

出國報告〈出國類別：出席國際會議〉

**2017 Towards a Natural Classification &
Industrial Utilization of the Fungi**

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出國期間：106年1月10日
 至106年1月14日
報告日期：106年03月29日

摘 要

本次” 2017 Towards a Natural Classification & Industrial Utilization of the Fungi” 於泰國皇后大學(Mae Fah Luang University)舉辦，由真菌研究卓越中心主辦，結合英國真菌學會前主席的EB Gareth Jones教授與美國、英國、泰國、菲律賓、印度、中國、台灣、香港、澳門等地區的真菌學家，發表論文50餘篇、張貼論文100餘篇，共舉辦3天會議。對於目前的真菌研究，不論在傳統形態分類及真菌多樣性調查方面，提供了最新的研究及訊息，在植物病原真菌方面，以中國的發表資料可以提供台灣未來防疫檢疫之參考。在水生菌方面，能夠了解在各真菌多樣性豐富之區域，目前研究之現況。本筆者自身也發表了一篇水生菌的研究，與會中也與各國學者有良好的互動與討論，對未來的研究有很大的助益。

目 次

壹、計畫起源與目的.....	1
貳、參訪行程.....	1
參、會後心得與建議.....	4
肆、附件.....	5

壹、計畫起源與目的

2017 Towards a Natural Classification & Industrial Utilization of the Fungi於泰國皇后大學(Mae Fah Luang University)舉辦，由真菌研究卓越中心主辦，為亞洲科學家提供一個交流平台，結合英國真菌學會前主席的EB Gareth Jones教授與美國、英國、泰國、菲律賓、印度、中國、台灣、香港、澳門等地區的真菌學家，會中發表論文50餘篇、張貼論文100餘篇，共舉辦3天會議。近年來的真菌研究，真菌分類系統發展有急遽的變化，傳統形態分類、真菌多樣性調查方面、生物學中分子數據的使用和真菌的生物技術用途，皆提供了最新的研究及訊息，能夠了解在各真菌多樣性豐富區域目前研究之現況。

貳、參訪行程

臺灣日期	泰國日期	活動行程
1/10(二)	1/10(二)	臺北桃園(台灣桃園國際機場)8:40→11:35泰國曼谷(曼谷蘇汪納篷國際機場)，泰國曼谷轉機13:35→14:45泰國清萊(清萊國際機場)
1/11(三)	1/11(三)	參加會議及訪問研究中心
1/12(四)	1/12(四)	參加會議及皇太后大學
1/13(五)	1/13(五)	參加會議及論文討論交流
1/14(六)	1/14(六)	泰國清萊(清萊國際機場) 9:45→11:05泰國曼谷(曼谷蘇汪納篷國際機場)，泰國曼谷轉機14:30→19:10臺北桃園(台灣桃園國際機場)

本次所發表的論文中，筆者認為有幾項研究值得注意，可以提供我們很好的參考訊息，概述如下：

泰國學者在木質分解水生真菌的調查及多樣性論文報告中，說明木質分解水生真菌在自然界生態的角色，也是生態環境的指標，這類真菌會產生酵素及抗生物質，也可能是植物或動物的病原菌，本次總共發表論文報告包含了3綱24目48科175屬，其中於泰國發現了7個新屬38個新種，這些調查結果包含子囊菌和不完全菌，可以作為

目前台灣地區調查研究之參考。

論文中也報導於泰國紅樹林的真菌多樣性，包含真菌的特性、棲息環境、作為腐生或分解者，也可以寄生在藻類動物，也可共生成為地衣的真菌。演講中提到水生真菌在世界上的熱點(Hot spot)，這些熱點都是最佳的研究地點。同時也報導泰國水生真菌種類多樣性相對高的地區，總共可達六千多種。

另中國大陸的學者報導有關於深海下真菌多樣性及二次代謝物的研究，可作為台灣未來研究真菌的參考，希望在未來真菌調查中，能採集更多樣性之菌種，且能針對二次代謝物研究作為醫療上等使用。

英國與中國學者共同發表分解木質素水生真菌的調查，在湄公河總共獲得612活體菌株，115屬226種真菌，這些真菌包含子囊菌、絲孢菌等，均由活菌體以DNA作親緣關係鑑定，完成親源樹狀圖。

