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Cover images: 1. Begonia holosericeoides (female flower and habit) (Begoniaceae; Ardi et al.); 2. Abaxial cuticles of Alseodaphne rhododendropsis (Lauraceae; Nishida & van der Werff); 3. Dipodium puspitae, Dipodium purpureum (Orchidaceae; O'Byrne); 4. Agalmyla exannulata, Cyrtandra coccinea var. celebica, Codonoboea kjellbergii (Gesneriaceae; Kartonegoro & Potter).

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CERCOSPORA BRUNFELSIICOLA (FUNGI, MYCOSPHAERELLACEAE), A NEW TROPICAL CERCOSPOROID FUNGUS ON BRUNFELSIA UNIFLORA

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ABSTRACT

HIDAYAT, I. & MEEBOON, J. 2014. *Cercospora brunfelsiicola* (fungi, Mycosphaerellaceae), a new tropical cercosporoid fungus on *Brunfelsia uniflora. Reinwardtia* 14(1): 211 – 217. — *Cercospora brunfelsiicola* on *Brunfelsia uniflora* is proposed as a new species based on a combination of molecular phylogenetic and morphological data analyses. The molecular phylogenetic analysis based on combined multilocus analyses of the Internal Transcribed Spacer (ITS), part of the elongation factor $1-\alpha$ gene (EF1- α), and part of the calmodulin (CAL) gene regions showed that *C. brunfelsiicola* is phylogenetically distinguishable from other *Cercospora* species, including members of the *C. apii s. l.* complex. Morphologically, *C. brunfelsiicola* differs from other closely related *Cercospora* species, in particular *C. acaciae-mangii*, by forming lesions with indistinct margin, larger stromata [(32) 48.5 ± 10.6 (68) µm diam.], and filiform to narrowly obclavate conidia [(45) 59 ± 9.1 (72) × (2.5) 2.5 ± 0.2 (3) µm].

Key words: Fungi, Hyphomycetes, leaf spot, phylogeny, taxonomy.

ABSTRAK

HIDAYAT, I. & MEEBOON, J. 2014. *Cercospora brunfelsiicola* (jamur, Mycosphaerellaceae), jenis jamur cercosporoid daerah tropis pada *Brunfelsia uniflora*. *Reinwardtia* 14(1): 211 – 217. — *Cercospora brunfelsiicola* Hidayat & Meeboon yang ditemukan pada bercak daun *Brunfelsia uniflora* diusulkan sebagai spesies baru berdasarkan kombinasi hasil analisis data morfologi dan analisis filogenetik sekuen DNA gabungan dari daerah *Internal Transcribed Spacer* (ITS), sebagian daerah gen *elongation factor* $1-\alpha$ gene (EF1- α) dan gen *calmodulin* (CAL). Hasil analisis menunjukkan bahwa *C. brunfelsiicola* secara filogenetik terpisah dari sekuen DNA *Cercospora* terdekat, termasuk anggota *C. apii s.l.* Secara morfologi, *C. brunfelsiicola* dapat dibedakan dari spesies *Cercospora* terdekat, khususnya *C. acaciae-mangii*, karena memiliki warna gejala pada daun kecoklatan dengan garis batas yang tidak jelas, stromata lebih besar [diameter (32) 48,5 ± 10,6 (68) µm] dan memiliki bentuk konidia *obclavate* [(45) 59 ± 9,1 (72) × (2,5) 2,5 ± 0,2 (3) m].

Kata kunci: Bercak daun, filogeni, Hifomisetes, jamur, taksonomi.

INTRODUCTION

Cercospora Fresen. is an anamorph-typified ascomycete genus, now considered and used as holomorph genus covering species only forming Cercospora-like asexual morphs as well as species with such asexual and Mycosphaerella-like sexual morphs (Braun et al., 2013). More than 3000 names have been described worldwide (Crous et al., 2000; Crous & Braun, 2003) see also http:// www.mycobank.com/MycoTaxo.aspx]. Members of this genus are commonly found as saprobes, secondary invaders and plant pathogens causing leaf spot or leaf blight (Crous & Braun, 2003). The morphological characteristics of pigmented conidiophores, thickened conspicuously and darkened conidiogenous loci (scars) and conidial

hila and scolecosporous, mostly acicular, pluriseptate, hyaline conidia, are typical for the genus *Cercospora* (Crous & Braun, 2003). Recent studies of cercosporoid fungi from Thailand have revealed several new species and new records of *Cercospora* on wild plants and economically important cultivated plants (Meeboon *et al.*, 2007a, b, c; Nakashima *et al.*, 2010; To–anun *et al.*, 2009, 2011; Phengsintham *et al.*, 2012, 2013).

