GenBank (Table 1).

Phylogenetic analyses. − Sequences (Table 1) were obtained from GenBank. DNA sequences for each gene region (small subunits ribosomal RNA (SSU) and large subunits ribosomal RNA (LSU), were initially aligned using Bioedit (Hall, 2004). Further improvements of the data set were carried out in MAFFTv6 (Katoh *et al.,* 2002; Katoh & Toh, 2008), online sequence alignment was edited under the default settings (mafft.cbrc.jp/alignment/server/). All absent genes were coded as missing data.

Phylogenetic analyses of the combined LSU and SSU data were performed using maximum likelihood (ML) and maximum parsimony (MP) algorithms. Maximum likelihood (ML) analyses was performed in RAxML (Stamatakis, 2006) implemented in raxmlGUI v.0.9b2 (Silvestro & Michalak, 2010). Maximum parsimony analyses were performed by PAUP v. 4.0b10 (Swofford, 2002) using the heuristic search option with 1,000 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. The Tree Length (TL), Consistency Indices (CI), Retention Indices (RI), Rescaled Consistency Indices (RC) and Homoplasy Index (HI) were calculated for each tree generated. Maxtrees 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 1,000 replicates, each with 10 replicates of random stepwise addition of taxa (Hillis & Bull, 1993). Phylogenetic trees were visualized with FigTree (Rambaut, 2012).

RESULTS

Phylogenetic analyses

A combined dataset of LSU and SSU gene regions of representative taxa of families in Massarineae (Bambusicolaceae, Didymosphaeriaceae, Lentitheciaceae, Massarinaceae, Morosphaeriaceae, and Trematosphaeriaceae) was used to show the placement of new. Bootstrap support (BS) values of MP and ML (equal or above 70%) are shown on the upper branches.

We carried out separate analyses for LSU (not shown). The tree topology of LSU tree was very similar to the combined gene tree (LSU and SSU) but bootstrap values were low. We did not carry out single gene analyses for SSU gene as most of the strains in *Massarinaceae* lack SSU sequences.

Table 1. Strains used in this study. Type strains are in bold and newly generated sequences are in bold and marked with an asterisk

Taxon	*Culture collection number*	*GenBank Accession number*	
		LSU	*SSU*
Alloconiothyrium aptrooti	**CBS 981.95**	JX496235	
Bambusicola bambusae	**MFLUCC 11-0614**	JX442035	JX442039
Bambusicola massarinia	**MFLUCC 11-0389**	JX442037	JX442041
Bambusicola splendida	**MFLUCC 11-0439**	JX442038	JX442042
Bimuria novae-zelandiae	**CBS 107.79**	AY016356	AY016338
Byssothecium circinans	CBS 675.92	GU205217	GU205235
Corynespora leucadendri	CBS 135133	KF251654	
Deniquelata barringtoniae	**MFLUCC 110422**	JX254655	JX254656
Kalmusia brevispora	KT 1466	AB524600	AB524459
Kalmusia brevispora	KT 2313	AB524601	AB524460
Kalmusia ebuli	CBS 123120	JN644073	JN851818
Kalmusia scabrispora	KT 2202	AB524594	AB524453
Karstenula rhodostoma	CBS 690.94	GU301821	GU296154
Katumotoa bambusicola	**MAFF 239641**	AB524595	AB524454
Murilentithecium clematidis	**MFLUCC 14-0561**	KM408758	KM408759
Keissleriella cladophila	CBS 104.55	JX681090	GU296155
Lentithecium aquaticum	CBS 123099	GU301823	GU296156
Lentithecium arundinaceum	CBS 123131	GU456320	GU456298
Lentithecium fluviatile	CBS 122367	GU301825	GU296158
Lentithecium fluviatile	CBS 123090	FJ795450	FJ795492
Lentithecium lineare	IFRD 2008	FJ795435	FJ795478
Massarina cisti	CBS 266.62	FJ795447	FJ795490
Massarina eburnea	CBS 473.64	GU301840	GU296170
Montagnula opulenta	CBS 168.34	NG 027581	
Morosphaeria ramunculicola	JK 5304B	GU479794	GU479760
Neottiosporina paspali	CBS 331.37	EU754172	EU754073
Paraconiothyrium brasiliense	**CBS100299**	JX496124	AY642523
Paraconiothyrium estuarinum	**CBS 109850**	JX496129	AY642522
Paraconiothyrium minitans	CBS 122788	EU754173	EU754074
Paraphaeosphaeria michotii	CBS 652.86	GQ387581	GQ387520
Paraphaeosphaeria michotii	CBS 591.73	GU456326	GU456305
Phaeosphaeriopsis glaucopunctata	**MFLUCC 13-0265**	KJ522477	KJ522481
Phaeosphaeriopsis musae	**BS 120026**	GU301862	GU296186
Phaeosphaeriopsis triseptata	MFLUCC 13-0347	KJ522480	KJ522483
Phragmocamarosporium hederae*	**MFLUCC 13-0552**	KP842915	KP842918
Phragmocamarosporium platani*	**MFLUCC 14-1191**	KP842916	KP842919
Pleospora herbarum	CBS 191.86	JX681120	GU238232
Pseudocamarosporium propinquum	**MFLUCC 13-0544**	KJ813280	KJ819949
Pseudocamarosporium tilicola	MFLUCC 13-0550	KJ813281	KJ819950
Setoseptoria phragmitis	CBS 114966	KF251753	
Setoseptoria phragmitis	CBS 114802	KF251752	
Stagonospora paludosa	**CBS 135088**	KF251760	
Stagonospora cf paludosa	**CBS 130005**	KF251757	
Stagonospora pseudocaricis	**CBS 135132**	KF251762	
Stagonospora pseudopaludosa	**CPC 22654**	KF777239	
Stagonospora trichophoricola	**CBS 136764**	KJ869168	
Stagonospora uniseptata	**CBS 135090**	KF251767	
Suttonomyces clematidis*	**MFLUCC 14-0240**	KP842917	KP842920
Trematosphaeria pertusa	CBS 122368	FJ201990	FJ201991