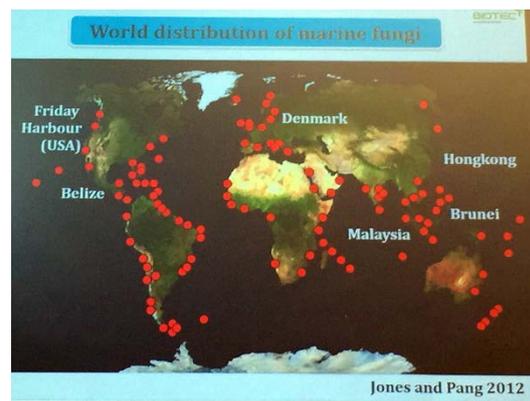
學者報導關於內生真菌的研究，內生真菌是近幾年來會感染植物但不會引起病害的一種真菌，希望能藉由對內生真菌的研究與認識，提供一些新的偵測方法，以利於未來研究。

學者發表利用水生真菌清除海上油污污染的研究。

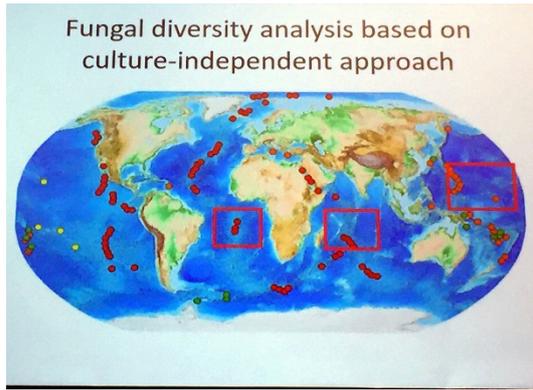
在植物病原菌方面，中國大陸雲南的花卉栽培調查了幾樣相關的植物病原菌，針對蘋果銹病的調查，發現2個新種以及6個新紀錄種，此銹病調查結果也可以作為台灣未來防疫檢疫之參考。



圖一、英國真菌學會前任理事長EB Gareth Jones教授演講



圖二、水生真菌於世界上的熱點(Hot spot)



圖三、深海所調查的真菌

Results

Morphological characteristics of *Gymnosporangium* species recognized in this study

Species	Host plant	Host part	Geographical origin	Host plant	Host part	Geographical origin	Host plant	Host part	Geographical origin	Host plant	Host part	Geographical origin	Host plant	Host part	Geographical origin	Host plant	Host part	Geographical origin
<i>G. cubense</i>	citrus	fruit	China															
<i>G. japonicum</i>	citrus	fruit	China															
<i>G. kobei</i>	citrus	fruit	China															
<i>G. shanghaiense</i>	citrus	fruit	China															
<i>G. sinense</i>	citrus	fruit	China															
<i>G. yunnanense</i>	citrus	fruit	China															

Species name was given mainly based on Kern (1973).

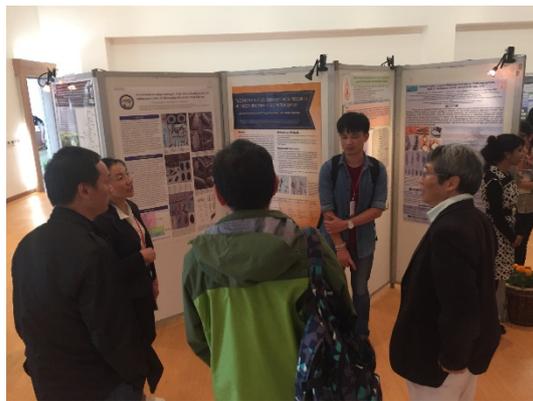
圖四、中國大陸蘋果銹病調查結果



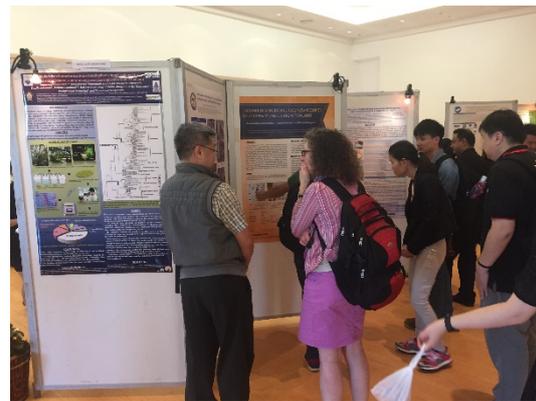
圖五、本次發表之海報



圖六、發表海報張貼證明



圖七、作者與與會人員共同討論論文發表



圖八、共同發表人吳博士於會場講解論文內容



圖九、作者很榮幸與EB Gareth Jones
教授合影，討論所發表之論文

參、會後心得與建議

本次所發表的論文在鑑定將上命名為新屬，會議期間也跟與會學者進行交換經驗與心得分享，共同討論而獲取許多寶貴資訊。學者也提出建議，對於未來本菌提供更多的證據為發表新屬新種來作為佐證，得到很多的助益。

