

# ***Colletotrichum* spp. and other fungi associated with anthracnose on *Coffea arabica* L. in Mérida State, Venezuela**

Sari Ramon Mohali Castillo<sup>1,2</sup>, Stephan Miller<sup>2</sup>, Jane Stewart<sup>2</sup>

<sup>1</sup>Centro de Estudios Forestales y Ambientales de Postgrado (CEFAP), Laboratorio de Fitopatología, Facultad de Ciencias Forestales y Ambientales, Universidad de Los Andes, Mérida 5101-A, Venezuela. <sup>2</sup>Department of Agricultural Biology, Colorado State University, Ft. Collins, Colorado, 80523, USA

Corresponding author: Sari Ramon Mohali Castillo (sarirmohali@gmail.com)

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## **ABSTRACT**

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In tropical and subtropical regions worldwide, diseases can be major limiting factors to coffee (*Coffea arabica*) production, a highly valued crop internationally. Our aim was to identify *Colletotrichum* spp. and other fungal species associated with Coffee Berry Disease (CBD) and anthracnose on coffee twigs, which can greatly inhibit crop production. Concatenated phylogenetic analyses of ApMat and GS loci were used to identify two *Colletotrichum* species. *Colletotrichum siamense* was isolated from symptomatic mature and green berries that were both infested and uninfected with Coffee Berry Borer (CBB) and from twigs displaying anthracnose symptoms. *Colletotrichum alienum* was isolated from twigs showing anthracnose symptoms. Along with these two *Colletotrichum*

species, association of *Fusarium incarnatum* (= *Fusarium semitectum*) and *Fusarium solani* was found. Identification of *Fusarium* species was obtained through combined datasets of partial TEF1 and RPB2. *Fusarium* isolates came from ripe coffee fruits displaying symptoms of CBD, infested or not with CBB, and coffee twigs. In addition, concatenation of four gene regions (ITS, TEF1, CAL, TUB2) allowed the identification of another fungus, together with isolates from coffee twigs with anthracnose, *Diaporthe pseudomangiferae*. This is the first report of *Colletotrichum siamense* and *Colletotrichum alienum*, along with the fungi *Fusarium solani* and *Diaporthe pseudomangiferae*, associated with berry diseases on *Coffea arabica* in the state of Mérida, Venezuela.

**Keywords:** Coffee Berry Disease, *Diaporthe pseudomangiferae*, *Fusarium incarnatum*, *Fusarium solani*

## **RESUMEN**

Mohali-Castillo, S.R.; Miller, S.; Stewart, J. *Colletotrichum* spp., y otros hongos asociados con la antracnosis en *Coffea arabica* L. en el estado Mérida, Venezuela. *Summa Phytopathologica*, v.48, n.3, p.99-111, 2022.

En las regiones tropicales y subtropicales de todo el mundo, las enfermedades pueden ser factores limitantes importantes para la producción de café (*Coffea arabica*), un cultivo muy valorado a nivel internacional. Nuestro objetivo era identificar *Colletotrichum* spp., y otras especies de hongos asociadas con la enfermedad de las Bayas o Cerezas del café (CBD) y de la antracnosis en las ramitas de café, que pueden inhibir en gran medida la producción de cultivos. Se utilizaron análisis filogenéticos, concatenando los locus ApMat y GS para identificar dos especies de *Colletotrichum*. Se aisló *Colletotrichum siamense* desde bayas verdes y maduras sintomáticas que estaban infestadas y no por Broca del fruto del cafeto (CBB) y desde ramitas que presentaban síntomas de antracnosis. *Colletotrichum alienum* se aisló de ramitas que mostraban síntomas

de antracnosis. Junto con estas dos especies de *Colletotrichum*, se encontraron asociados *Fusarium incarnatum* (= *Fusarium semitectum*) y *Fusarium solani*. La identificación de la especie *Fusarium* se realizaron utilizando conjuntos de datos combinados del parcial TEF1 y RPB2. Los aislamientos de *Fusarium* provinieron de frutos de café maduros que mostraban síntomas de CBD, infestados o no con CBB y ramitas de café. Asimismo, mediante la concatenación de cuatro regiones genéticas (ITS, TEF1, CAL, TUB2) se identificó otro hongo junto con aislamientos de ramitas de café con antracnosis, *Diaporthe pseudomangiferae*. Este es el primer reporte de *Colletotrichum siamense* y *Colletotrichum alienum*, junto con los hongos *Fusarium solani* y *Diaporthe pseudomangiferae*, asociados con enfermedades de las bayas en *Coffea arabica* en el estado de Mérida, Venezuela.

**Palabras Claves:** Enfermedad de las Bayas o Cerezas del Café, *Diaporthe pseudomangiferae*, *Fusarium incarnatum*, *Fusarium solani*.

## **RESUMO**

Mohali-Castillo, S.R.; Miller, S.; Stewart, J. *Colletotrichum* spp. e outros fungos associados à antracnose em *Coffea arabica* L. no estado de Mérida, Venezuela. *Summa Phytopathologica*, v.48, n.3, p.99-111, 2022.

Nas regiões tropicais e subtropicais do mundo todo, as enfermidades podem ser fatores limitantes importantes para a produção do café (*Coffea arabica*), que possui grande valor no mercado internacional. O objetivo do presente trabalho foi identificar as espécies de *Colletotrichum* spp. e de outros fungos associados a queda dos frutos do café (QFC) e a antracnose dos ramos que podem reduzir a produtividade. Foram utilizados análises filogenéticas, de locos ApMat e GS. Foi identificado *Colletotrichum siamense* nos frutos verdes e maduros sintomáticos infestados ou não pela broca do café (BFC) como também nos ramos com sintomas de antracnose

onde se isolou *Colletotrichum alienum*. Associados a outras espécies de *Colletotrichum*, foi isolado do fungo *Fusarium incarnatum* (= *Fusarium semitectum* e *Fusarium solani*), identificados com a combinação TEF e RPB2. Mediante a amplificação de regiões genéticas (ITS, TEF1, CAL, TUB2), foi possível identificar outro fungo nos ramos com antracnose: *Diaporthe pseudomangiferae*. Este é o primeiro relato da ocorrência de *Colletotrichum siamense* e *Colletotrichum alienum*, junto com os fungos *Fusarium solani* e *Diaporthe pseudomangiferae*, associados com os frutos de *Coffea arabica* no estado de Mérida, Venezuela.

**Palavras Chaves:** Quadra dos frutos de café, *Diaporthe pseudomangiferae*, *Fusarium incarnatum*, *Fusarium solani*.

*Coffea arabica* L. is considered one of the most important crops worldwide, contributing significantly to the economy of different countries. The largest global producers of green *Coffea arabica* include Brazil, Colombia, Ethiopia and Honduras; meanwhile, in Venezuela, *Coffea arabica* production has faced a steady decline since 2007 (18). Biotic agents, particularly fungal agents, are known as major limiting factors to coffee production. Increased fungal pressure can greatly impact food security in certain countries, especially those where coffee is a major income source for small-scale growers concerning purchase of food and supplies for grain cultivation (1).

