无性丝孢真菌分类研究

张修国　主编

TAXONOMIC CLASSIFICATION OF HYPHOMYCETES

科学出版社

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北京

内 容 简 介

本书系统介绍了我国南方地区凋落枯枝无性暗色丝孢真菌系统分类研究的成果，先后从19个省（直辖市、自治区）不同生境及不同植被类型采集标本，基于传统的真菌系统分类技术，合格描述鉴定了4个新属（*Cladosporiopsis*、*Parablastocatena*、*Sativumoides*、*Sinomyces*）；系统开展了*Corynespora*、*Heteroconium*及*Solicorynespora*等60余个暗色丝孢真菌属的分类研究，修订了*Lomaantha*属级特征，评价了*Ulocladium*等属种形态学划分标准与分类框架，订正了*Sporidesmium*及*Ulocladium*属内部分疑难种的分类地位，澄清了*Pseudoacrodictys*等属种分类的混乱，补充或完善了*Piricaudiopsis*等多个属的种级分类检索表，合格描述新种139个、新组合2个、中国新记录61个及若干已报道种。相关分类研究成果先后发表于*Fungal Biology*、*Mycologia*、*Mycological Progress*、*Mycoscience*等国际学术期刊。

本书可供国内外从事真菌分类、植物病理、植物保护和生物多样性研究的科研工作者及高等院校相关专业的教师和研究生参考，也可作为农林生产单位真菌诊断和鉴定的工具书。

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前　言

山东农业大学植物保护学院真菌及真菌资源利用研究室自2001年创立以来，紧紧围绕无性丝孢真菌多样性、真菌资源利用、真菌分子遗传学与人才培养四大核心任务，依托学院一级学科博士点和博士后流动站的学科体系，形成了一支专业知识扎实、研究素质较强，以硕士生和博士生为主的科研队伍，营造了奋发进取、献身科学的研究氛围。经多年研究积淀，建成了无性丝孢真菌分类研究平台：①配置了从事真菌形态学及分子遗传学研究的仪器设备，结合学科公共实验条件构建了具有国内外先进水平的技术平台；②积累了丰富的文献资料，拥有多部无性丝孢真菌专著：*Conidial Fungi from Cuba: I-II*、*Dematiaceous Hyphomycetes*、*Deuteromycotina de Cuba. Hyphomycetes II-IV*、*Fungi Cubense I-III*、*Fungi of Northwestern China*、*Hifomicetes Demaciáceos de Sierra del Rosario, Cuba*、*Higher Fungi of Tropical China*、*Hyphomycetes*、*Icones Microfungorum a Matsushima Lectorum*、*Matsushima Mycological Memoirs No.*1-10、*Microfungi of the Solomon Islands and Papua-New Guinea*、*More Dematiaceous Hyphomycetes*、*Ninety-nine Conidial Fungi from Cuba and Three from Canada*、*Patterns of Development in Conidial Fungi*、*Sporidesmium, Endophragmiella and Related Genera from China*、*The Fifth Kingdom*、*The Genera of Hyphomycetes*（1980版, 2011版）、*The Genera of Hyphomycetes from Soil*、*The Synnematous Genera of the Fungi Imperfecti*、*Mycological Papers*（共38卷）、《中国真菌志》（共17卷）、《中国真菌总汇》和《河北小五台山菌物》，并汇集了*Acta Botánica Cubana*、*Canadian Journal of Botany*、*Ceská Mykologie*、*Cryptogamie Mycologie*、*Current Science*、*Fungal Diversity*、*Kavaka*、*Indian Phytopathology*、*Journal of the Indian Botanical Society*、*Mycologia*、*Mycological Progress*、*Mycological Research*、*Mycotaxon*、*New Zealand Journal of Botany*、*Nova Hedwigia*、*Studies in Mycology*、*Sydowia*、*Transactions of the British Mycological Society*、《菌物学报》和《菌物研究》等多种真菌（植物）分类学期刊相关论文，构建了中国无性丝孢真菌分类文献信息平台；③凝聚团队力量，加强国内外同行学者合作与交流，先后与加拿大滑铁卢大学Bryce Kendrick教授，加拿大农业与农业食品部S. J. Hughes教授，古巴热带农业基础研究所R. F. Castañeda-Ruíz教授，新西兰菌物标本馆Eric H. C. McKenzie教授，美国农业部农业研究中心Nichole R. O'Neill博士、Gary J. Samuels博士，美国马萨诸塞大学E. G. Simmons博士，法国昂热国家农艺研究院Bruno Le Cam博士，印度果阿大学D. J. Bhat教授及荷兰微生物菌种保藏中心（CBS）等建立了长期的学术交流与合作，交换多份具重要研究价值的标本材料，并承蒙惠赠部分文献资