The combined LSU and SSU data consists of 45 taxa with *Pleospora herbarum* (CBS 191.86) as the outgroup taxon. The data set consists of 1814 characters (LSU = 1-810 bp and SSU = 810-1814 bp) after alignment of which included in ML and MP analyses (TL = 865, CI = 0.535, RI = 0.726, RC = 0.389, HI = 0.465). Of the included base pairs, 1200 sites are conserved, while 365 and 249 sites are variable and parsimony informative respectively. Our new collections with phragmospores *viz*. *Phragmocamarosporium platani* and *P. hederae* cluster in Lentitheciaceae and group with the type strain of *Murilentithecium clematidis* Wanasinghe *et al.* (MFLUCC 14-0561) with high bootstrap (MP: 91%; ML: 90%). The taxon with muriform conidia *viz. Suttonomyces clematidis* groups in Massarinaceae, as the sister branch to *Stagonospora* and *Neottiosporina* clade with lower bootstrap values (54% and 72% in MP and ML analyses respectively) (Fig. 1). Tree topology of the ML analysis (not shown) was almost similar with the MP tree.

TAXONOMY

Phragmocamarosporium Wijayawardene, Yong Wang bis & K.D. Hyde, gen. nov.

Index Fungorum number: IF551084; *Facesoffungi Number*: FoF 00465

Etymology: In reference to the genus resembling the genus *Camarosporium* but which lacks longitudinal septa

Saprobic and *endophytic* on twigs of *Hedera helix* and *Platanus* sp. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* pycnidial, sub-epidermal, black, gregarious, unilocular, globose to sub-globose, with a centrally located papillate ostiole. *Pycnidial wall* with outer wall layer of dark brown cells of *textura angularis*, with inner-most layer of hyaline, thin cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* simple to branched at the base, smooth, short or long, phialidic, hyaline. *Conidia* medium brown, clavate or ellipsoid to subcylindrical, with obtuse apex and truncate base, straight to curved, (2-)3(-4)-transverse septate, rarely with 1 longitudinal septum, constricted at the septa.

Notes: The genus *Phragmocamarosporium* is introduced to place our collections from *Hedera helix* (Germany) and *Platanus* sp. (China). Currently the genus comprises two species *viz*. *Phragmocamarosporium hederae* and *P. platani*. Both species grouped with *Murilentithecium clematidis* in Lentitheciaceae with high bootstrap support. Wanasinghe *et al.* (2014) reported *M. clematidis* has an asexual state with muriform conidia from culture, hence we propose *Phragmocamarosporium* to accommodate our collection which has conspicuous phragmospores.