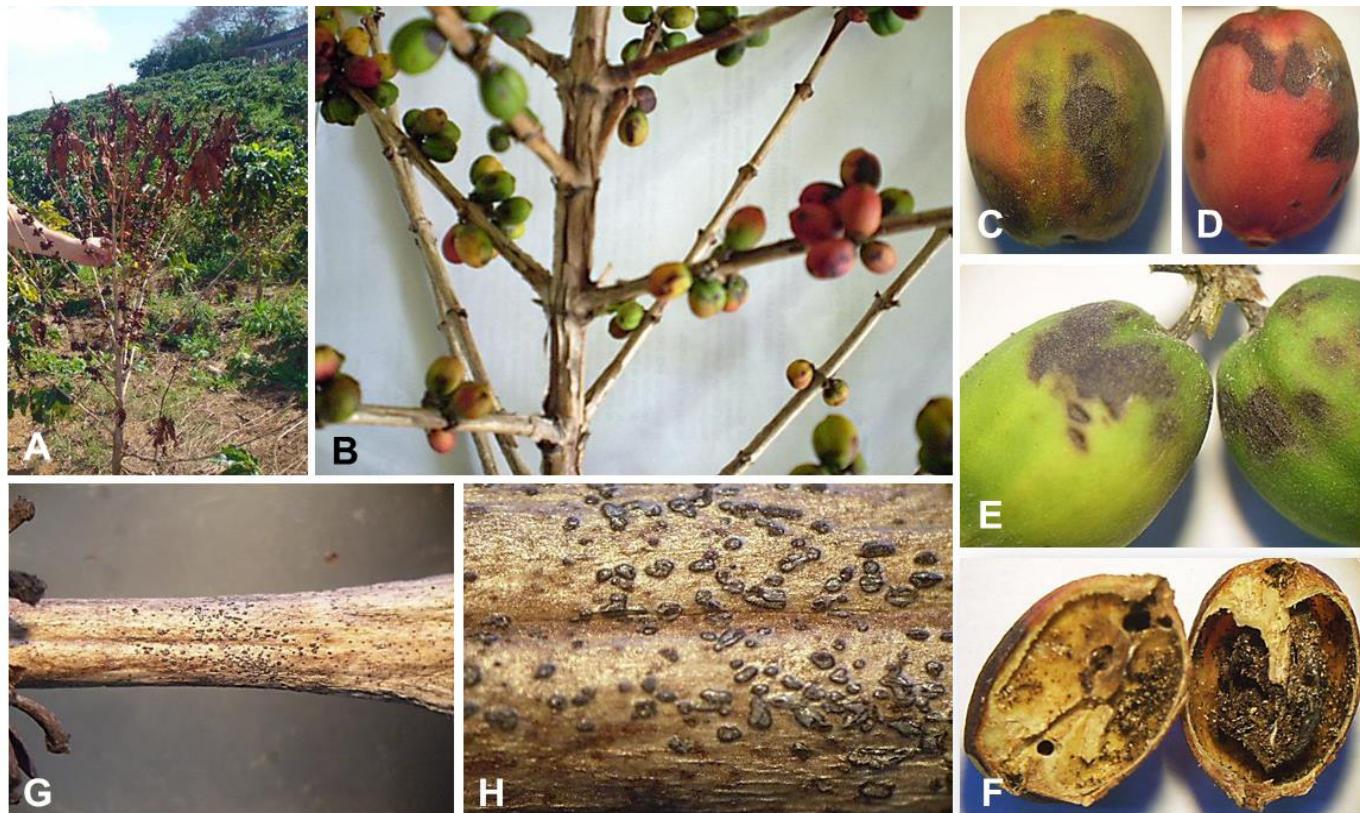
Pathogens of the genus *Colletotrichum* are responsible for anthracnose diseases on several economically important crops, and *Colletotrichum gloeosporioides* Penz. is the predominant pathogen in tropical and subtropical regions (5, 8, 35, 42, 53). *Colletotrichum* species have been reported on coffee as endophytes, epiphytes or pathogens (42) capable of causing leaf necrosis, coffee berry diseases and dieback (35).

*Colletotrichum kahawae* subsp. *kahawae* has been reported in multiple African countries, including Kenya, Angola, Cameroon and Malawi (54), causing Coffee Berry Disease (CBD), damaging green berries and inducing premature fruit drop and/or fruit mummification (37). This disease reduces yields by as much as 70-80% (14).

Even though *C. kahawae* is most virulent, sixteen *Colletotrichum* species have been identified on *Coffea arabica*, and six of them are presently reported in Vietnam and Mexico (5, 35). There are reports of *Colletotrichum asianum* Prihastuti, L. Cai & K.D. Hyde, *C. fructicola* Prihastuti, L. Cai & K.D. Hyde, *C. siamense* Prihastuti, L. Cai & K.D. Hyde, and *C. cordylinicola* Phoulivong, L. Cai & K.D. Hyde

causing diseases on green and red berries in Laos and Thailand (41, 42); *Colletotrichum acutatum* Simmonds also causes minor disease on ripening berries (31). In Mexico, at least six *Colletotrichum* species were identified causing anthracnose on fruits and leaves of *C. arabica*, including *C. gloeosporioides*, *C. siamense*, *C. gigasporum* E.F. Rakotoniriana & F. Munauton, *C. theobromicola* Delacr., *C. karstii* Y.L. Yang, Zuo Y. Liu, K.D. Hyde & L. Cai and one *Colletotrichum* sp. (5). In Costa Rica, *Colletotrichum costaricense* Damm, P.F. Cannon & Crous was isolated as pathogenic/endophytic on berries of *C. arabica* (6, 19). In Brazil, *Colletotrichum boninense* Moriwaki, Toy, Sato & Tsukib., and *C. gloeosporioides* have been reported on *C. arabica* and *Coffea canephora* L. trees, producing dieback and necrosis on leaves and berries (9). Furthermore, *Colletotrichum coffeatum* Noak & Pflanzenk. and *C. gloeosporioides* have also been reported as endophytic on healthy leaves of *C. arabica* in Brazil (36). In Colombia, *Colletotrichum gigasporum* was reported as an endophytic fungus on *C. arabica* (43).

For Venezuelan coffee production, there is little information about the involved diseases. In 1984 and 1985, *C. arabica* fields were surveyed in Lara and Portuguesa States, Venezuela, to determine the causal agent of leaf and branch anthracnose, fruit diseases and tree dieback. *Colletotrichum gloeosporioides* was identified, at altitudes between 700 and 1300 m, as the causal agent of anthracnose (29, 30). *Colletotrichum capsici* (Syd.) E. J. Butler & Bisby and a species similar to *C. gossypii* Southworth were reported as the causal agents of basal rot on coffee plants in Trujillo State (51). The aim of the present study was to characterize *Colletotrichum* species and fungal species associated with anthracnose and CBD in Venezuela using both morphological and genetic species identifications.



**Figure 1.** Coffee plant with anthracnose symptom. (A) Dead coffee plant due to anthracnose; (B) Berries with anthracnose symptoms or coffee berry disease (CBD); (C, D) CBD on ripe berries; (E) CBD on unripe or green berries; (F) Coffee berry borer (CBB); (G, H) Black acervuli on coffee twig with anthracnose.

## MATERIALS AND METHODS

**Isolation of fungal species from infected coffee berries and twigs**  
Samples were collected in two parishes from Antonio Pinto Salina Municipality ( $8^{\circ}24'33.12''$  N,  $71^{\circ}39'5.4''$  W), Mesa de Las Palmas parish and Agropecuaria Las Canales farm, Santa Cruz de Mora parish, both belonging to Mérida State, Venezuela. Fungi were isolated from green and mature fruits symptomatic of CBD, infested or not with CBB, and from twigs with anthracnose (Figure 1). Samples were transferred to the Phytopathology Laboratory of the School of Forestry Engineering, University of Los Andes (ULA), Mérida State, Venezuela. Fungi were isolated from anthracnose lesions on infected berries and twigs by excising  $5 \times 5$  mm margins of infected tissue. The tissues were then dipped in 1% sodium hypochlorite for 1 minute, immersed in 70% ethanol for 1 minute, rinsed three times with sterile water and finally dried in sterile tissue paper. Samples were placed on water-agar and incubated at room temperature, 25–28°C. The growing edges of any fungal hyphae, developing from the tissues, were then transferred aseptically to potato dextrose agar (PDA; 20 g potato dextrose agar in 1L distilled water; Difco Laboratories, Detroit, MI). Fungi were identified following sporulation. Single spore subcultures were obtained according to the procedure described by Choi et al. (4). After overnight room temperature incubation, single germinated spores were picked up with a sterile needle, transferred to PDA and incubated at 25°C for 7 days or until mycelia were observed growing from the samples. Fungal mycelium was sub-cultured onto PDA and hyphal tipping methods were performed to obtain pure cultures.