During the study of diversity of *Cercospora* and allied genera in Thailand (2008–2010), we found *Cercospora* leaf spot on an ornamental plant identified as *Brunfelsia uniflora* [syn. *B. hopeana*] at Royal Flora Garden, Chiang Mai. This plant belongs to family Solanaceae, originally from South America and now widely cultivated as ornamental plant. *Brunfelsia uniflora* is also recognized as

medicinal plants for diuretic, antirheumatic and anti –inflammatory (Plowman, 1977). In this report, *Cercospora* specimen on *B. uniflora* from Thailand is proposed as a new species based on a combination of morphology and molecular phylogenetic analyses involving ITS rDNA, part of the elongation factor $1-\alpha$ (EF1- α) gene and part of the calmodulin (CAL) gene region.

MATERIALS AND METHODS

Collection and Observation

Specimens of *Cercospora* leaf spot on *B. uniflora* were collected from Royal Flora, Chiang Mai Province, Thailand. Magnifying lenses of $10 \times$ and $20 \times$ magnifications were used during the

observation of symptoms in the field. Specimens showing the presence of *Cercospora* caespituli were placed in plastic bags for further examination. The collecting bags were sealed and labeled as follows: name of host plant, collection site, collector/s and collection date.

Macroscopic characteristics were observed using a stereo microscope (Olympus SZX7) to check the fungal caespituli on the leaf spots in detail. The examination of microscopic characters was carried out by means of an Olympus BX53 light microscope using oil immersion (1000×). Specimens for observation were prepared by hand sectioning. Water and Shear's solution were used as mounting media. Thirty conidia. hila. conidiophores, conidiogenous loci and 10 stromata



Fig. 1. Phylogenetic tree based on combination of ITS, partial EF1– α , and CAL genes region representing placement of members of *C. brunfelsiicola* within *Cercospora s.str*. Bootstrap support \ge 50% from Maximum Parsimony analysis are shown on the nodes.

were measured for each specimen. Line drawings were prepared at a magnification of $400 \times$ or $1000 \times$. Single spore isolation was carried out following the method outlined by Choi *et al.* (1999) with a modification. Dried herbarium specimens were deposited in the BIOTEC Herbarium (BBH), Thailand. Cultures were deposited at BIOTEC culture collection (BCC), Thailand and LIPI microbial culture collection (LIPIMC), Indonesia.

DNA Extraction, Polymerase Chain Reaction (PCR), and Sequencing

A culture of *Cercospora* isolated from *B. uniflora* was grown on potato dextrose broth (PDB, Difco) and incubated on waterbath shaker (100 rpm) (Taitec Personal–11) for 10 days at 28°C prior to DNA extraction. Fungal mycelia were harvested in a 1.5 ml tube with 500 μ l miliQ water. Mycelial cell–walls were homogenized mechanically using

Table 1. GenBank	accession num	ber of cerc	osporoid fung	i used in	this study.