料。Bruno Le Cam博士、R.F. Castañeda-Ruíz教授、Bryce Kendrick教授及Nichole R. O'Neill博士等先后访问过本研究室。国内著名菌物学家魏江春院士、李玉院士、庄剑云研究员、戴玉成研究员、李泰辉研究员、郭良栋研究员、陈双林教授、图力古尔教授及郑维发教授等曾对本研究室的分类研究给予指导，中国科学院微生物研究所庄文颖院士、郭英兰研究员、郭林研究员等关注本研究室的发展并提供帮助，拓展了国内同行的联系与交流，提升了研究水平与创新能力。

研究室自创立以来，先后从四川、重庆、贵州、湖南、海南、云南、广东、广西、福建、江苏、安徽、河南、山东、陕西、河北、新疆、辽宁、吉林和黑龙江等19个省（直辖市、自治区）不同生境及植被类型区域采集若干研究标本，描述鉴定了4个新属（*Cladosporiopsis*、*Parablastocatena*、*Sativumoides*及*Sinomyces*），并系统开展了*Corynespora*、*Heteroconium*及*Solicorynespora*等60余个暗色丝孢真菌属的分类研究，修订了*Lomaantha*的属级特征，评价了*Ulocladium*等属种形态学划分标准，订正了*Sporidesmium*及*Ulocladium*属内疑难种的分类地位，澄清了*Pseudoacrodictys*等属种分类的混乱，补充或完善了*Piricaudiopsis*等多个属的种级分类检索表，合格描述新种139个、新组合2个、中国新记录61个及若干已报道种，充实了《中国真菌志：砖格分生孢子类Ⅱ》和《中国真菌志：砖格分生孢子类Ⅲ》编研内容，为深入探索无性丝孢真菌分类研究提供技术积累与经验借鉴，具重要的真菌分类学及真菌资源学意义。新种主模式保存于山东农业大学植物病理学标本室（HSAUP），副模式保存于中国科学院微生物研究所菌物标本馆（HMAS），部分种菌株保存于荷兰微生物菌种保藏中心（CBS）。

相关分类成果先后于*Fungal Biology*、*Mycologia*、*Mycological Progress*、*Mycoscience*、*Nova Hedwigia*、*Cryptogamie Mycologie*、*Sydowia*及*Mycotaxon*等8种国际SCI源期刊发表科学论文72篇，国内一级学报《菌物学报》及核心期刊《菌物研究》发表6篇，培养（含在读）真菌分类学博士4名、硕士7名，2人次的毕业论文被评为“山东省优秀硕士学位论文”，3人次被评为“山东省优秀毕业生”，1人次荣获中国菌物学会“菌物杯”青年科技创新奖。

现将本研究室真菌分类研究论文汇集成册供同行参考，希望本论文集能够促进同行学者间的交流与合作，营造更加浓厚的研究氛围，鼓励更多青年学者投入到菌物研究，更好地促进我国菌物学科的发展。恭请各位同行专家及读者提出宝贵建议。

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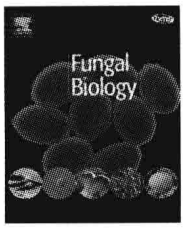

Sinomyces: a new genus of anamorphic *Pleosporaceae*

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ABSTRACT

Sinomyces gen. nov. is described for *Ulocladium alternariae* and two new species from China. These three species differ from *Ulocladium* in producing simple conidiophores with a single, cicatrized apical pore or 1 or 2 short, uniperforate, geniculate sympodial proliferations. Phylogenetic analysis of partial DNA sequences of the glyceraldehyde-3-phosphate dehydrogenase gene (*gpd*) gene and a fragment of the *Alternaria alternata* major allergen (Alt a 1) gene, using Maximum-Parsimony (MP), Maximum-Likelihood (ML) and Bayesian approaches, indicates that *Sinomyces* is distinct within the *Alternaria–Stemphylium* complex, although its closest relatives could not be determined. *Sinomyces alternariae* comb. nov. and the new species *Sinomyces obovoideus* and *Sinomyces fusoideus* are proposed.