### Morphological analyses

Mycelial plugs (5-mm diameter) were taken from the periphery of actively growing cultures and transferred to 9-cm Petri dishes containing PDA and malt extract agar (MEA, Difco Laboratories, Detroit, MI, USA). Following incubation at room temperature (25°C) for 7 days, colony characteristics and pigment production were noted; colony diameters were measured after 7-to-10-day growth. Colony coloration was rated according to Rayner (45). Cultures were examined periodically for ascoma development. Conidia produced on PDA and MEA were mounted in lactophenol to obtain dimensions and perform morphological analyses. If a fungus was not sporulating on PDA and MEA, morphological characteristics were described from synthetic nutrient-poor agar (SNA). Hyphal appressoria were observed on colonies grown on PDA. At least 50 measurements per structure were taken at  $\times 1000$  magnification under a compound light microscope (Nikon Eclipse Ci).

### DNA extraction, amplification and sequencing

DNA was extracted from 7-day-old axenic cultures, grown on half-strength potato dextrose agar medium (1/2 PDA: 10 g potato dextrose agar in 1L distilled water; Difco Laboratories, Detroit, MI) added of 0.1 g streptomycin sulphate (Sigma-Aldrich, USA). Cultures were grown on sterile MF-Millipore membrane filters (Millipore Sigma, Burlington, MA) and incubated at 25°C. DNA was extracted, using the ZR Fungal/Bacterial DNA MiniPrep (Zymo Research, Irvine, CA), following the manufacturer's protocol. Polymerase chain reactions (PCR) were performed with a reaction mixture that consisted of 30 ng fungal genomic DNA, 2.5 µl of 10x Standard Tag Reaction Buffer (New England BioLabs (NEB), Ipswich, MA), 0.5 µl of 10 mM dNTP (Roche Applied Science, Penzberg, Germany), 1 µl of each of 10 µM primer, 0.125 µl Taq DNA polymerase (NEB), and sterile deionized water for

a total volume of 25 µl. For certain fungal genera, 1.5 µl MgCl<sub>2</sub> had to be included in the PCR reaction mixture for amplification (Roche Diagnostics, Mannheim, Germany). PCR products were cleaned with ExoSAP-IT PCR Product Cleanup (Thermo Fisher Scientific, Grand Island, NY) and sequenced at Eurofins Scientific ([www.eurofinsus.com](http://www.eurofinsus.com)).

Several genes were amplified and sequenced for phylogenetic species recognition considering the isolates within each genus, including 5.8S rDNA and two flanking internal transcribed spacers (ITS), partial sequence of the translation elongation factor 1-α (TEF1), glutamine synthetase (GS), Apn2-Mat1-2 intergenic spacer and partial mating type (Mat1-2) gene (ApMat), calmodulin (CAL), β-tubulin (TUB2), and RNA polymerase II second largest subunit (RPB2). Primer pairs were used for the following genera: **Colletotrichum** sp.: GS: GSLF2 (TACACGAGSAAAAGG ATACGC) and GSLR1 (AGRCGCACATTGTCAGTATCG) (25); **ApMAT**: AMF1 (TCATTCTACGTATGTGCCG) and AMR1 (CCAGAAATACACCGAACCTGC) (50); **Fusarium** sp.: **TEF1**: EF1 (ATGGGTAAGGA(A/G)GACAAGAC) and EF2 (GGA(G/A)GTA CCAGT(G/C)ATCATGTT) (38); **RPB2**: fRPB2-5f2 (GGGGWGAYCAGAAGAAGGC) and fRPB2-7cr (CCCATRGCTTGYTTRCCCAT) (27); **Diaporthe** sp.: **ITS**: ITS1F (CTTGGTCATTAGAGGAAGTAA) (11) and ITS4 (TCCTCCGCTTATTGATATGC) (55); **TEF1**: EF1-728F (CATCGAGAAGTTCGAGAAGG) and EF1-986R (TACTTGAAGGAACCCTTACC) (2); **CAL**: CAL-228F (GAGTTCAAGGAGGCCTTCTCCC) and CAL-737R (CATCTTCTGGCCATCATGG) (2); **TUB2**: Bt2a (GGTAACCAAATCGGTGCTGTTTC) and Bt2b (ACCCTCAGTAGTGTAGTGACCCTGGC) (12), respectively.

PCR thermal cycle programs were performed as described by each previous author. The optimum annealing temperatures were: ApMat, GS, ITS, TEF1 (EF1-728F+ EF1-986R): 55°C; TUB2: 55 or 60°C; TEF1 (EF1+EF2) and CAL: 61°C; RPB2: 62°C. Some isolates required a change in the annealing temperatures due to either excessive or no bands amplified at the original annealing temperature.

### Phylogenetic analyses

Phylogenetic analyses compared the sequenced isolates from the current study with holotypes and ex-types of closely related taxa. Preliminary sequence alignments for each locus and genus were completed using either ClustalX v. 2.1 (22) or BioEdit version 7.2.5 (15). Sequence data for closely related species considering genus were obtained from GenBank (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Manual adjustments and concatenation of loci were conducted using MAFFT for final alignments (20, 21) within Geneious Pro v. 9.0.5.

Maximum likelihood (ML) and Bayesian inference (BI) algorithms were used to reconstruct phylogenies for alignments using PhyML and MrBayes v. 3.2.1 (46) in Geneious v6.1.3 (Biomatters Inc.). A best-fit substitution model for each dataset was selected using the Bayesian Information Criterion (BIC) implemented in DT ModSel (33). Models HKY+G, SYM+I+G and TrN+I+G were chosen for the combined loci for *Colletotrichum*, *Fusarium* and *Diaporthe*, respectively. For ML analyses within PhyML, phylogenies were run with 1000 bootstraps. Bayesian Markov Chain Monte Carlo analyses were carried out using MrBayes (17). Six chains were run for 2000000 generations and trees were sampled every 100 generations. The first 25000 trees were discarded as burn-in, the remaining trees were used to estimate posterior probabilities (PP) for the majority rule consensus tree. Phylogenies

were estimated for each locus separately and multiple loci together for each genus.

Phylogenies for multiple loci datasets were estimated using Bayesian analyses, implemented in Bayesian Evolutionary Analysis Sampling Trees (BEAST v1.7.5) (7). BEAST does not use concatenation, but rather co-estimates the individual gene trees embedded inside the summary species tree. Bayesian Evolutionary Analysis Utility (BEAUTi), version 1.7.5, was used to create XML-formatted input files for BEAST v1.7.5. In BEAST, a Markov Chain Monte Carlo algorithm was used to sample the posterior distribution of trees by conducting five independent runs of 100 million generations each using a constant size tree prior, strict molecular clock, and uniform priors. Trees were sampled every 1000 generations and the first 20% were discarded as burn-in. Post burn-in trees were combined with the program Log Combiner (BEAST v1.7.5), and chains were assumed to converge when the average standard deviation of

split frequencies was < 0.01. The maximum clade credibility tree with posterior probability of each node was computed with the program Tree Annotator (BEAST v1.7.5). Log files and tree files were visualized in Tracer v1.5 (<http://tree.bio.ed.ac.uk/software/tracer/>) and FigTree v1.3.1 (<http://tree.bio.ed.ac.uk/software/figtree/>), respectively.

## RESULTS AND DISCUSSION

Isolates were divided into five groups according to mycelium growth, color on culture media, and conidial shape and size after 8 days. Two groups of *Colletotrichum* and *Fusarium* and one *Diaporthe* were separated.