No.	Species	Strain Code	GenBank Accession Number		
			ITS	EF	CAL
1	Cercospora brunfelsiicola	RF5	AB859638	AB863025	AB863026
2	Cercospora acaciae-mangii	CPC 10526T	AY752141	AY752176	AY752235
3	Cercospora acaciae-mangii	CPC 10550	AY752139	AY752172	AY752231
4	Cercospora senecionis-walkeri	CBS 132636	JX143649	JX143408	JX142916
5	Cercospora apii	CBS 116455	AY840519	AY840486	AY840417
6	Cercospora apiicola	CBS 116457	AY840536	AY840503	AY840434
7	Cercospora armoraciae	MUCC 768	JX143554	JX143308	JX142816
8	Cercospora apii	CBS 152.52	AY840515	AY840482	AY840413
9	Cercospora apiicola	CPC 10248	AY840539	AY840506	AY840437
10	Cercospora beticola	CBS 116456	AY840527	AY840494	AY840425
11	Cercospora cf. flagellaris	CBS 132674	JX143606	JX143364	JX142872
12	Cercospora capsici	MUCC 574	JX143569	JX143325	JX142833
13	Cercospora chenopodii	CBS 132620	JX143571	JX143327	JX142835
14	Cercospora cf. citrulina	MUCC 588	JX143582	JX143340	JX142848
15	Cercospora tezpurensis	CS 2012T	KC351743	KC513746	KC513745
16	Cercospora zeae-maydis	CBS 117758	DQ185075	DQ185087	DQ185111
17	Cercospora zeina	CPC 11998	DQ185082	DQ185094	DQ185118
18	Cercospora beticola	CPC 5123	DQ233327	DQ185094	DQ233405
19	Cercospora cf. helianthicola	MUCC 716	JX143615	JX143374	JX142882
20	Cercospora cf. ipomoeae	MUCC 442	JX143618	JX143377	JX142885
21	Cercospora kikuchii	CBS 135.28	DQ835071	DQ835089	DQ835135
22	Cercospora lactucae-sativae	MUCC 570	JX143623	JX143382	JX142890
23	Cercospora cf. nicotianae	CBS 132632	JX143631	JX143390	JX142898
24	Cercospora punctiformis	CBS 132626	JX143638	JX143397	JX142905
25	Cercospora cf. richardiicola	MUCC 138	JX143643	JX143402	JX142910
26	Cercospora rodmanii	15-GTOX	GQ884185	GQ884191	GQ884195
27	Cercospora sojina	CPC 17977	JX143674	JX143434	JX142942
28	Cercospora zeae-maydis	CBS 117757	DQ185074	DQ185086	DQ185110
29	Cercospora zebrina	CBS 118790	GU214657	KF253248	KF253963
30	Cercospora zeina	CPC 11995T	DQ185081	DQ185093	DQ185117
31	Cercospora cf. zinniae	CBS 132676	JX143757	JX143519	JX143027
32	Pseudocercospora thailandica	CPC 10621	AY752159	AY752189	AY752251
33	Pseudocercospora thailandica	CPC 10547	AY752156	DQ835102	AY752248

plastic pestle. The mycelia were then centrifuged using a Centrifuge MiniSpin (Eppendorf, Germany) at 14.500 rpm for 10 minutes. DNA was extracted from the mycelia with a PHYTOPURETM DNA extraction kit (GE Healthcare, UK) according to the manufacturer's instruction. DNA amplification was performed by polymerase chain reaction (PCR) of using primer pairs ITS5 (5' -GGAAGTAAAAGTCGTAACAAGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') for ITS (Internal Transcribed Spacer) region (White et 1990). EF1-728F al., (5' -CATCGAGAAGTTCGAGAAGG-3') and EF1-986R (5'-TACTTGAAGGAACCCTTACC-3') for part of Elongation Factor $1-\alpha$ region, and CAL-228F (5'-GAGTTCAAGGAGGCCTTCTCCC-3') (5'-CAL-737R and CATCTTTCTGGCCATCATGG-3') for Calmodulin region (Carbone & Kohn, 1999). For the ITS region, PCR was performed in a 25 ml volume as follows: nuclease free water 10 µl, Go Taq® Green Mastermix (Promega, Madison, USA) 12.5 µl, ITS5 dan ITS4 primer 0.5 µl for each primer, DMSO 0.5 µl, and DNA template 1 µl. The PCR reaction was done using TaKaRa thermocycler (TaKaRa, Japan) as follows: initial denaturation at 95°C for 90 s, followed by 35 cycles of 95°C for 30 s, 55°C for 30 s, 72°C for 90 s, and final extension of 72°C for 5 min. PCR reactions for EF and CAL genes were performed in 25 mL reaction volumes as follow: each reaction containing nuclease free water 8.75 µl, Go Taq® Green Mastermix (Promega, Madison, USA) 12.5 µl, forward and reverse primer 0.625 µl for each primer, DMSO 0.5 µl, and DNA template 2 µl. PCR was performed in a TaKaRa thermocycler (TaKaRa, Japan) with the following program: 94°C for 5 min, 35 cycles {94°C for 30 s, 52°C for 30 s, 72°C for 30 s} and followed by a final extension of 7 min at 72°C (Groenewald et al., 2005). PCR results were visualized using electrophoresis method in a 1% agarose gel at 100 V for 30 min. Agarose gel was soaked in an ethidium bromide for 60 mins and visualized under UV light (Printgraph). PCR products were sent to 1stBase (Malaysia) for DNA sequencing.