Introduction

The *Alternaria–Stemphylium* complex, which comprises the genera *Alternaria* Nees, *Embellisia* E.G. Simmons, *Nimbya* E.G. Simmons, *Stemphylium* Wallr., and *Ulocladium* Preuss, and, encompasses many species, among which are several economically important plant pathogens. Simmons (1967) surveyed *Alternaria*, *Stemphylium* and *Ulocladium* and emphasized the shapes of juvenile and mature conidia and the modes of conidiophore proliferation. He resurrected *Ulocladium* for species having obovoid and nonbeaked conidia. *Embellisia* was distinguished primarily on the basis of the thick, dark and rigid septa in the conidia, while *Nimbya* produced distoseptate conidia (Simmons 1971, 1989). Inderbitzin *et al.* (2006) combined molecular and morphological characters in proposing a new genus in the *Alternaria* group, *Crivellia* Inderb. *et al.*, which was monotypic for *Crivellia papaveracea* (De Not.) Inderb. & Shoemaker and was characterized by having cylindrical phragmoconidia.

Recent molecular analyses have revealed that *Alternaria*, *Crivellia*, *Embellisia*, *Nimbya* and *Ulocladium* form a large clade that is in a sister-group relationship with *Stemphylium*, but many of the morphologically defined genera are polyphyletic (Pryor & Gilbertson 2000; Pryor & Bigelow 2003; Hong *et al.* 2005; Inderbitzin *et al.* 2006). Thus morphological characters can be misleading. Runa *et al.* (2009) analyzed the ITS, *gpd* and Alt a 1 sequences of 13 *Ulocladium* species and found only ten species grouped into a well-supported clade. *Ulocladium alternariae* (Cooke) E.G. Simmons and *Ulocladium oudemansii* E.G. Simmons, which possessed the key conidium characteristics of *Ulocladium*, clustered as a separate clade sister to the core *Ulocladium* clade. Conidiophores of *U. alternariae* terminate in a single pore, or occasionally proliferate once sympodially as a geniculation to form a second, uniperforate conidiogenous locus. This is distinct from the conidiophores of typical *Ulocladium* species that produce a sympodial succession of geniculate conidiogenous loci (Simmons 1967).

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During investigations of anamorphic *Pleosporaceae* in China from 2004–2008, we obtained many strains of *Alternaria* spp., *Stemphylium* spp. and *Ulocladium* spp. from leaves of diverse plants and rotten wood. Among them, two species, similar to *U. alternariae* in morphology, were isolated from the leaves of *Tamarix ramosissima* and *Daucus carota*, respectively. Because neither could be identified to any of the known species of *Ulocladium* they appeared to be new. In the current study we characterize the morphology of these fungi and determine their phylogenetic relationships using sequences of Alt a 1 and *gpd* genes. In light of its unusual morphology in *Ulocladium*, phylogeny and morphology of *U. alternariae* are studied.

Materials and methods

Morphological analysis

Diseased leaves of *Tamarix ramosissima* and *Daucus carota* were collected from Xinjiang and Sichuan provinces in China. Single-conidium cultures were taken from necrotic leaf spots and incubated on potato-dextrose agar (PDA; 20 g white potato boiled and filtered, 20 g dextrose, 20 g agar, 1 L distilled water) at 4 °C. Morphological observations are based on cultures grown on potato-carrot agar (PCA; 20 g white potato boiled and filtered, 20 g carrot boiled and filtered, 20 g agar, 1 L distilled water). 'Standard conditions' for the study of morphology are defined as: growth on PCA at ambient temperature (20–23 °C) and under cool-white fluorescent light 35–40 cm above the culture surface, with an 8 h on and 16 h off light cycle (Simmons & Roberts 1993). The holotypes (dried culture) of the new species were deposited in the Herbarium of the Department of Plant Pathology, Shandong Agricultural University (HSAUP). Reference strains were maintained in HSAUP and the collection of the Centraalbureau voor Schimmelcultures (CBS) Utrecht, The Netherlands.

Conidium germination was studied on PCA, at ambient temperature (20–23 °C) and under cool-white fluorescent light 35–40 cm above the culture surface, with an 8 h on and 16 h off light cycle (Simmons & Roberts 1993). The statistics presented here are based on measurement of 50 mature conidia and 30 conidiophores at 100× magnification in lactic acid.