### *Colletotrichum Corda*

Sixteen isolates of *Colletotrichum* spp. (CSM 143-1, CSM 143-2,

**Table 1.** GenBank and culture collection accession numbers of *Colletotrichum* spp. included in the current study.

Species	Accession number	Host	Locality	Collector	GenBank accession number	
					GS	ApMat
<i>Colletotrichum aenigma</i>	ICMP 18608	<i>Persea americana</i>	Israel	S. Freeman	JX010078	KM360143
<i>C. aeschynomenes</i>	ICMP 17673	<i>Aeschynomene virginica</i>	USA	D. TeBeest	JX010081	KM360145
<i>C. alatae</i>	CBS 304.67	<i>Dioscorea alata</i>	India	K.L. Kothari/J. Abramham	JX010065	KC888932
<i>C. alienum</i>	ICMP 12071	<i>Malus domestica</i>	New Zealand	P.R. Johnston	JX010101	KM360144
<i>C. alienum</i>	LF322	<i>Camellia sinensis</i>	China	F. Liu	KJ954982	KJ954545
<i>C. alienum</i>	<b>CSM 145</b>	<i>Coffea arabica</i> -twigs	Venezuela	<b>S. R. Mohali</b>	<b>MG584613</b>	<b>MG584592</b>
<i>C. alienum</i>	<b>CSM 146</b>	<i>Coffea arabica</i> -twigs	Venezuela	<b>S. R. Mohali</b>	<b>MG584612</b>	<b>MG584591</b>
<i>C. alienum</i>	<b>CSM 147</b>	<i>Coffea arabica</i> -twigs	Venezuela	<b>S. R. Mohali</b>	<b>MG584611</b>	<b>MG584590</b>
<i>C. alienum</i>	<b>CSM 156</b>	<i>Coffea arabica</i> -twigs	Venezuela	<b>S. R. Mohali</b>	<b>MG584610</b>	<b>MG584589</b>
<i>C. alienum</i>	<b>CSM 157</b>	<i>Coffea arabica</i> -twigs	Venezuela	<b>S. R. Mohali</b>	<b>MG584609</b>	<b>MG584588</b>
<i>C. aotearoa</i>	ICMP 18537	<i>Coprosma</i> sp.	New Zealand	B. Weir	JX010113	KC888930
<i>C. asianum</i>	CBS 130418	<i>Coffea Arabica</i> (berry)	Thailand	H. Prihastuti	JX010096	FR718814
<i>C. aeschynomenes</i>	ICMP 17673	<i>Aeschynomene virginica</i>	USA	D. TeBeest	JX010081	KM360145
<i>C. camelliae</i>	LC1364	<i>Camellia sinensis</i>	China	P. Tan	KJ954932	KJ954497
<i>C. clidemiae</i>	ICMP 18658	<i>Clidemia hirta</i>	USA	S.A Ferreira/K. Pitz	JX010129	KC888929
<i>C. cordylinicola</i>	ICMP 18579	<i>Cordyline fruticosa</i>	Thailand	S. Phoulivong	JX010122	JQ899274
<i>C. fructicola</i>	CBS 130416	<i>Coffea Arabica</i> (berry)	Thailand	H. Prihastuti	JX010095	JQ807838
<i>C. gloeosporioides</i>	CBS 112999	<i>Citrus sinensis</i>	Italy	G. Goidánich	JX010085	JQ807843
<i>C. henanense</i>	LF238	<i>Camellia sinensis</i>	China	M. Zhang/R. Zang	KJ954960	KJ954524
<i>C. horii</i>	ICMP 10492	<i>Diospyros kaki</i>	Japan	N. Nishihara	JX010137	JQ807840
<i>C. jiangxiense</i>	LF687	<i>Camellia sinensis</i>	China	Y. Zhang	KJ955051	KJ954607
<i>C. jiangxiense</i>	LF684	<i>Camellia sinensis</i>	China	Y. Zhang	KJ955048	KJ954604
<i>C. kahawae</i>	ICMP 17816	<i>Coffea arabica</i>	Kenya	D.M. Masaba	JX010130	JQ894579
<i>Colletotrichum musae</i>	CBS 116870	<i>Musa</i> sp.	USA	M. Arzanlou	JX010103	KC888926
<i>C. nupharicola</i>	CBS 470.96	<i>Nuphar lutea</i> subsp. <i>polysepala</i>	USA	D.A. Johnson	JX010088	JX145319
<i>C. psidii</i>	CBS 145.29	<i>Psidium</i> sp.	Italy	M. Curzi	JX010133	KC888931
<i>C. queenslandicum</i>	ICMP 1778	<i>Carica papaya</i>	Australia	J.H. Simmonds	JX010104	KC888928
<i>C. salsolae</i>	ICMP 19051	<i>Salsola tragus</i>	Hungary	D. Berner	JX010093	KC888925
<i>C. siamense</i>	LF139	<i>Camellia</i> sp.	China	F. Liu	KJ954938	KJ954503
<i>C. siamense</i>	LF177	<i>Camellia oleifera</i>	China	F. Liu	KJ954943	KJ954508
<i>C. siamense</i>	CBS130417, ICMP 18578	<i>Coffea arabica</i>	Thailand	H. Prihastuti	JX010094	JQ899289
<i>C. siamense</i> (syn. <i>C. hymenocallidis</i> )	CBS125378, ICMP 18642	<i>Hymenocallis americana</i>	China	Y. L. Yang	JX010100	JQ899283 <i>continued...</i>

**Table 1.** Continuation

Species	Accession number	Host	Locality	Collector	GenBank accession number	
					GS	ApMat
<i>C. siamense</i>	CSM 143-1	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584608	MG584587
<i>C. siamense</i>	CSM 143-2	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584607	MG584586
<i>C. siamense</i>	CSM 144	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584606	MG584585
<i>C. siamense</i>	CSM 148	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584605	MG584584
<i>C. siamense</i>	CSM 149	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584604	MG584583
<i>C. siamense</i>	CSM 150	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584603	MG584582
<i>C. siamense</i>	CSM 151	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584602	MG584581
<i>C. siamense</i>	CSM 152	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584601	MG584580
<i>C. siamense</i>	CSM 153	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584600	MG584579
<i>C. siamense</i>	CSM 154	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584599	MG584578
<i>C. siamense</i>	CSM 155	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584598	MG584577
<i>C. siamense</i>	CSM 158	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584597	MG584576
<i>C. siamense</i>	CSM 159	<i>Coffea arabica</i> -twigs	Venezuela	S. R. Mohali	MG584596	MG584575
<i>C. siamense</i>	CSM 163	<i>Coffea arabica</i> -ripe fruit	Venezuela	S. R. Mohali	MG584595	MG584574
<i>C. siamense</i>	CSM 166	<i>Coffea arabica</i> -ripe fruit	Venezuela	S. R. Mohali	MG584594	MG584573
<i>C. siamense</i>	CSM 167	<i>Coffea arabica</i> -ripe fruit	Venezuela	S. R. Mohali	MG584593	MG584572
<i>Colletotrichum theobromicola</i>	CBS 124945, ICMP18649	<i>Theobroma cacao</i>	Panama	E. J. Rojas	JX010139	KC790726
<i>C. ti</i>	ICMP 4832	<i>Cordyline</i> sp.	New Zealand	J.M. Dingley	JX010123	KM360146
<i>C. tropicale</i>	CBS 124949	<i>Theobroma cacao</i>	Panama	E.I. Rojas/L.C. Mejia/ Z. Maynard	JX010097	KC790728
<i>C. viniferum</i>	CBS 130644	<i>Vitis vinifera</i> , cv. 'Hongti'	China	L.J. Peng	JN412784	KJ623242
<i>C. xanthorrhoeae</i>	CBS 127831	<i>Xanthorrhoea preissii</i>	Australia	F.D. Podger	JX010138	KC790689

ICMP: International Collection of Microorganisms from Plants, Auckland, New Zealand; LC: Working collection of Lei Cai, housed at CAS, China; LF: Working collection of Fang Liu, housed at CAS, China; CBS: Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, The Netherlands; CSM: Personal culture collection deposited in the Department of Bioagricultural Sciences & Pest Management, Colorado State University, USA.