Type species: *Phragmocamarosporium platani* Wijayawardene, Yong Wang bis & K.D. Hyde.

Phragmocamarosporium platani Wijayawardene, Yong Wang bis & K.D. Hyde **sp. nov.**

Index Fungorum number: IF551085; *Facesoffungi Number* : FoF 00466

Etymology: After the host genus *Platanus* on which the fungus was found

Saprobic on branch of *Platanus* sp. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 100-320 µm high, 150-300 µm diam., pycnidial, sub-epidermal, black, gregarious, unilocular, with a centrally located papillate ostiole. *Pycnidial wall* with outer 4-5 cell layers of dark brown cells of *textura angularis*, with inner 2-3 layers of hyaline cells. *Conidiophores* reduced to conidiogenous cells.

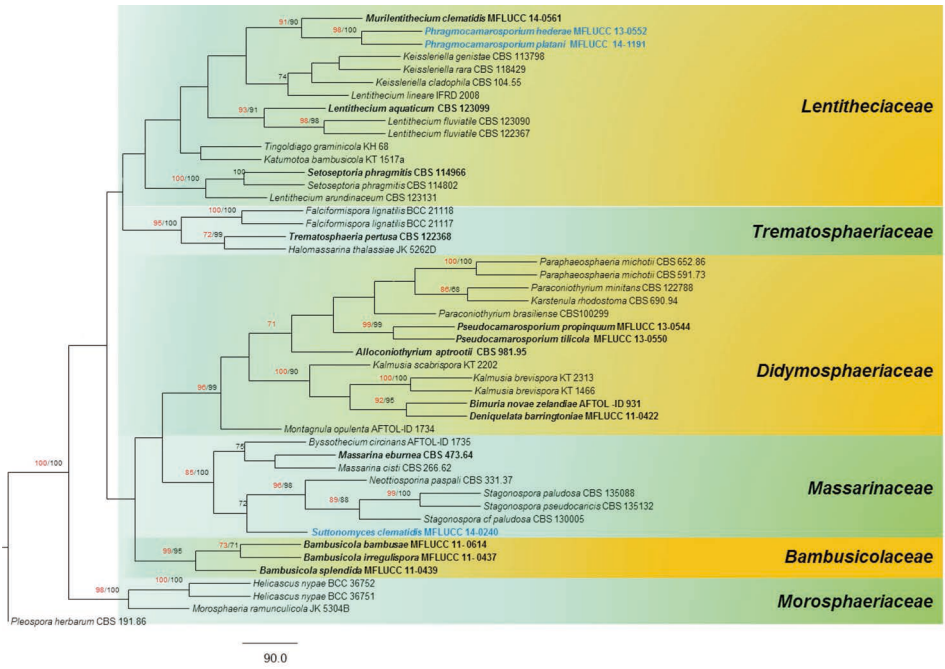

Fig. 1. One of the 1000 most parsimonious trees resulting from the combined analysis of LSU and SSU nucleotide sequence data. Bootstrap support values (>7 0%) for maximum parsimony (MP) and maximum likelihood (ML) analyses are given at the nodes in red and blue respectively. Ex-type isolates are in bold and newly generated strains are in blue.

Conidiogenous cells simple, smooth, short, 1.5-3 × 1.5-2.5 µm, phialidic, hyaline. *Conidia* 12-13 × 5-7.5 µm ($\bar{x}$ = 12.2 × 6 µm, n = 20), medium brown, clavate or ellipsoid to subcylindrical, with obtuse apex and truncate base, 3-4-transverse septate, rarely 1 longitudinal septa, constricted at the septa.

Culture characteristics: On PDA white from above and light brown from reverse, even margin, zonate, cottony, attaining a diam. of 2.5 cm in 7 days at 18°C.

Material examined: China, Guizhou Province, Huaxi, on branch of *Platanus* sp., 20 July 2012, Nalin Wijayawardene, NNW G0928-1 (MFLU 15-0164), living cultures MFLUCC 14-1191, GUCC N87.