DNA extraction, PCR amplification, DNA sequencing

Thirty-six strains belonging to 35 species were used for phylogenetic analyses. Among them, the two unknown strains from *Tamarix ramosissima* and a strain of *Crivellia* were sequenced *de novo*; all other sequences were retrieved from GenBank (Table 1). Genomic DNA was isolated from mycelium grown on PCA plates following the protocol of Pryor & Gilbertson (2000). Portions of Alt a 1 and *gpd* gene regions were amplified using the primers targeting the conserved regions of these genes in several species of *Ulocladium* and *Alternaria* (Hong *et al.* 2005). Reaction mixtures contained 5 μL of 10× ThermoPol reaction buffer [200 mM Tris–HCl, pH 8.3, 100 mM KCl, 100 mM $(NH_4)_2SO_4$ and 1 % Triton X-100], 5 μL of 10 mM $MgSO_4$, 20 ng template genomic DNA, 4 pM of each primer, 4 μL of 2.5 mM dNTPs, 2.5 U of AmpliTaq polymerase (TaKaRa, Dalian, China); total volume was adjusted to 50 μL with deionized water. The PCR thermal cycling program of Alt a 1 and *gpd* regions was conducted using previously described reaction conditions (Pryor & Gilbertson 2000; Hong *et al.* 2005). The PCR products were purified using DNA fragment Purification Kit Ver. 2.0 (TaKaRa). PCR products were cloned into the pGM-Teasy vector following the manufacture's protocol of the pEASY-T3 Cloning Kit (China) and transformed into DH5α. Sequences were performed with an ABI PRISM 3730 DNA autosequencer using either dRhodamine terminator or Big Dye Terminator chemistry (Applied Biosystems Inc., Foster City, California). The sequences of both strands of each fragment were determined for sequence confirmation.

Phylogenetic analysis

Alt a 1 and *gpd* sequences were aligned using Clustal X 1.81 (Thompson *et al.* 1997). The alignments were improved manually where necessary, and deposited in TreeBASE (TB2: S10509). Alignment gaps were treated as missing data and all characters were unordered and of equal weight. Phylogenetic analyses were performed with PAUP* 4.0b10 (Swofford 2002). A partition homogeneity test (Swofford 2002) was run to determine whether sequence data for *gpd* and Alt a 1 genes regions could be combined.

MP analysis, in which searches for most parsimonious trees was conducted with the heuristic search algorithm with tree-bisection-reconnection (TBR) branch swapping. For each search, 1000 replicates of random stepwise sequence addition were performed and 100 trees were saved per replicate. Optimal trees were identified using heuristic searches based on 1000 random addition replicates retaining clades compatible with the 50 % majority rule in the bootstrap consensus tree.

For ML analysis, MODELTEST v. 3.06 (Posada & Crandall 1998) was used to identify the model of DNA substitution that best fits. MODELTEST analyses using Akaike Information Criterion (AIC) selected the GTR + G + I model of nucleotide frequencies (A = 0.2336, C = 0.3332, G = 0.2204, and T = 0.2128) with the shape parameter of the gamma distributed ($a = 1.1627$) to accommodate rate variations among sites. Confidence values were estimated using bootstrap analysis (100 replicates), which were summarized as a 50 % majority rules consensus tree in PAUP.

The model of evolution in Bayesian analysis was also GTR + G + I estimated by MODELTEST v. 3.06. Posterior probabilities (PP) (Rannala & Yang 1996; Zhaxybayeva & Gogarten 2002) were determined by Markov Chain Monte Carlo sampling (MCMC) in MrBayes v. 3.1 (Ronquist & Huelsenbeck 2003). Four simultaneous Markov chains were run for 600 000 generations and trees were sampled every 100th generations (resulting 6001 total trees). Burn-in was set at 25 100 generations (i.e. 251 trees), well after the likelihood values converged to stationary, leaving 5750 trees from which the consensus trees and PP were calculated. Bayesian analyses were repeated five times for improved sampling of tree space and to guard against local optima in searches.

Results

Morphological and cultural studies

In culture on PCA under standard conditions the three unknown isolates were fast growing with yellow brown to dark brown,

Table 1 – Species and sequences database accession numbers used in this study.