附件

會議議程表-1

Program Overview					
Time	Day 1 : 11 January 2017	Time	Day 2 : 12 January 2017	Time	Day 3 : 13 January 2017
08:30-09:00	Registration	08:30-09:00	Registration	08:30-09:00	Registration
09:00-09:30	Center of Excellence in Fungal Research and COEIC2017 Opening Ceremony	09:00-09:30	Phylogeny and Evolution of fungi Chairman Prof. Gareth Jones Dr. Saranyaphath Boonmee	09:00-09:30	The ecological and economic roles of fungi across the SE Asian region Chairman Dr. Samantha Chandranath Karunarathna Dr. Peter Mortimer
09:30-10:20	<p style="text-align: center;">Marine and Freshwater Fungi Chairman Prof. Kevin Hyde Prof. Ka-Lai Pang</p> <p>Keynote Speaker Prof. E. B. Gareth Jones: Former President of the British Mycological Society (1992), England "Taxonomy and diversity of wood-degrading marine fungi"</p>		Keynote Speaker Dr. Rajesh Jeewon: Senior Lecturer, Faculty of Science, University of Mauritius, Mauritius "Establishing new fungal species: Ramifications & Recommendations"		Dr. Peter Mortimer: Kunming Institute of Botany, China : "Landscape scale distribution models and diversity of mushrooms in SE Asian forest systems"
10:20-10:40	Coffee Break	09:30-09:50	Keynote Speaker Dr. Eric Mckenzie: Former Senior Research Scientist of Landcare Research, New Zealand "OF, ON—did something change? 'One Fungus, One Name' and its effects on the basidiomycete fungi"	09:30-09:50	Dr. Samantha Chandranath Karunarathna: Cultivation of novel species from SE Asia
10:40-11:00	Veera Sri-Indrasudhi: An updated checklist of Thai lignicolous freshwater fungi	09:50-10:10	Sajeewa S.N. Maharachchikumbura : Current taxonomic status of the Sordariomycetes	09:50-10:10	Dissanayake Mudiyansele Naveen Jayalal: Prevalence of marketable wild mushrooms and their contribution to the rural economy in Xishuangbanna, Southwest China
11:00-11:20	Dr. Satinee Suetrong: Area-based collaborative research for conservation: distribution and occurrence of mangrove fungi in Thailand	10:10-10:30	Coffee Break	10:10-10:30	Xia Luo : The macrofungal diversity and community composition at different abiotic and biotic factors
11:20-11:40	Zhuhua Luo : Fungal diversity in deep sea sediments of the Pacific Ocean and their secondary metabolites	10:30-10:50	Qian Chen: Biodiversity in the family Didymellaceae, from plants to caves	10:30-10:50	Coffee Break
11:40 -12:00	Zong-Long Luo : "Lignicolous freshwater fungi of the greater Mekong subregion"	10:50-11:10	Dr. Sung-Yuan Hsieh: The sporangial development in <i>Pythiogeton</i> spp.	10:50-11:10	Supeni Sufaati: Confirming some <i>Scleroderma</i> from Papua, Indonesia using ITS rDNA
		11:10-11:30	Dr. Jian Kui Liu: Phylogenetic assessment of Dothideomycetes	11:10-11:30	Dr. Nattawut Boonyuen: <i>Parafuscospora Garethia</i> sp. nov., and some interesting fungal taxa isolated from Thai aquatic habitats
12:00-12:20	Resurreccion Bitoon Sadaba : Manglicolous fungi in bunker C oil contaminated mangrove forests in Taklong Island, Guimaras, Philippines	11:30-11:50	Dhanushka N. Wanasinghe : Multigene phylogeny and taxonomic revision of camarosporium-like taxa; introducing Camarosporiellaceae fam. nov. and <i>Camarosporiella</i> gen. nov. in Pleosporineae	11:30-11:45	Nilam Wulandari: Research Progress of the <i>Phyllachora</i> species of Sorghum in Bogor, Indonesia
12:20-13:30	Lunch Break	11:50-13:00	Lunch Break	12:00-13:00	Pheng Phengsingkum: Checklist of Lao Fungi
	Lunch Break		Lunch Break		Lunch Break