Notes: *Phragmocamarosporium platani* has 2-4 transverse septa and 1 longitudinal septum observed rarely from the sporulated cultures. However, we have not observed conidia with longitudinal septa in specimen from host material.

Other species:

Phragmocamarosporium hederae Wijayawardene, R.K. Schumacher & K.D. Hyde sp. nov.

Index Fungorum number: IF551086; *Facesoffungi Number* : FoF 00467
Etymology: After the genus *Hedera* on which the fungus was found

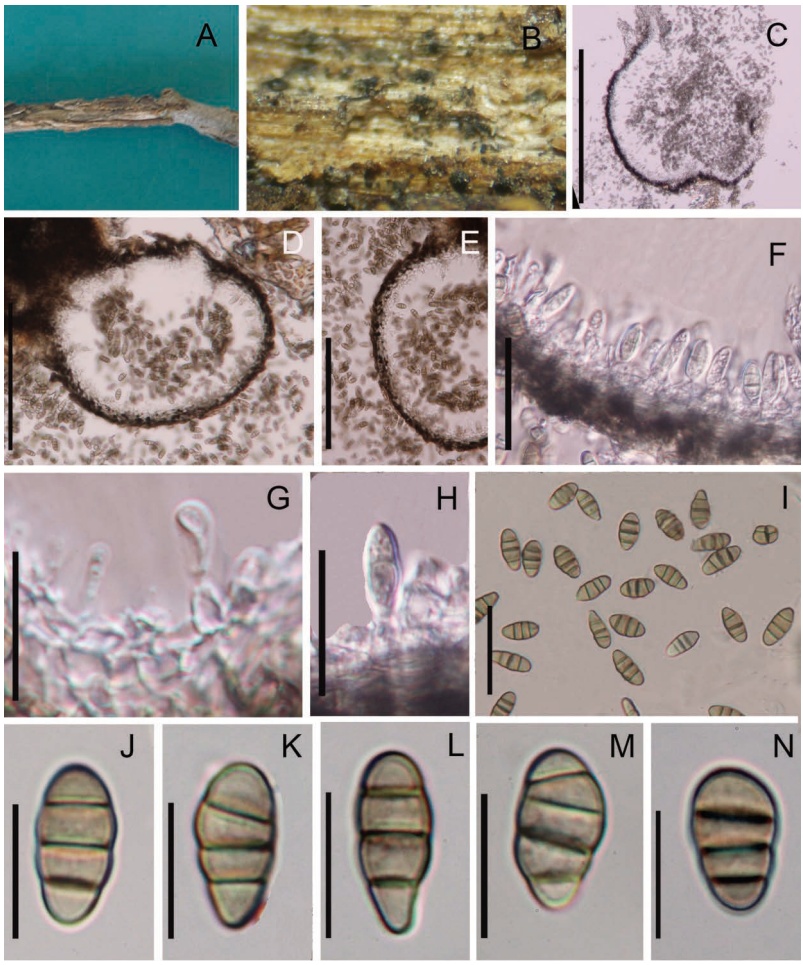

Fig. 2. *Phragmocamarosporium platani* (holotype) **A.** Branch of *Platanus* sp. **B.** Pycnidia on branch. **C, D.** Cross section of pycnidium. **E.** Pycnidial wall. **F-H.** Developing conidia attached to conidiogenous cells. **I-N.** Conidia. **Scale bars:** C 150 µm, D 100 µm, E 100 µm, F-H 10 µm, I 15 µm, J-N 10 µm.

Saprobic on twigs of *Hedera helix*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 80-110 µm high, 100-140 µm diam., pycnidial, sub-epidermal, black, gregarious, unilocular, globose to sub-globose, with a centrally located papillate ostiole. *Pycnidial wall* with outer 3-4 layers of dark brown cells of *textura angularis*, with inner layer of thin, hyaline cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* simple to simple branch at the base, smooth, long, 8-10 × 1.5-2.5 µm, phialidic, hyaline. *Conidia* 9-11 × 3-4.5 µm ($\bar{x}$ = 10.2 × 3.9 µm, n = 20), medium brown, clavate or ellipsoid to sub-cylindrical, with obtuse apex and truncate base, straight to curved, (2-)3(-4)- transverse septate, constricted at the septa.