Species name	Collection no.[a]	GenBank no.	
		gpd	Alt a 1
Alternaria alternata	EGS 34-016	AY278808	AY563301
Alternaria arborescens	EGS 39-128	AY278810	AY563303
Alternaria brassicae	BMP 0322	AY562414	AY563309
Alternaria brassicicola	EEB 2232	AY278813	AY563311
Alternaria cetera	EGS 41-072	AY562398	AY563278
Alternaria cinerariae	EGS 33-169	AY562413	AY563308
Alternaria ethzedia	EGS 37-143	AY278795	AY563284
Alternaria euphorbiicola	EGS 42-049	AY562417	AY563314
Alternaria japonica	ATCC 13618	AY278814	AY563312
Alternaria longipes	EGS 30-033	AY278811	AY563304
Alternaria macrospora	DDG Am1	AY278805	AY563294
Alternaria metachromatica	EGS 38-132	AY562404	AY563285
Alternaria mouchaccae	EGS 31-061	AY562399	AY563279
Alternaria petroselini	EGS 09-159	AY278799	AY563288
Alternaria photistica	EGS 35-172	AY562402	AY563282
Alternaria porri	ATCC 58175	AY278806	AY563296
Alternaria radicina	ATCC 96831	AY278797	AY563286
Alternaria solani	ATCC58177	AY278807	AY563299
Alternaria sonchi	EGS 46-051	AY562412	AY563307
Alternaria smyrniii	EGS 37-093	AY278801	AY563289
Sinomyces fusoideus 1	CBS 124114	**HM209081**	**HM209085**
Sinomyces fusoideus 2	HSAUP1986	**HM209082**	**HM209086**
Sinomyces obovoideus	CBS 123375	EU862547	EU862546
Sinomyces alternariae	BMP 0352	AY278815	AY563316
Crivellia papaveracea	CBS 427.50	**HM209083**	**HM209084**
Embellisia allii	EGS 38-073	AY278827	AY563322
Embellisia telluster	EGS 33-026	AY562419	AY563325
Nimbya caricis	EGS 13-094	AY278826	AY563321
Nimbya scirpicola	EGS 19-016	AY278825	AY563320
Stemphylium botryosum	ATCC 42170	AY278820	AY563274
Ulocladium atrum	ATCC 18040	AY278818	AY563318
Ulocladium botrytis	ATCC 18043	AY278817	AY563317
Ulocladium chartarum	ATCC 18044	AY278819	AY563319
Ulocladium consortiale	CBS 201-67	FJ266494	FJ266509
Ulocladium solani	CBS 123376	EU855805	EU855801
Ulocladium subcucurbitae	CBS 121491	EU855803	EU855807

Newly generated sequences in bold.

a ATCC, American Type Culture Collection, Manassa, VA, USA; BMP, B.M. Bryor, Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA; CBS, Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands; DGG, D.G. Gilchrist, Department of Plant Pathology, University of California, Davis, CA 95616, USA; EEB, E.E. Butler, Department of Plant Pathology, University of California, Davis, CA 95616, USA; EGS, E.G. Simmons, Mycological Services, Crawfordsville, IN 47933,USA.

cottony colonies that attained 35–45 mm diam in 7 d. Conidiophores typically arose from the tip cell of a hypha that was morphologically and functionally distinct from vegetative hyphae. A single conidium was produced from a pore at the tip of the conidiophore; occasionally the conidiogenous cell proliferated sympodially to form 1 or 2 uniperforate geniculations, each of which produced a single conidium. Conidia were dictyosporous, yellow brown to dark brown and obovoid to fusiform, tapering from a broad apex to a narrow base. Additionally, conidia did not produce 'false beaks' (i.e. secondary conidiophores arising from conidia still attached to the conidiogenous cell).

Phylogenetic analyses

The size of DNA fragments was of 449–451 bp for Alt a 1, and 472–508 bp for *gpd*. Alignment of the Alt a 1-*gpd* fragments resulted in a 966-character data set. Of these, 349 characters were parsimony informative, and 516 were constant. Results of the PHT between the two loci ($P = 0.113$) indicated the Alt a 1 and *gpd* data sets could be combined and analyzed. *Stemphylium botryosum* was used as outgroup based on results from previous studies (Pryor & Gilbertson 2000; Pryor & Bigelow 2003; Hong *et al.* 2005).