CSM 144, CSM 148, CSM 149, CSM 150, CSM 151, CSM 152, CSM 153, CSM 154, CSM 155, CSM 158, CSM 159, CSM 163, CSM 166, CSM 167) presented colonies white to pale brown, reverse pale yellow, aerial mycelium greyish white, dense, cottony; conidia one-celled, smooth-walled, guttulate, hyaline, fusiform with obtuse to slightly rounded ends, sometimes oblong, 8-18.5 x 4-8.5  $\mu\text{m}$  (mean = 12.7 x 5.5  $\mu\text{m}$ , n = 50). Other five isolates (CSM 145, CSM 146, CSM 147, CSM 156, CSM 157) had colonies cottony, grey aerial mycelium and orange conidial ooze, reverse dark grey to pale orange in center; conidia were one-celled, cylindric with broadly rounded ends, 13-21 x 3-6  $\mu\text{m}$  (mean = 15.5 x 5.0  $\mu\text{m}$ , n = 50) (54) (Table 1).

Bayesian and maximum likelihood phylogenetic trees were generated for a concatenated dataset of ApMat and GS loci with 1838 base pairs. The phylogenies included 21 isolates of *Colletotrichum* species from the present study and 26 additional closely-related taxa and were rooted with *C. xanthorrhoeae* CBS 127831 (Table 1). Sixteen *C. siamense* isolates and five *Colletotrichum alienum* B. Weir & P.R. Johnst. isolates formed two separate and well-supported clades with values of BS/PP = 78/0.98 for *Colletotrichum siamense* and BS/PP = 94/0.97 for *C. alienum* (Figure 2).

Coffee production has often been limited by CBD, which is caused by *Colletotrichum kahawae* in Kenya and other countries of Eastern Africa. At high altitudes, CBD is particularly devastating, damaging green berries and inducing premature fruit drop and fruit mummification, leading to production losses of 50 to 80% (16, 34).

Interestingly, *Colletotrichum siamense* was isolated from symptomatic CBD in green and mature fruits, infested or not with CBB, and from twigs with anthracnose symptoms, whereas *C. alienum* was only isolated from twigs with anthracnose. *Colletotrichum siamense* was first identified and reported in isolates from lesions in healthy berry tissues, as well as from the surface of coffee berries in northern Thailand (42). In three municipalities in Puebla State, Mexico, *C. siamense* was isolated from leaves showing typical and atypical *Cercospora* lesions, as well as from symptomatic unripe fruits of coffee trees (5). In Chiapas, Mexico, 21 fungal genera were isolated from coffee berries infested with CBB by *Hypothenemus hampei*; however, *Colletotrichum* was not present in these isolates (40). In the current study, *C. siamense* was found associated with CBB in coffee grown in Venezuela.

*Colletotrichum alienum* was isolated and identified for the first time on ripe fruit rot from *Persea americana* in Australia (54), later in Israel (47), on *Malus domestica* fruit rot in New Zealand (54), associated with anthracnose diseases on *Proteaceae* in Australia, South Africa and Europe (24), and on *Nerium oleander* in Australia (48). This is the first report of such a species affecting coffee in Venezuela; however, as this species was recently named and separated from the *C. gloeosporioides* complex, it will likely be found in numerous regions where species within the *C. gloeosporioides* complex have been found (54). Recently, 80 *Colletotrichum* isolates from an Australian culture collection were analyzed on a molecular phylogenetic level, and *C. alienum* was distinguished from other species within the *C. gloeosporioides* species



**Figure 2.** Phylogenies generated from Bayesian analysis based on combined ApMat and GS sequences of *Colletotrichum* species. The phylogenies were rooted with *C. xanthorrhoeae* CBS 127831. Bootstrap test  $\geq 50\%$ : 1000 replicates and Bayesian posterior probabilities  $\geq 0.50$  (BS/PP) are highlighted by arrows. The isolates included in the current study are in bold and oblique. The phylogeny includes annotation of species boundaries for taxa that belong to the *C. gloeosporioides* complex. Bootstrap (BS) values below 50% are marked with a hyphen (-) on the phylogenetic trees.

complex using GS sequences (49, 54).

Sequence data of the concatenated ApMat and GS loci have served as a barcode for species identification of isolates belonging to the *C. gloeosporioides* species complex. Recently, Lui et al. (26) used these loci to re-construct a phylogenetic tree of *Colletotrichum* species from *Camellia* spp., highlighting that the topology of ApMat-GS phylogram was similar to that of a phylogram encompassing sequence data from 8 loci (25). Mating-related genes have been suggested to evolve at a faster rate and have a higher sequence variability, which dominates the topology of the multi-locus phylogram (25), allowing ApMat-GS to be informative for species identification.

### **Fusarium Link ex Grey.**

Four isolates of *Fusarium* spp. (CSM 134, CMS 135, CMS 137, CMS 138) had cultures showing dense aerial mycelia, initially white to beige or brown with age; Chlamydospores present; Macroconidia 3 to 5 septate, apical cell curved and tapering to a point, basal cell foot-shaped, 20-41.5 x 2.0-4.5 µm (mean = 19.3 x 3.1 µm, n = 50). Other cultures of five isolates (CSM 136, CMS 139, CSM 140, CSM 141, CSM 142) usually are white to cream with sparse mycelium; Chlamydospores abundant; Macroconidia 5 to 7 septate, wide and straight, apical cell blunt and rounded, basal cell straight to almost cylindrical, 13.5-44 x 3.0-6 µm (mean = 20.5 x 3.6 µm, n = 50); Microconidia oval to ellipsoid, 0 or 1 septum (23, 28) (Table 2).

The combined datasets of the partial TEF1 and RPB2 was comprised of 1659 base pairs from 27 taxa collected from this study and 43 reference species (Table 2). *Fusarium lyarnte* RBG5331 served as the outgroup. Four *F. incarnatum* (Roberge) Sacc (= *Fusarium semitectum*

Berk. & Ravenel) isolates clustered together with reference species, forming a *Fusarium incarnatum-equiseti* species complex (FIESC). Five *Fusarium solani* (Mart.) Sacc/ sexual morph *Neocosmospora solani* (Mart.) L. Lombard & Crous isolates clustered together. The BS and PP values for each *F. incarnatum* and *F. solani* well-support clades were BS/PP = 100/1 (Figure 3).

*Fusarium* species have long been known as latent pathogens of different tree species, existing as endophytes before causing disease (3). Numerous *Fusarium* species have previously been reported on coffee, as an endophyte or as a pathogen. The present study found *Fusarium incarnatum* and *F. solani* associated with anthracnose and as endophytes. In Colombia, Hawaii, Mexico and Puerto Rico, *Fusarium* sp. was the second most common endophyte out of 843 isolated fungi, while *Colletotrichum* sp. was the most commonly isolated species (52). A survey conducted from 1979 to 1981 in Puerto Rico, to evaluate anthracnose incidence and severity, found that *Fusarium stilbooides* (Wollenb.), *F. oxysporum* (Schltdl.) and *F. semitectum* were associated with anthracnose symptoms (32), indicating that multiple *Fusarium* are capable of causing anthracnose on coffee. In Minas Gerais, Brazil, *Fusarium equiseti* (Corda) Sacc. and *F. semitectum* were found to be associated with the mycobiota, both internally and externally, on four coffee bean cultivars (*C. arabica*) without observable symptoms (39) and, similar to our study, *Fusarium incarnatum* was reported on coffee beans in Campo Elias Municipality, Trujillo State, Venezuela (51).