Culture characteristics: On PDA white from above and very light brown from reverse, with thin mycelium, zonate, uneven margin, cottony, slow growing, attaining a diam. of 2.5 cm in 7 days at 18°C.

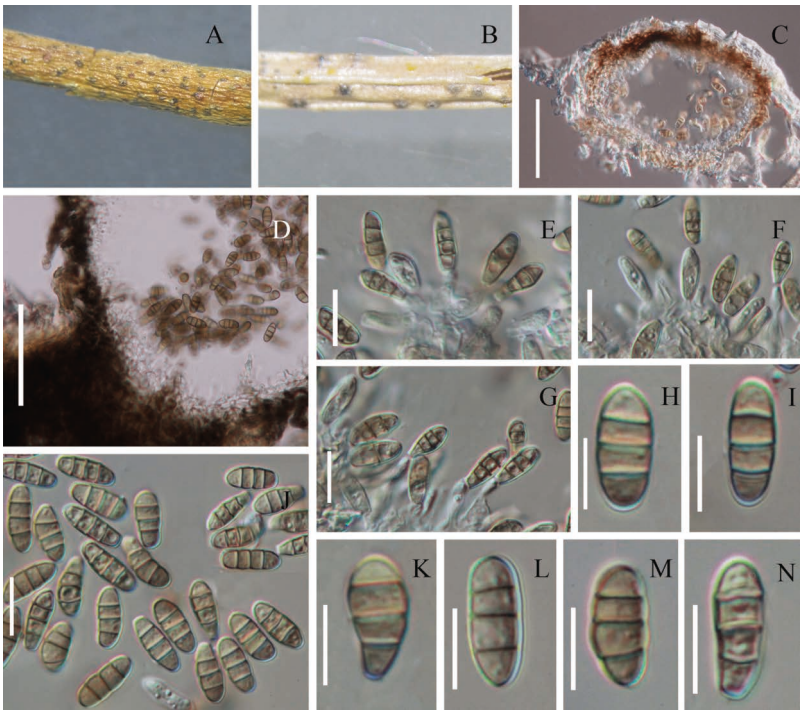

Fig. 3. *Phragmocamarosporium hederae* (holotype). **A, B.** Pycnidia on host material. **C.** Cross sections of pycnidium. **D.** Pycnidial wall. **E-G.** Developing conidia attached to conidiogenous cells. **H-N.** Conidia. **Scale bars:** C 75 μm, D 30 μm, E-N 5 μm.

Material examined: Germany, near Berlin, park, on a twig of *Hedera helix* L. (*Araliaceae*), 18 May, 2013, Rene Klaus Schumacher, NNW GER 014/8 (MFLU 15-0165), living cultures MFLUCC 13-0552, GUCC 8.

Notes: Ellis and Everhart (1900) reported *Camarosporium hederae* Ellis & Everh. which lacks longitudinal septa (phragmospores) from *Hedera helix*. *Phragmocamarosporium hederae* is similar with *Camarosporium hederae* as both share phragmospores and medium brown conidia. However, the conidial dimensions of both species are quite distinct as *Camarosporium hederae* (7-10 × 5-7 μm) has wider conidia, while *Phragmocamarosporium hederae* has narrower conidia (9-11 × 3-4.5 μm).

Phragmocamarosporium hederae has longer conidiogenous cells (8-10 × 1.5-2.5 μm) and smaller conidia (9-11 × 3-4.5 μm), while *P. platani* (type species) has shorter conidiogenous cells (1.5-3 × 1.5-2.5 μm) and larger conidia (12-13 × 5-7.5 μm). Hence we propose new species to place our collection from *Hedera helix*.

Suttonomyces Wijayawardene, Camporesi & K.D. Hyde, gen. nov.

Index Fungorum Number: IF551091; *Facesoffungi Number* : FoF 00468

Etymology: In honour of B.C. Sutton who predicted the heterogeneity of genus *Camarosporium* based on morphology.

Saprobic on branch of *Clematis vitalba*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* pycnidial, dark brown to black, solitary, superficial, unilocular, globose to sub-globose, with a centrally located papillate ostiole. *Pycnidial wall* with outer thick wall layer of dark brown cells of *textura angularis*, inner most layer hyaline, thin. *Paraphyses* present, hyaline, aseptate, tapering to obtuse apex, cylindrical, not abundant. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* simple, continuous, smooth, blastic to percurrent proliferation. *Conidia* pale brown to dark brown, oblong, with a truncate base, obtuse at the apex, straight to curved, muriform, with 1-2 transverse septa and occasionally 1 longitudinal septa, smooth-walled, guttulate when young and occasionally even at maturity.