Parsimony analysis yielded six equally parsimonious trees of 1339 steps with a consistency index (CI) = 0.5063, retention index (RI) = 0.6824, rescaled consistency index (RC) = 0.3455, homoplasy index (HI) = 0.4937. The MP tree (Fig 1), which was obtained from the analysis of combined DNA sequences of gpd and Alt a 1, grouped *Ulocladium alternariae* and the two unknown strains clustered independently of each other in one clade with a high bootstrap support (100 %). Two strains isolated from *Tamarix* formed a branch with 100 % bootstrap

Fig 1 – Phylogenetic tree of *Sinomyces* and five similar genera of anamorphic *Pleosporaceae* generated from MP analysis based on combined data set of Alt a 1 and *gpd* sequences. Number in the front of '/' represents parsimony bootstrap values and number after the '/' represents ML bootstrap values. Bootstrap values <70 % are not shown. Thickened branches indicate Bayesian PP ≥95 %. The tree is rooted with *Stemphylium botryosum*.

support. The strain isolated from *Daucus* was joined to this branch with high bootstrap support (80 %). *Ulocladium alternariae* formed a strongly supported subclade in a sister relationship to the clade that included the *Tamarix* and *Daucus* strains. Based on MP phylogenetic analysis (Fig 1), and consistent with previous results (Pryor & Bigelow 2003; Hong *et al.* 2005), *Embellisia*, the *Alternaria infectoria* group and *Nimbya* formed a single, well-supported clade. The analysis revealed several well-supported terminal clades, including *Sinomyces*, but there was no internal support to show relationships among the clades. The topologies generated from ML and Bayesian analyses were essentially similar to that of the parsimony analysis. The ML and Bayesian trees were therefore not shown, but the bootstrap values of ML (≥70 %) and statistically-supported clades (≥95 %) are marked in the parsimony trees (Fig 1).

Taxonomy

Phylogenetic analyses (MP, ML and Bayesian) for the two gene regions (Alt a 1 and *gpd*) indicate that *Ulocladium alternariae* and the *Daucus* and *Tamarix* strains are distinct from any of the genera of the *Alternaria* group (Fig 1). This result is consistent with morphological observations.

Conidiophores of *U. alternariae* and the *Daucus* and *Tamarix* strains produce few, more or less widely spaced conidiogenous loci. As a result the conidia always appear to be solitary. This differs from typical *Ulocladium*, where conidia appear to be held in clusters because of the close spacing of the conidiogenous loci, which tend to repeatedly proliferate sympodially. Moreover, conidia of some typical *Ulocladium* species produce short conidiophores directly and when conidia arise from these secondary conidiophores, they are closely spaced and appear to be catenate. We have not observed this in *U. alternariae* or the *Daucus* and *Tamarix* strains. These fungi are similar to *Alternaria* because of their simple conidiophores and terminal conidiogenous loci (Simmons 1967). However, *Alternaria* is distinguished by its ovoid apically tapered, often catenate conidia. Conidia of *U. alternariae* and the *Daucus* and *Tamarix* strains are dictyosporous, which distinguishes them from *Crivellia*, *Embellisia* and *Nimbya* (Simmons 1971, 1989; Inderbitzin *et al.* 2006), which have phragmosporous conidia. Finally, *U. alternariae* and the *Daucus* and *Tamarix* strains differ from *Stemphylium* by the sympodial/geniculate proliferation of the conidiogenous cells; conidiogenous cells in *Stemphylium* proliferate percurrently.

The combined molecular/phylogenetic and morphological observations strongly indicate that *U. alternariae* does not belong in *Ulocladium* but that it cannot be accommodated in any of the genera that are close to *Ulocladium*. The results also show that the two unknown fungi that we isolated, respectively from *Daucus* and *Tamarix*, are closely related but distinct from each other but are closely related to *U. alternariae*. Thus we propose a new genus for them:

Sinomyces Yong Wang bis & X.G. Zhang, **gen. nov.**
MycoBank no.: 513490
Etym.: Sino (Latin) referring to the country of collection.
Typus: *Sinomyces fusoideus* Yong Wang bis & X.G. Zhang

Anamorphic Pleosporaceae. *Mycelium* ex hyphis, simplicia vel ramosa, septatae, subhyalinae, laeves. *Conidiophora* copiosa, recta vel acclivia, simplicia vel ramose, ex lateribus hypharum submersarum aeriarumque oriunda, sympodiala, septata, subhyalinae vel aureo-brunnea, simplicia, terminals vel raro semel vel bis crebre unus-terebro genicula, laevis. *Conidia* solitaria, obovoidea vel fusoidea, aureo-brunnea vel atro-brunnea, ad quin exhibitio reprobate rostrum. *Mycelium* subhyaline simple or branched, septate, smooth. *Conidiophores* abundant, subhyaline to pale brown, erect or ascending from submerged and aerial hyphae, simple or branched, sympodial, septate, smooth, simple with an apical pore or 1 or 2 uniperforate geniculations present at times, originating laterally or apically from attached, primary conidium. *Conidia* solitary, obovoid or fusoid, golden brown to dark brown, without producing a false beak.