會議議程表-2

12:20-13:30	Lunch Break	11:50-13:00	Lunch Break	12:00-13:00	Lunch Break
	Plant Pathology Chairman Dr. Eric Mckenzie Dr. Sinang Hongsanan		Fungal systematic Chairman Dr. Putarak Chomnunti Dr. Ratchadawan Cheewangkoon		Fungal Biotechnology Chairman Dr. Nattawut Boonyuen Miss. Benjarong Thongbai
13:30-14:00	Keynote Speaker Dr. Joanne Elizabeth Taylor: BBSRC funded researcher for PROTREE project, Royal Botanic Garden Edinburgh, United Kingdom "The tree microbiome as part of the extended phenotype?"	13:00-13:30	Keynote Speaker Prof. D J Bhat: Goa University, India : 'Conidiogenesis in Ascomycota: A perusal from current taxonomic perspective'	13:00-13:30	Keynote Speaker Prof. Dr. Marc Stadler: Head of the Research Department Mikrobielle Wirkstoffe (MWIS) Germany "Phylogeny and functional biodiversity of the Xylariaceae"
14:00-14:20	Prof. Dr. Cai Lei: Ecological speciation of plant pathogenic fungi	13:30-14:20	Dr. Dongqin Dai : Bambusicolous ascomycetes	13:30-14:20	Miss Birthe Förster : New compounds from the Hohenbuehelia
14:20-14:40	Thilini Chethana & Ishara Manawasighe: Comparative genome and transcriptome analyses reveal adaptations for plant cell wall degradation in <i>Lasiodiplodia theobromae</i>	14:20-14:40	Yahui Gao: The systematics study on Diaporthe	14:20-14:40	Ji-Chuan Kang: The rise of medicinal mushrooms in the pharmaceutical industry
14:40-15:00	Sehroon Khan : <i>Ampelomyces</i> (Pleosporales) as a potential biocontrol agent against powdery mildew of rubber (<i>Hevea brasiliensis</i>)	14:40-15:00	Yong Wang: Phylogeny and taxonomy of fungal pathogens in orchid plants in southwestern China	14:40-15:00	Maythasith Konkarn : Sustainable agricultural systems in Thailand : The perspective of entomopathogenic fungi as potential biological control agents of insect pests
15:00-15:20	Coffee Break	15:00-15:30	Qing Tian: "Determining family and genus limits in ascomycota: Melanommataceae and Chaetothyriales as model systems"	15:00-15:20	Assoc. Prof. Dr. Rulin Zhao: A phylogenetic overview of Basidiomycota and allied phyla with the divergence times of higher level taxa
15:20-15:40	Bussakan Punlerdmate: "Epiphytic yeasts as plant disease biocontrol agents"	15:30-15:50	Indunil C. Senanayake: "Revision of Sydowiellaceae"	15:20-15:40	Coffee Break
15:40-16:00	Ying Zhang: Biodiversity of Botryosphaeriaceae in China - the tip of the iceberg	15:50-16:10	Coffee Break		Ranking and Evolution Chairman Dr. Sinang Hongsanan
16:00-16:20	Gayuh Rahayu: Genetic diversity of <i>Fusarium oxysporum</i> fsp. Cubense, from several regions in Indonesia based on their ISSR Profiles			15:40-16:00	Milan C. Samarakoon: "Evolutionary events for the ranking of taxa - is it possible?"
16:20-16:40	Nisachon Tamakaew : Diversity of Fungi causing Tar spot disease in Chiang Mai province.	16:10-17:10	Poster Presentation	16:00-16:20	Ausana Mapook: "Muyocoprionales ord. nov., and Palawaniaceae, a new family in the Dothideomycetes with their divergence time estimates"
16:40-17:00	Asha Dissanayake & Ruvishika Jayawardena : Grape fungal diseases.			16:20-16:40	Chayanard Phukhamsakda: "The evolution of Massariaceae with Longipedicellataceae fam. nov."
17:00-21:00	Welcome Dinner (Banquet)			16:40-17:00	Closing ceremony