Notes: Our new strain clusters in Massarinaceae and groups with the *Neottiosporina-Stagonospora* clade. *Neottiosporina* is characterized by hyaline conidia with basal and apical appendages and *Stagonospora* is characterized with hyaline, smooth, conidia with several transverse septa (Sutton, 1980). Currently, there are no known camarosporium-like taxa reported in Massarinaceae (Hyde *et al.,* 2013; Wijayawardene *et al.,* 2014c). Hence, we introduce *Suttonomyces* for our new taxon. However, *Paracamarosporium* Wijayawardene & K.D. Hyde and *Pseudocamarosporium* Wijayawardene & K.D. Hyde have been reported in Didymosphaeriaceae, Massarinae (Wijayawardene *et al.,* 2014b). *Suttonomyces* is morphologically distinct from *Camarosporium sensu stricto* and *Pseudocamarosporium sensu stricto* because the latter genera lack paraphyses (Sutton, 1980; Wijayawardene *et al.,* 2014b). Nevertheless, *Paracamarosporium* possess paraphyses (type species *P. psoraleae* (Crous & M.J. Wingf.) Wijayawardene & K.D. Hyde *fide* Wijayawardene *et al.* 2014b) which is similar to *Suttonomyces* (Fig. 4), but we did not observe microconidia in the culture of *Suttonomyces clematidis,* as in *P. psoraleae* (Crous *et al.,* 2013). These distinct morphological characters of camarosporium-like taxa in Massarinae are further supported by molecular data analyses (Fig. 1).

Type species: *Suttonomyces clematidis* Wijayawardene, Camporesi & K.D. Hyde.

Suttonomyces clematidis Wijayawardene, Camporesi & K.D. Hyde sp. nov.

Index Fungorum Number: IF 551092; *Facesoffungi Number* : FoF 00469

Etymology: Named after the generic name of host

Saprobic on branches of *Clematis vitalba*. **Sexual morph:** Not observed. **Asexual morph**: *Conidiomata* 160-210 µm high, 180-220 µm wide, pycnidial, dark brown to black, solitary, superficial, unilocular, globose to sub-globose, with a centrally located papillate ostiole. *Pycnidial wall* with 7-10 wall layers of dark brown cells of *textura angularis,* inner most layer hyaline, thin. *Paraphyses* 80-100 × 3-4 µm, hyaline, aseptate, cylindrical, not abundant. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* continuous, smooth, blastic to percurrent proliferation. *Conidia* 8-11.5 ×5-7 µm (mean = 9.6-5.8 µm, n = 20), pale brown to dark brown, oblong, with truncate base, apex obtuse, straight to curved, muriform, with 1-2 transverse septa and occasionally 1 longitudinal septa, smooth-walled, guttulate when young and occasionally at maturity.

Culture characteristics: On PDA white from above and very light brown from reverse, with thin mycelium, uneven margin, slow growing, attaining a diam. of 3 cm in 7 days at 18°C.

Material examined: Italy, Forlì-Cesena [FC] Province, Acquapartita - Bagno di Romagna, on twigs of *Clematis vitalba*, 6 December 2013, Erio Camporesi, NNW IT1560 (MFLU 15-0166), living cultures MFLUCC 14-0240 = GUCC 18.