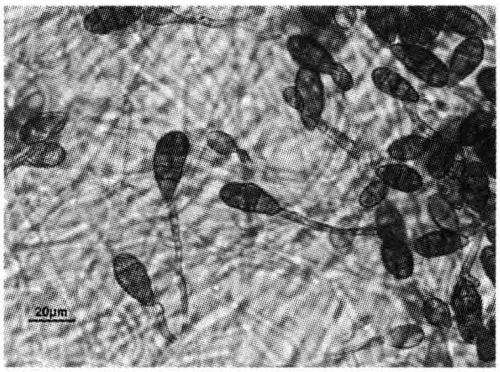

Fig 2 – *Sinomyces fusoideus* from the holotype. Conidiophores and conidia (40× magnification).

Sinomyces fusoideus Yong Wang bis & X.G. Zhang, **sp. nov.** (Figs 2 and 3)
MycoBank no.: 513491
Etym.: fusoideus (Latin) referring to the fusoid conidia of this fungus.

Coloniae in PCA, 35–40 diam in seven diebus ad 23 °C, auctus velosi, sporulatione abunda, conspicue concentrice zonata. *Hyphae* vegetativae septatae, ramosae, subhyalinae, 4–5 µm crassae, laeves. *Conidiophora* copiosa, recta vel acclivia, simplicia vel ramosa, ex lateribus hypharum praecipue submersarum aeriarumque oriunda, pallide-brennea, septata, 25–60 × 3.5–4 µm ($M = 43 \times 3.7$ µm, $n = 30$), terminals vel raro semel vel bis crebre unus-terebro genicula, laeves. *Conidia* 31–39 × 11–15 µm ($M = 36 \times 13$ µm, $n = 50$), solitaria, obclavata vel fusoidea, aureo-brunnea vel atro-brunneae, 3–6 transverse septata et 1–3 longiseptata, laeves vel dense pustulata, ad quin exhibitio reprobate rostrum.

Holotype: **China**: Xinjiang Province: Kashi, 40°12′30″N, 76°30′27″E, on diseased leaves of *Tamarix ramosissima*,

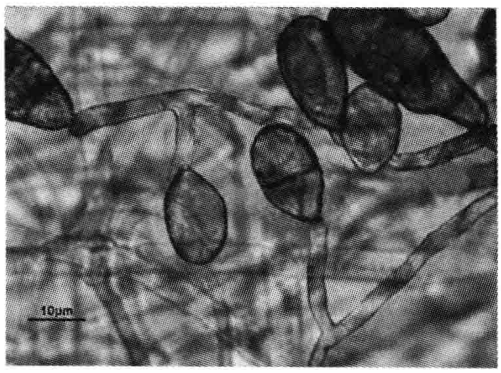

Fig 3 – *Sinomyces fusoideus* from the holotype. Sporulation apparatus (100× magnification).

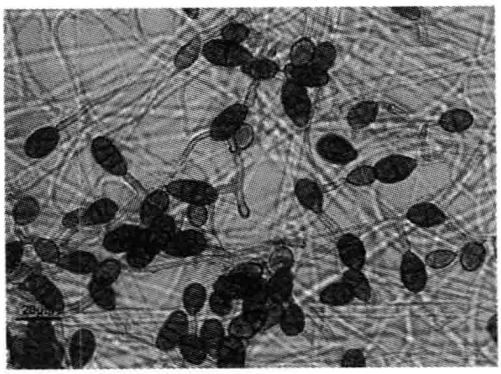

Fig 4 – *Sinomyces obovoideus* from the holotype. Conidiophores and conidia (40× magnification)

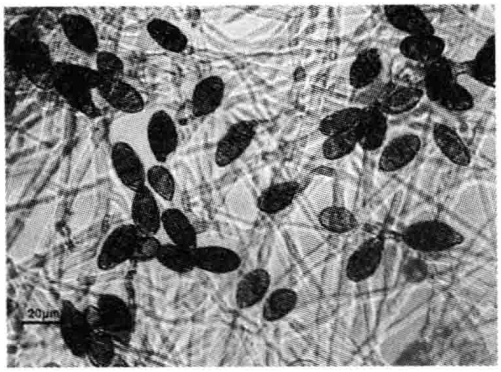

Fig 6 – *Sinomyces alternariae* from the living cultures of BMP 0352. Conidiophores and conidia (40× magnification).