張貼海報



Wenhsuimyces chiayiensis gen. et sp. nov., a hyphomycete on submerged culm of *Miscanthus floridulus* from Taiwan

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Abstract

Wenhsuimyces chiayiensis gen. et sp. nov. from decaying culm of *Miscanthus floridulus* submerged in a freshwater stream of Alishan area, Chiayi County, Taiwan, is described and illustrated. It produces large ovoid muriform solitary thallic conidia which are dark brown to black, but encased in a layer of subhyaline peripheral cells. The conidia are produced singly at an oblique angle to the conidiophores which are borne from superficial hyphae on the natural substratum. The genus is compared with other similar dictyosporous hyphomycetes: *Acrodactys*, *Berkleasium*, *Coleodictyospora*, *Hermatomyces*, *Kostermansinda*, *Monodictys*, *Tamhinispora*, and *Waihonghopes*. Conidia of this fungus germinated readily in culture, but growth was slow. It produced abundant chlamydospores in culture but no sporulation was observed. Although its sexual morph is presently unknown, the phylogenetic relationship of this fungus is inferred to be a member of the Tubeufiaceae by comparing the partial 28S segment and the internal transcribed spacer regions of the nucleolar ribosomal RNA gene.

INTRODUCTION

During a survey of microfungi occurring on plant litter submerged in a stream of Alishan area, Chiayi County, Taiwan, we found an extraordinary dematiaceous hyphomycete producing large ovoid muriform solitary thallic conidia on a decaying culm of *Miscanthus floridulus*. The conidia were produced singly at an oblique angle to the conidiophores which arose from superficial hyphae on the natural substratum. Under the stereomicroscope, the mature conidia were black and glistening, whereas the young ones were white and thus resembling rice kernels. Higher magnification of the conidia revealed that the conidia were dictyosporous, but the mature ones were dark brown to black and thus the central septa were often obscured. Such somewhat opaque conidia, however, were unique in having a pale external wall comprising of a single layer of hyaline or pale olivaceous peripheral cells. A literature search has revealed that this fungus on submerged wood has not been previously described. As it cannot be suitably placed in any of the known genera of Hyphomycetes, it is described and illustrated in this paper as a new genus. The genus is compared with morphologically similar fungi: *Acrodactys*, *Berkleasium*, *Coleodictyospora*, *Hermatomyces*, *Kostermansinda*, *Monodictys*, *Tamhinispora*, and *Waihonghopes*. We have successfully grown this fungus in pure culture, all from single-spore isolation using the method described by Goh. Colony morphology is described. DNA extraction of this fungus was from these pure cultures and used for molecular studies. Its phylogenetic relationship was inferred by comparing the concatenated ITS-5.8S-ITS2 (ITS barcode) and the partial 28S segment (LSU) of the nuc rDNA.

RESULTS

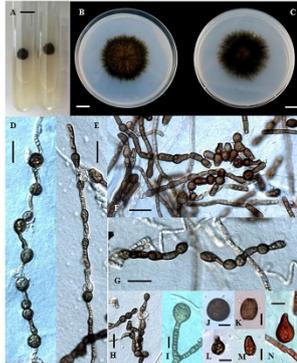
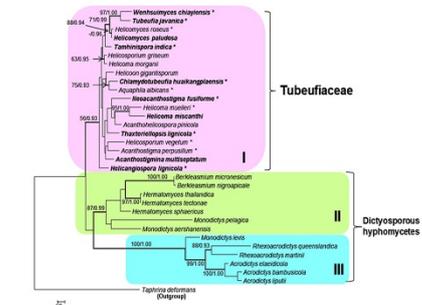


Fig. 1. *Wenhsuimyces chiayiensis* (BCRC-FU39757, ex-type culture). Cultural characteristics: A. Colonies on PDA slants produced from single-spores. B, C. Colonies on PDA plates from surface (B) and reverse (C). D-H. Hyphae and chlamydospores. I. A developing terminal chlamydospore. J-N. Detached chlamydospores. Bars: A-C = 1 cm, D-H = 20 μ m, I-N = 10 μ m.