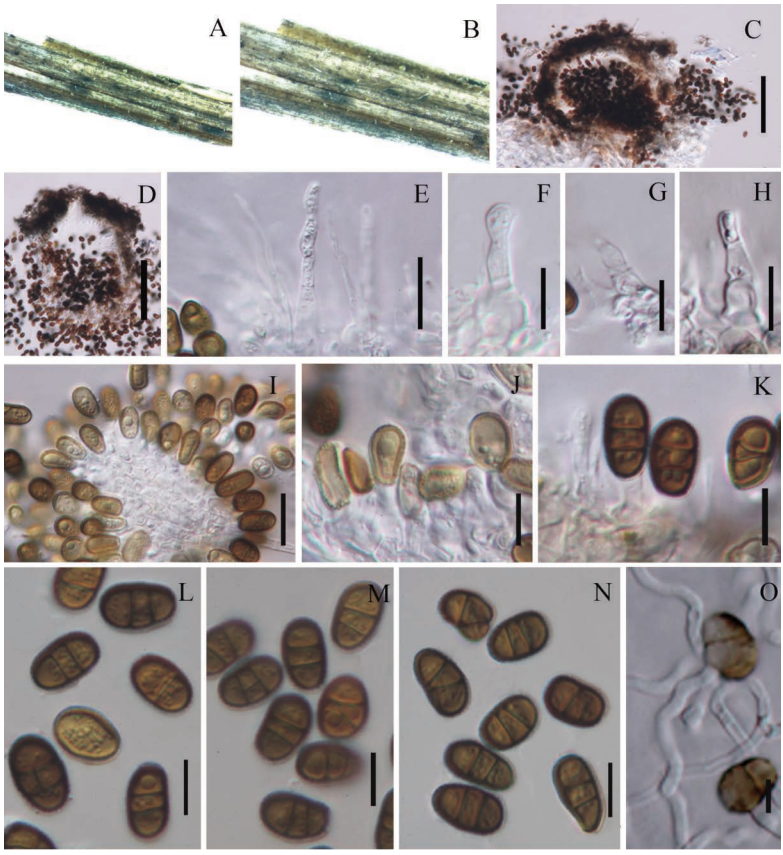

Fig. 4. *Suttonomyces clematidis* (holotype). **A, B.** Conidiomata on host. **C, D.** Cross sections of conidiomata. **E.** Paraphyses. **F-H.** developing conidia. **I-K.** Mature conidia attach to conidiogenous cells. **L-N.** Conidia. **O.** germinating conidia. **Scale bars:** C, D 250 μm, E 40 μm, F-N 20 μm.

Notes: Wijayawardene *et al.* (2014a) described *Camarosporium clematidis* Wijayawardene *et al.* from the same host *viz. Clematis vitalba*. However, *C. clematidis* is phylogenetically and morphologically (as it lacks paraphyses) distinct from *Suttonomyces clematidis* (Wijayawardene *et al.*, 2014a).

DISCUSSION

Ellis and Everhart (1900) introduced *Camarosporium hederae* Ellis & Everh. with conspicuous phragmosporous conidia (occasionally with a longitudinal septum) from *Hedera helix*. However, the genus *Camarosporium* Schulzer is characterized with muriform conidia, *viz.* several transverse and longitudinal septa (Schulzer, 1870; Sutton, 1980; Wijayawardene *et al.*, 2014a). Nevertheless, our collection of *Phragmocamarosporium hederae* (9-11 × 3-4.5 μm) from *Hedera helix*

has narrower conidia than *C. hederae* (7-10 × 5-7 µm). Furthermore, *P. hederae* is phylogenetically quite distinct from *Camarosporium sensu stricto* (Wijayawardene *et al.*, 2014a).

It is essential to clarify the generic concept of *Camarosporium* as it comprises of over 500 names in Index Fungorum (2014). In recent studies, several genera have been introduced to accommodate camarosporium-like taxa (Crous *et al.*, 2014; Wijayawardene *et al.*, 2014c). However, it is important to recognize that some of the *Camarosporium* species are morphologically quite distinct from the type species, *viz*. *C. quaternatum* (Hazsl.) Schulz. *C. propinquum* (Sacc.) Sacc with proliferating phialidic conidiogenesis, *C. psoraleae* Crous & M.J. Wingf. with paraphyses and microconidia and *C. hederae* with phragmospore conidia are good examples of such exceptions. Recent molecular-based studies confirm the heterogeneity of *C. propinquum* and *C. psoraleae* and hence the genera *Pseudocamarosporium* and *Paracamarosporium* were introduced by Wijayawardene *et al.* (2014c). Our collection with muriform conidia *viz*. *Suttonomyces clematidis* confirms the heterogeneity of camarosporium-like taxa as it shows a phylogenetic lineage distinct from *Camarosporium sensu stricto* (Wijayawardene *et al.*, 2014a, b). Therefore, it is important to rely on molecular-based studies to confirm the generic placements of camarosporium-like taxa.

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