*Fusarium solani* and *Fusarium* sp. have been reported as part of the mycobiota associated with the cuticle, gut, feces and galleries of CBB, *Hypothenemus hampei*, in coffee plantations in Chiapas, Mexico (40). Interestingly, in the current study, *Fusarium incarnatum* and

**Table 2.** GenBank and culture collection accession numbers of *Fusarium* spp. included in the current study.

Species	Accession number	Host	Locality	Collector	GenBank accession number	
					TEF1	RPB2
<i>Fusarium avenaceum</i>	FRC R-09495	-	-	-	GQ915502	GQ915486
<i>F. aywerte</i>	RBG5743	-	Australia	RBG	KP083250	KP083278
<i>F. beomiforme</i>	RBG4549	-	Australia	RBG	HQ667157	HQ646396
<i>F. burgessii</i>	RBG5319	Soil	Australia	B. Wang/A. Fraser	HQ667149	HQ646392
<i>F. coicis</i>	RBG5368	<i>Coix gasteenii</i>	Australia	RBG	KP083251	KP083274
<i>F. commune</i>	NRRL28387	<i>Dianthus caryophyllus</i>	The Netherlands	NRRL	AF246832	JX171638
<i>F. culmorum</i>	RBG3558	-	Australia	RBG	HQ667167	HQ646401
<i>F. fujikuroi</i>	NRRL13566	<i>Oryza sativa</i>	Taiwan	NRRL	AF160279	EF470116
<i>F. gaditijirri</i>	F15048	<i>H. triticeus</i>	Australia	L. W. Burgess	AY639634	HQ662690
<i>F. goolgardi</i>	RBG5411	<i>Xanthorrhoea glauca</i>	Australia	D. M. Robinson/M. H. Laurence	KP101123	KP083280
<i>F. hostae</i>	RBG3994	-	Australia	RBG	HQ667160	HQ646390
<i>F. incarnatum</i>	CBS 132194	-	-	-	KF255470	KF255542
<i>F. incarnatum</i>	CBS 132894	-	-	-	KF255480	KF255545
<i>F. incarnatum</i>	CSM 134	<i>Coffea arabica</i>	Venezuela	S. R. Mohali	MG049934	MG049943
<i>F. incarnatum</i>	CSM 135	<i>Coffea arabica</i>	Venezuela	S. R. Mohali	MG049933	MG049942
<i>F. incarnatum</i>	CSM 137	<i>Coffea arabica</i>	Venezuela	S. R. Mohali	MG049932	MG049941
<i>F. incarnatum</i>	CSM 138	<i>Coffea arabica</i>	Venezuela	S. R. Mohali	MG049931	MG049940
<i>F. lyarnte</i>	RBG5331	-	Australia	RBG	EF107118	HQ662691
<i>F. miscanthi</i>	RBG4177	-	Australia	RBG	HQ667166	HQ662693
<i>F. mundagurra</i>	RBG5717	From soil Carnarvon Gorge National Park	Australia	S. M. Dunstan/M. H. Laurence	KP083256	KP083276

*continued...*

**Table 2.** Continuation

Species	Accession number	Host	Locality	Collector	GenBank accession number	
					TEF1	RPB2
<i>F. napiforme</i>	NRRL13604	<i>Pennisetum typhoides</i>	Namibia	A.Lübben	AF160266	EF470117
<i>Fusarium nelsonii</i>	NRRL13338	Soil	Australia	NRRL	GQ505402	GQ505466
<i>F. newnesense</i>	RBG5443	-	Australia	RBG	KJ397074	KP083277
<i>F. nisikadoi</i>	RBG4043	-	Australia	RBG	HQ667165	HQ662692
<i>Fusarium nelsonii</i>	NRRL13338	Soil	Australia	NRRL	GQ505402	GQ505466
<i>F. newnesense</i>	RBG5443	-	Australia	RBG	KJ397074	KP083277
<i>F. nisikadoi</i>	RBG4043	-	Australia	RBG	HQ667165	HQ662692
<i>F. oxysporum</i>	RBG5413	-	Australia	RBG	HQ667161	HQ646385
<i>F. oxysporum</i>	RBG5414	-	Australia	RBG	HQ667163	HQ646388
<i>F. oxysporum</i>	CSM 105	<i>Theobroma cacao</i>	Venezuela	S. R. Mohali	MF436042	MF447156
<i>F. oxysporum</i>	CSM 109	<i>Theobroma cacao</i>	Venezuela	S. R. Mohali	MF436041	MF447155
<i>F. proliferatum</i>	NRRL43665	Contact lens	USA	NRRL	EF452996	EF470035
<i>F. pseudograminearum</i>	RBG3580	-	Australia	RBG	HQ667168	HQ646400
<i>F. redolens</i>	RBG4173	-	Australia	RBG	HQ667159	HQ646391
<i>F. sibiricum</i>	NRRL53429	<i>Avena sativa</i>	Russia	L. S. Malinovskaya/ E. A. Pirjazeva	HM744683	HQ154471
<i>F. solani</i>	CBS 138564	<i>Homo sapiens</i>	Turkey	-	KT272100	KT272102
<i>F. solani</i>	CBS 131775	wheat	Iran	M. Davari	JX118990	JX237778
<i>F. solani</i>	CSM 103	<i>Theobroma cacao</i>	Venezuela	S. R. Mohali	MF436040	MF436050
<i>F. solani</i>	CSM 250	<i>Theobroma cacao</i>	Venezuela	S. R. Mohali	MF436033	MF436046
<i>F. solani</i>	<b>CSM 136</b>	<i>Coffea arabica</i>	Venezuela	<b>S. R. Mohali</b>	<b>MG049930</b>	<b>MG049938</b>
<i>F. solani</i>	<b>CSM 139</b>	<i>Coffea arabica</i>	Venezuela	<b>S. R. Mohali</b>	<b>MG049929</b>	<b>MG049939</b>
<i>F. solani</i>	<b>CSM 140</b>	<i>Coffea arabica</i>	Venezuela	<b>S. R. Mohali</b>	<b>MG049928</b>	<b>MG049937</b>
<i>F. solani</i>	<b>CSM 141</b>	<i>Coffea arabica</i>	Venezuela	<b>S. R. Mohali</b>	<b>MG049927</b>	<b>MG049936</b>
<i>F. solani</i>	<b>CSM 142</b>	<i>Coffea arabica</i>	Venezuela	<b>S. R. Mohali</b>	<b>MG049926</b>	<b>MG049935</b>
<i>F. tjaetaba</i>	RBG5361	<i>Sorghum interjectum</i>	Australia	J.L. Walsh.	KP083263	KP083275
<i>F. verticillioides</i>	NRRL43656	Contact lens	USA	NRRL	EF452987	EF470026

RBG: Royal Botanic Gardens Trust, Sydney, New South Wales, Australia; NRRL: Agricultural Research Service Culture Collection, Peoria, Illinois USA; F: University of Sydney, Sydney, New South Wales, Australia; CBS: Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, The Netherlands. CSM: Personal culture collection deposited in the Department of Bioagricultural Sciences & Pest Management, Colorado State University, USA; FRC: Fusarium Research Center, Penn State University, University Park, USA; -: not provided in literatures.

*F. solani* were isolated from ripe coffee fruits, with or without CBD infestations in Mérida, Venezuela, indicating that there may not be a close association of these *Fusarium* species with CBB.