Y. Wang, Jul. 2006, HSAUP2708 (dry agar culture), holotype designated herewith. Living ex type culture. CBS 124114 = HSAUP2708.

Colonies 35–40 mm diam in 7 d at 23 °C on PCA, yellow brown to dark brown, rapidly covering entire 9-cm-diam Petri dish. Concentric zonation of growth pronounced; sporulation abundant. *Mycelium* subhyaline, hyphae branched, smooth, septate, 4–5 μm wide. *Conidiophores* abundant, erect or ascending from submerged and aerial hyphae, simple or branched, dilute brown, septate, smooth, 25–60 × 3.5–4 μm ($M = 43 \times 3.7$ μm, $n = 30$), simple with an apical pore or occasionally 1 or 2 close, uniperforate geniculations. Conidia 31–39 × 11–15 μm ($M = 36 \times 13$ μm, $n = 50$), solitary, obclavate to fusoid, golden brown to dark brown, 3–6 transverse septa and 1–3 longitudinal septa, smooth to depressed pustulate, lacking a false beak (secondary conidiophores).

Additional specimens examined: on diseased leaves of *Tamarix ramosissima*. **China**: Xinjiang Province: Yili, 43°14′35″N, 85°21′43″E, Y. Wang, Sep. 2008 (HSAUP1986).

Sinomyces obovoideus Yong Wang bis & X.G. Zhang, **sp. nov.** (Figs 4 and 5)

MycoBank no.: 513492

Etym.: obovoideus (Latin) referring to the conidial shape.

Coloniae in PCA 40–45 diam in seven diebus temperatura 23 °C, auctus velosi, sporulatione abunda, conspicue concentrice zonata. *Hyphae* vegetativae septatae, ramosae, subhyalinae, 3.5–4 μm crassae, laeves. *Conidiophora* copiosa, recta vel acciivia, simplicia vel ramosa, ex lateribus hypharum praecipue submersarum aeriarumque oriunda, subhyalinae, septata, 20–50 × 3–3.5 μm ($M = 40 \times 3.2$ μm, $n = 30$), terminals vel raro 1–2 crebre unus-terebro genicula, laeves. *Conidia* 18–26 × 13–17 μm ($M = 22.5 \times 15$ μm, $n = 50$), solitaria, obovoidea vel ellipsoidea, atro-brunneae, 2–3 transverse septata et 2–3 longiseptata, laeves vel dense pustulata, ad quin exhibitio reprobate rostrum.

Holotype: **China**: Sichuan Province: Leshan, 29°21′36″N, 103°26′24″E, on diseased leaves of *Daucus carota*, Y. Wang, Jul. 2005, HSAUP1144 (dried culture), holotype

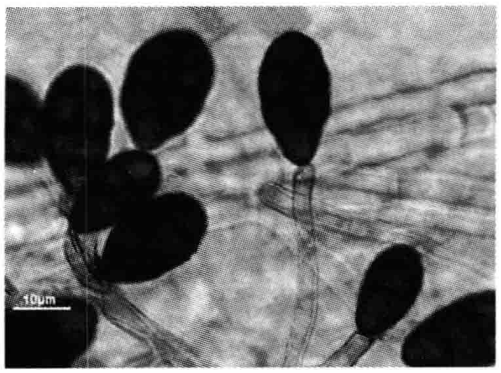

Fig 5 – *Sinomyces obovoideus* from the holotype. Sporulation apparatus (100× magnification).

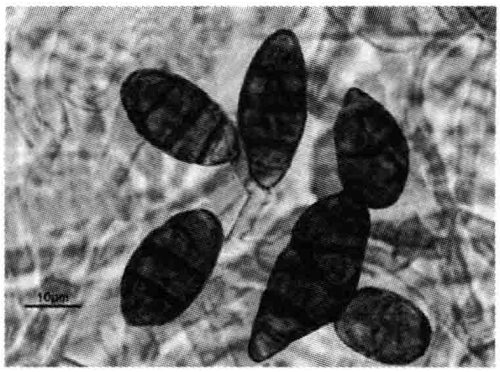

Fig 7 – *Sinomyces alternariae* from the living cultures of BMP 0352. Sporulation apparatus (100× magnification).