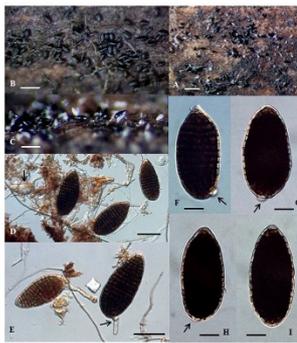


Fig. 2. *Wenhsuimyces chiayiensis* (TNM F33075, holotype). A-C. Colonies on natural substratum; note the developing conidia which are white and resemble rice kernels. D. Young conidia, three nearly mature ones are uniform and pigmented. Arrow points to a developing conidium which is hyaline at its early stage. E. Two nearly mature conidia which are uniform and still attaching at an oblique angle to their conidiophore. Arrow points to the delimiting septum at the base of a conidium. F-I. Mature conidia which are nearly pigmented and nearly opaque, but encased by a single layer of hyaline peripheral cells. Arrows point to the off-centred base of conidia. Bars: A = 500 μ m, B = 250 μ m, C = 100 μ m, D = 50 μ m, E = 50 μ m, F-I = 20 μ m.

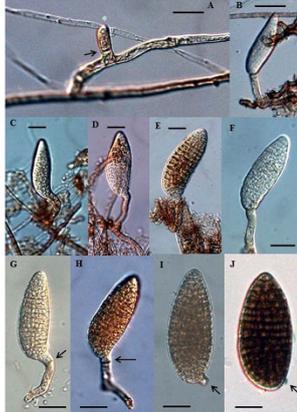


Fig. 3. *Wenhsuimyces chiayiensis* (TNM F33075, holotype). A. Developing conidiophore from superficial hypha. Arrow points to delimiting septum. Asterisk denotes the tip of the conoidal initial which is off-centred. B-D. Early stages of conoidal development at which the conoidal cells are hyaline. E-H. Middle stages of conoidal development at which conoidal cells become more and more pigmented except the single layer of peripheral cells which remain hyaline. Mycelium septation becomes more visible at these stages. Developing conidia are obliquely attached to the conidiophores. Arrows point to delimiting septum. I, J. Nearly mature conidia which are uniform and pigmented except the subhyaline out-wall. Arrows point to the off-centred base of conidia. Bars: A-C = 20 μ m.



Fig. 4. *Wenhsuimyces chiayiensis* (TNM F33075, holotype). Scanning electron micrographs. A-C. Mature conidia. Note that conidia are uniform, slightly constricted at the septa, but smooth-walled. D. Young conidia. Arrows point to conidiophores which are arising from superficial hyphae. Bars: A, B, E = 100 μ m, C, D = 200 μ m.

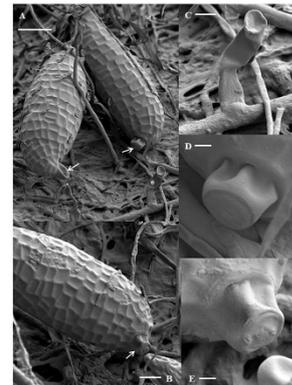


Fig. 5. *Wenhsuimyces chiayiensis* (TNM F33075, holotype). Scanning electron micrographs. A, B. Mature conidia, each with an off-centred, proconical base. Asterisk denotes conidiophore arising from superficial hypha. C. Higher magnification of conidiophore from A, D, E. Higher magnification of proconical base of conidia, from A and B, respectively. Note that the lumen is smooth, an evidence of subhyaline conoidal secretion. Bars: A = 200 μ m, B = 100 μ m, C = 50 μ m, D, E = 20 μ m.

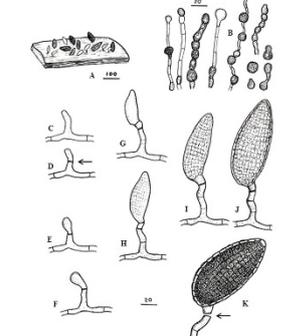


Fig. 6. *Wenhsuimyces chiayiensis* (TNM F33075, holotype). Diagrammatic representation. A. Colony on natural substratum. B. Chlamydospores and hyphae from culture. C-I. Serial representation of conidiogenesis. Arrow in I indicates the appearance of a delimiting septum before conoidal ontogeny. J. Nearly mature conidium which is dictyosporous, with a single layer of pale peripheral cells. K. Mature conidium which is uniform, with darkly pigmented central cells and a single layer of pale peripheral cells. Arrow denotes subhyaline conoidal secretion. Bars: A = 100 μ m, B-K = 20 μ m.