#### *Diaporthe* Nitschke (asexual morph *Phomopsis* (Sacc.) Bubák).

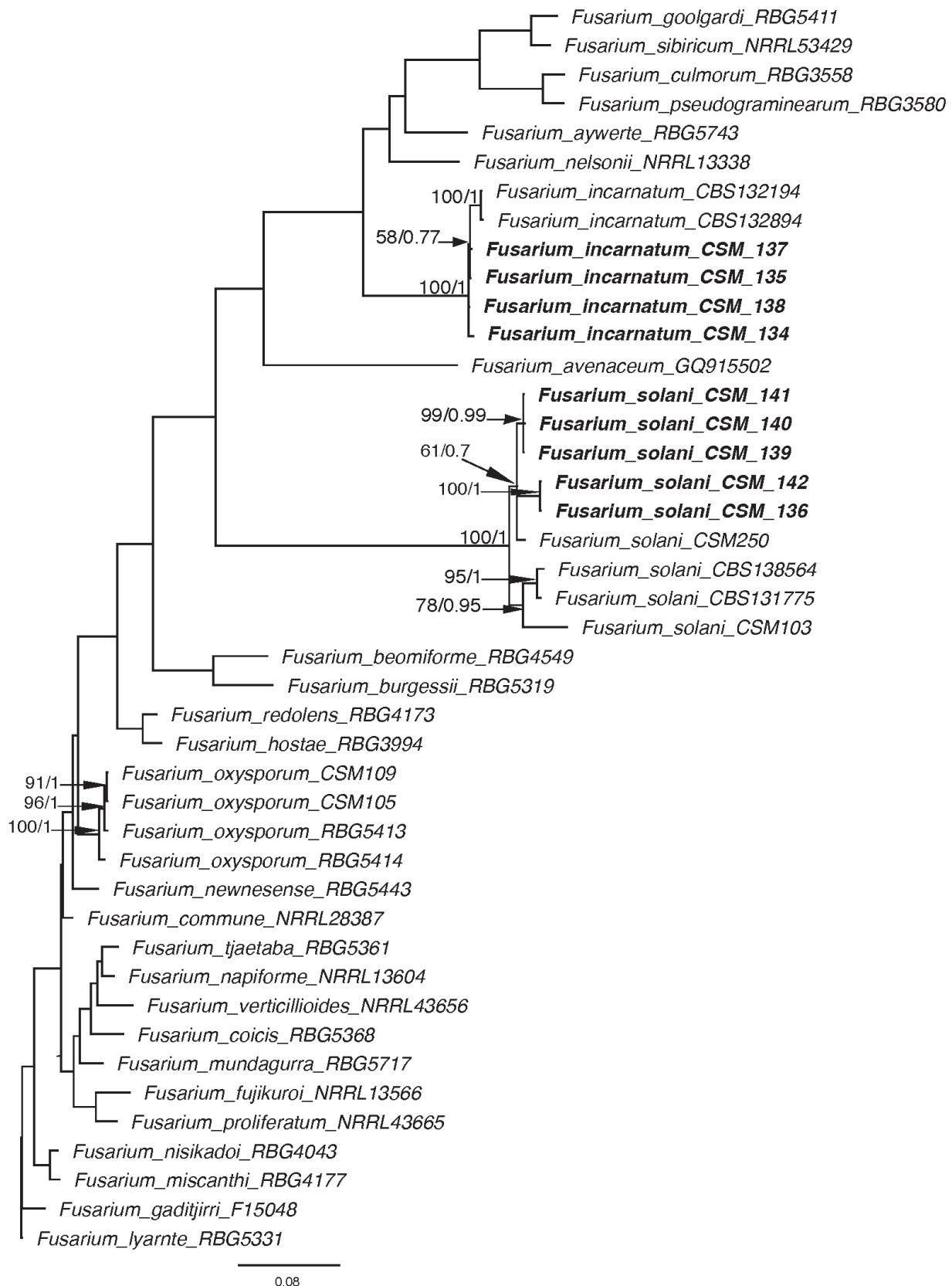
Three isolates (CSM 133, CSM 222, CSM 224) with similar characteristics to genus *Phomopsis*/sexual morph *Diaporthe* produced cultures with a surface dirty white to ochreous, reverse umber, very large, coalescing stromata with lodged, elongated pycnidia necks forming dense, cream-colored droplets of conidia. Alpha conidia abundant, base truncate, smooth, aseptate, hyaline, guttulate, fusiform, tapering towards both ends, apex acutely rounded, 5.5–10 x 2–3 µm (mean = 8.0 x 2.5 µm, n = 50), beta conidia not seen (13) (Table 3).

A concatenated dataset of four gene regions was used for *Diaporthe* species identification. The ITS, TEF1, CAL and TUB2 data had 2095 base pairs and included 03 taxa isolated in the current study plus 31 reference species of *Diaporthe*. *Diaporthella corylina* was included as an outgroup CBS 121124 (Table 3). Three *Diaporthe pseudomangiferae*

R.R. Gomes, C. Glienke & Crous isolates were clustered with BS/PP = 76/0.99 (Figure 4).

*Diaporthe* species (asexual morph = *Phomopsis*) have been previously isolated from coffee as both pathogens and endophytes around the globe; however, *Diaporthe* species have varied depending on location. In the present study, *Diaporthe pseudomangiferae* could be isolated from coffee twigs with anthracnose symptoms in Venezuela. *Phomopsis* sp. was previously isolated in Venezuela from a coffee leaf spot in Trujillo (51). In Puerto Rico, *Phomopsis* sp. was found on branches and dead nodes of coffee trees with *C. gloeosporioides* and mummified berries (32). Furthermore, *Diaporthe acutispora* Y.H. Gao & L. Cai and *Diaporthe yunnanensis* Y.H. Gao & L. Cai were also isolated from healthy leaves of *Coffea* sp. in Yunnan Province of China (10).

In Kenya, Rayner (44) isolated and reported *Phomopsis* sp. as a coffee endophyte after having sterilized the surfaces of healthy leaves, pedicels, stems, and green berries; an endophyte was also isolated from asymptomatic coffee tissues of berries and leaves in Colombia,