Phylogenetic Analysis

Nucleotide sequences obtained from the respective primer pairs (ITS5 and ITS4, EF1–728F and EF1–986R, CAL–228F and CAL–737R) were examined and refined by direct examination using Chromas Pro 1.41 software (Technelysium Pty Ltd., Australia). Sequences generated from the respective ITS, EF, and CAL regions were aligned with sequences retrieved from DNA databases (DDBJ, NCBI) using MUSCLE (Edgar, 2004) implemented

in MEGA 6 (Tamura *et al.*, 2013). *Pseudocercospora thailandica* strain CPC 10621 and *P. thailandica* strain CPC 10547 were used as outgroups in the analysis. Regions designated as ambiguously aligned were excluded from the analyses. GeneBank accession number, strain code, and taxon names used in this study are given in Table 1.

The phylogenetic analysis was conducted using the maximum parsimony (MP) method in PAUP* 4.0b10 (Swofford, 2002). The MP analysis was performed with the heuristic search option using the 'tree-bisection-reconstruction' (TBR) algorithm with 1000 random sequence additions to find the optimum tree. The stepwise addition option set as random and maximum tree number was set at 5000. Tree length (TL), consistency index (CI), retention index (RI), related consistency index (RC), and homoplasy index (HI) were also calculated. The Kishino-Hasegawa (KH) likelihood test (Kishino & Hasegawa, 1989) was carried out to compare the best tree topology obtained by the nucleotide sequence data with a constrained tree. The strength of the internal branches of the phylogenetic tree in MP analysis was tested with bootstrap (BS) analysis (Felsenstein, 1985) using 1000 replications. BS values of 50 % or higher are shown. Random sequence addition was used in the bootstrap analysis. All sites were treated as unordered and unweighted, and gaps treated as missing data. TreeGraph 2 (Stöver & Müller, 2010) was used to refine the phylogenetic tree. The partition homogeneity test (Farris et al., 1995) was carried out by using PAUP* to determine whether ITS, EF1 $-\alpha$, and CAL datasets were in conflict with 1000 replicates.

RESULTS

Phylogenetic Analysis

The alignment of the combined sequences from ITS, EF and CAL regions contained 33 sequences and 1120 total characters, of which 835 characters were constant, 40 characters were variable and parsimony-uninformative, 245 characters were parsimony-informative. The most parsimonius tree was generated in 515 steps (CI = 0.695, RI = 0.791, RC = 0.550, HI = 0.305). The phylogenetic tree generated from MP analysis showed that C. brunfelsiicola is phylogenetically distinguishable from other Cercospora sequences (Fig. 1). Sequences of C. brunfelsiicola formed an independent lineage and showed a close relationship to sequences of C. acaciae-mangii Crous, Pongpan. & M. J. Wingf. on Acacia mangium Willd. (Leguminosae) with 62% BS (bootstrap support). This clade is sister to a clade containing sequences of *C. tezpurensis* M. K. Meghvansi & Md. Haneef Khan on *Capsicum assamicum* Purkayastha & Singh, *C. rodmanii* on *Eichhornia crassipes* (Mart.) Solms, and *C.* cf. *richardiicola* on *Fuchsia×hybrida* with 94% BS.

Taxonomy

Cercospora brunfelsiicola Hidayat & Meeboon, *spec. nov.* – Fig. 2.

MYCOBANK MB805994

Cercospora brunfelsiicola differs from *C. acaciaemangii* and other closely related *Cercospora* species by forming lesions with indistinct margin, larger stromata [(32) 48.5 ± 10.6 (68) µm diam.], and filiform to narrowly obclavate conidia [(45) 59 ± 9.1 (72) × (2.5) 2.5 ± 0.2 (3) µm]. — Type: Thailand, Chiang Mai Province, Royal Flora Garden, on leaves of *Brunfelsia uniflora* (Pohl) D. Don [= *B. hopeana* (Hook.) Benth.] (Solanaceae), 27 July 2008, Jamjan Meeboon, RF5 (BBH 23764: Holotype). Ex-type culture: BCC32756, other culture: LIPIMC 774. GenBank accession number (ITS: AB859638, EF: AB863025, CAL: AB863026).

Leaf spots amphigenous, distinct, circular to angular, 2–7 mm diam. brown, sometimes forming larger lesions. margin indistinct. Caespituli mainly epiphyllous, dark or blackish, punctiform, scattered within the lesions. Stromata (32) 48.5 ± 10.6 (68) µm diam. (n = 10), intraepidermal, well-developed, composed of globular to angular, brown to blackish brown cells. Conidiophores numerous, in dense fascicles arising from stromata, (34) 98.5 ± 28.8 (151) × (2.5) 4 \pm 0.6 (5.5) µm (n = 30), rarely branched, subcylindrical, strongly geniculate, 2-5-septate, simple, straight, erect to decumbent, smooth, pale



Fig. 2. Cercospora brunfelsiicola sp. nov. (from holotype) a. Conidia. b. Stromata and conidiophores. (Scale bar = 50μm).

yellow to pale brown. Conidiogenous cells integrated, terminal, (10) 21.5 ± 8.2 (47.2) × (2.5) 4.1 ± 1.1 (4.8) µm long (n = 30), holoblastic, polyblastic. monoblastic to sympodially proliferating. Conidiogenous loci 2.5-3 µm diam. (n = 30), conspicuous, thickened and darkened. *Conidia* (45) 59 ± 9.1 (72) × (2.5) 2.5 ± 0.2 (3) µm (n = 30), solitary, filiform to narrowly obclavate, 4 straight, hyaline, smooth, -8-septate. base obconically truncate, with subacute apex, hila 2-2.5 μ m diam. (n = 30), thickened and darkened.

Distribution. Only known from its type locality.

Etymology. The new species is named after its host generic name.

DISCUSSION

The current study is the first report of Cercospora found on B. uniflora. About 12 species of Cercospora have been recognized on hosts of the plant family Solanaceae, viz, C. canescens Ellis & G. Martin (C. apii s. l.), C. lanugiflori Chupp & A.S. Mull. [on Solanum velutinum Dunal (= S. lanugiflorum Pittier)], C. nigri Tharp var. microsporae L. N. Bhardwaj & Y. S. Paul (on S. nigrum L.), C. nicandrae Chupp [on Nicandra physalodes (L.) Gaertn.)], C. nicotianicola J. M. Yen (on Nicotiana tabacum L.), C. physalidis Ellis (C. apii s. lat.), C. physalidis-angulatae J.M. Yen (on Physalis angulata L.), C. puyana Syd. (on S. trachycyphum Bitter), C. sciadophila (Speg.) Chupp (on S. violifolium Schott. ex Spreng), C. solanacea Sacc. & Berl. (on Solanum spp.), C. solani Thüm. (on Solanum spp.), and C. Solaninigri Chidd. (on S. nigrum) [Chupp, 1954; Crous & Braun, 2003]. Cercospora venezuelae var. indica Govindu & Thirum. and C. solanigena Bhartiya, R. Dubey & S. K. Singh are noted as uncertain species by Crous & Braun (2003) as type material could not be traced and due to the assumption that the original description was based on young conidia, respectively. Based on the morphological examination, C. brunfelsiicola is distinguishable from other Cercospora species found on hosts of the plant family Solanaceae by having strongly geniculate, densely fasciculate conidiophores and filiform to narrowly obclavate conidia with a few septa (Fig. 2). Cercospora brunfelsiicola differs from the plurivorous C. apii s. l. on Solanaceae (C. canescens, C. physalidis) by well-developed stromata, having numerous conidiophores in dense fascicles and strongly geniculate conidiophores. The filiform to narrowly

obclavate conidia of *C. brunfelsiicola* (Fig. 2) are apparently distinct from the long acicular conidia of *C. apii s.l.*

The molecular phylogenetic analyses based on combined sequence of ITS, EF1- α and CAL gene regions apparently showed that C. brunfelsiicola has a close phylogenetic relationship to C. acaciae -mangii (Groenewald et al., 2013). Cercospora brunfelsiicola is distinguishable from C. acaciaemangii on A. mangium, which was originally described from Thailand as well (Crous et al., 2004), by having lesions with indistinct margin, larger stromata [(32) 48.5 ± 10.6 (68) µm diam.] and filiform to narrowly obclavate conidia [(45) 59 \pm 9.1 (72) × (2.5) 2.5 ± 0.2 (3) μ m]. Cercospora acaciae-mangii was morphologically described by Crous et al. (2004) based on distinct symptom (lesions medium brown, surrounded by a raised, dark brown border), stromata lacking to welldeveloped (up to 30 µm diam.) and conidia acicular (50–350 \times 3.5–5 µm). In conclusion, our morphological data showed that the lesions with indistinct margin, densely fasciculate, strongly geniculate conidiophores and filiform to narrowly obclavate conidia are distinct characters that distinguish C. brunfelsiicola from other closely related Cercospora species and justify the introduction of a new species for this fungus.

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