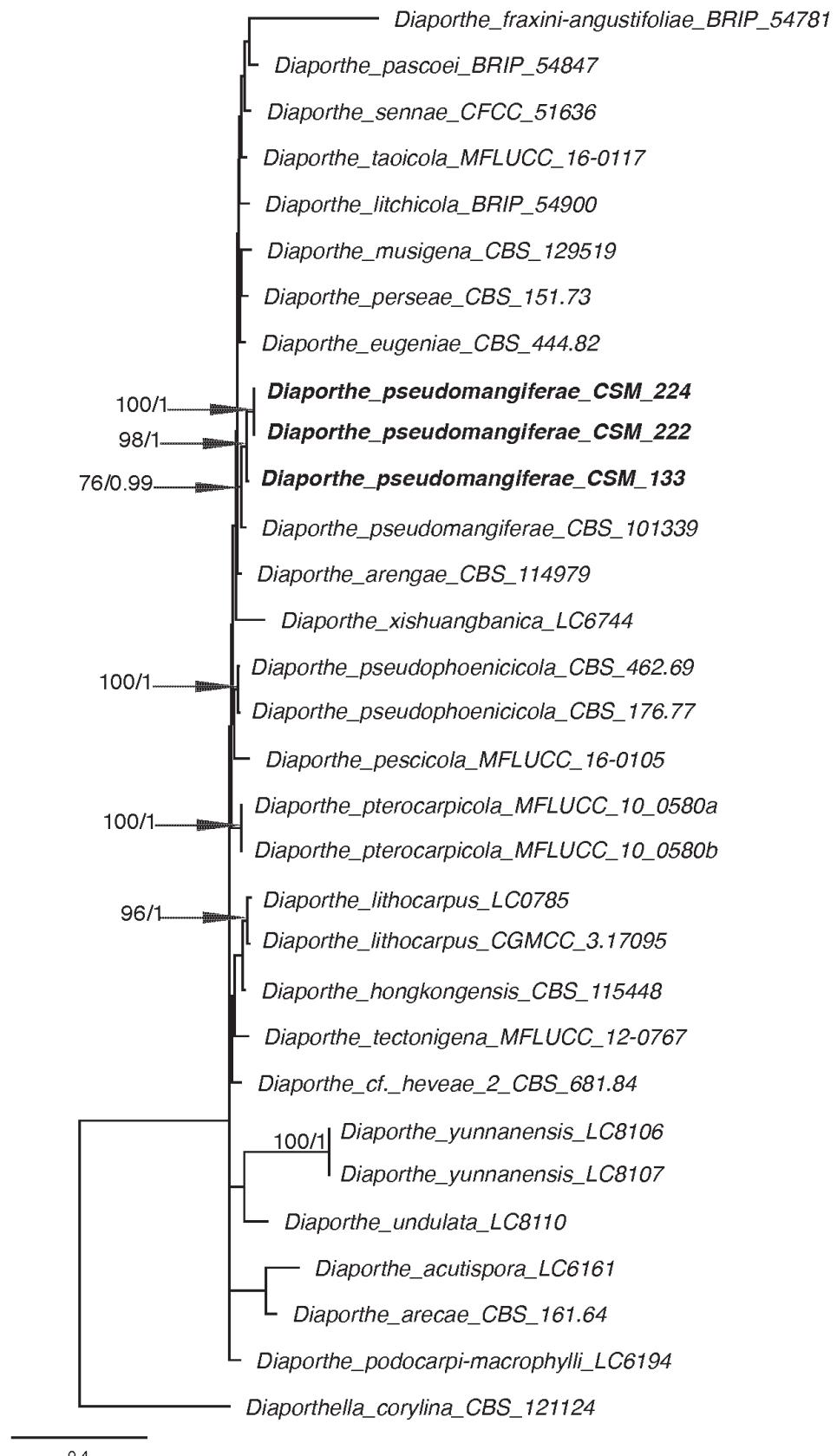


**Figure 3.** Phylogenies generated from Bayesian analysis based on combined EF1 and RPB2 sequences of *Fusarium* species. The phylogenies were rooted with *Fusarium lyarnte* (RBG 5331). Bootstrap test  $\geq 50\%$ :1000 replicates and Bayesian posterior probabilities  $\geq 0.70$  (BS/PP) are highlighted by arrows. The new coffee isolates included in the current study are in oblique and bold.

**Table 3.** GenBank and culture collection accession numbers of *Diaporthe* spp. included in the current study.

Species	Accession number	Host	Locality	Collector	GenBank accession number			
					ITS	TEF1	TUB2	CAL
<i>Diaporthe acutispora</i>	LC6161	<i>Coffea</i> sp.	China	W.J.Duan	KX986764	KX999155	KX999195	KX999274
<i>D. arecae</i>	CBS 161.64	<i>Areca catechu</i>	India	H.C. Srivastava	KC343032	KC343758	KC344000	KC343274
<i>D. arengae</i>	CBS 114979	<i>Arenga engleri</i>	Hong Kong	K.D. Hyde	KC343034	KC343760	KC344002	KC343276
<i>D. cf. heveae 2</i>	CBS 681.84	<i>Hevea brasiliensis</i>	India	K. Jayarathnam	KC343117	KC343843	KC344085	KC343359
<i>D. eugeniae</i>	CBS 444.82	<i>Eugenia aromatica</i>	West Sumatra	R. Kasim	KC343098	KC343824	KC344066	KC343340
<i>D. fraxini-angustifoliae</i>	BRIP 54781	<i>Fraxinus-angustifolia</i> subsp. <i>oxyacapa</i>	Australia	L. Smith	JX862528	JX852534	KF170920	-
<i>D. hongkongensis</i>	CBS 115448	<i>Dichora febrifuga</i>	Hong Kong	K.D. Hyde	KC343119	KC343845	KC344087	KC343361
<i>D. litchicola</i>	BRIP 54900	<i>Litchi chinensis</i>	Australia	K.R.E. Grice	JX862533	JX862539	KF170925	-
<i>D. lithocarpus</i>	LC0785	<i>Lithocarpus glabra</i>	China	W. Sun	KF576274	KF576249	KF576298	KF576226
<i>D. lithocarpus</i>	CGMCC 3.17095	<i>Lithocarpus glabra</i>	China	W. Sun	KF576285	KF576260	KF576309	KF576234
<i>D. musigena</i>	CBS 129519	<i>Musa</i> sp.	Australia	P.W. Crous & R.G. Shivas	KC343143	KC343869	KC344111	KC343385
<i>D. pascoei</i>	BRIP 54847	<i>Persea americana</i>	Australia	I.G. Pascoe	JX862532	JX862538	KF170924	-
<i>D. perseae</i>	CBS 151.73	<i>Perseae gratissima</i>	Netherlands Antilles	E. Laville	KC343173	KC343899	KC344141	KC343415
<i>D. pescicola</i>	MFLUCC 16-0105	<i>Prunus persica</i>	China	X. H. Li	KU557555	KU557623	KU557579	KU557603
<i>D. podocarpi-macrophylli</i>	LC6194	<i>Podocarpus macrophyllus</i>	China	W.J. Duan	KX986785	KX999156	KX999196	KX999275
<i>D. pseudomangiferae</i>	CBS 101339	<i>Mangifera indica</i>	Dominican Republic	P. de Leeuw	KC343181	KC343907	KC344149	KC343423
<i>D. pseudomangiferae</i>	CBS 388.89	<i>Mangifera indica</i>	Mexico	P. de Leeuw	KC343182	KC343908	KC344150	KC343424
<i>D. pseudomangiferae</i>	CSM 133	<i>Coffea arabica</i>	Venezuela	S.R. Mohali	MG576129	MG584619	MG584622	MG584616
<i>D. pseudomangiferae</i>	CSM 222	<i>Coffea arabica</i>	Venezuela	S.R. Mohali	MG576128	MG584618	MG584621	MG584615
<i>D. pseudomangiferae</i>	CSM 224	<i>Coffea arabica</i>	Venezuela	S.R. Mohali	MG576127	MG584617	MG584620	MG584614
<i>D. pseudophoenicicola</i>	CBS 462.69	<i>Phoenix dactylifera</i>	Spain	H.A. van der Aa	KC343184	KC343910	KC344152	KC343426
<i>D. pseudophoenicicola</i>	CBS 176.77	<i>Mangifera indica</i>	Iraq	M. S. A. Al-Momen	KC343183	KC343909	KC344151	KC343425
<i>D. pterocarpicola</i>	MFLUCC 10-0580a	<i>Piterocarpus indicus</i>	Thailand	D. Udayanga	JQ619887	JX275403	JX275441	JX197433
<i>D. pterocarpicola</i>	MFLUCC 10-0580b	<i>Piterocarpus indicus</i>	Thailand	D. Udayanga	JQ619888	JX275404	JX275442	JX197434
<i>D. sennae</i>	CFCC 51636	<i>Senna bicapsularis</i>	China	Q. Yang	KY203724	KY228885	KY228891	KY228875
<i>D. taoicola</i>	MFLUCC 16-0117	<i>Prunus persica</i>	China	X.H. Li	KU557567	KU557635	KU557591	-
<i>D. tectonigena</i>	MFLUCC 12-0767	<i>Tectona grandis</i>	Thailand	M. Doilom	KU712429	KU749371	KU743976	KU749358
<i>D. undulata</i>	LC8110	Unknown host	China	F. Liu	KY491545	KY491555	KY491565	-
<i>D. xishuangbanica</i>	LC6744	<i>Camellia sinensis</i>	China	F. Liu	KX986784	KX999176	KX999217	-
<i>D. yunnanensis</i>	LC8106	<i>Coffea</i> sp.	China	W.J. Duan	KY491541	KY491551	KY491561	KY491571
<i>D. yunnanensis</i>	LC8107	<i>Coffea</i> sp.	China	W.J. Duan	KY491542	KY491552	KY491562	KY491572
<i>Diaporthella corylina</i>	CBS 121124	<i>Corylus</i> sp.	China	L.N. Vassiljeva	KC343004	KC343730	KC343972	KC343246

CSM: Personal culture collection deposited in the Department of Bioagricultural Sciences & Pest Management, Colorado State University, USA; CBS: Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, The Netherlands; MFLUCC: Mae Fah Luang University Culture Collection; BRIP: Australian plant pathogen culture collection, Queensland; CGMCC: China General Microbiological Culture Collection Center; CFCC: China Forestry Culture Collection Center; LC: Working collection of Lei Cai, housed at Institute of Microbiology, CAS, China. -: not provided in literatures.



**Figure 4.** Phylogenies generated from Bayesian analysis based on combined ITS, TEF1, CAL and TUB2 sequences of *Diaporthe* species. The phylogenies were rooted with *Diaporthella corylina* CBS 121124. Bootstrap test  $\geq 75\%:1000$  replicates and Bayesian posterior probabilities  $\geq 0.99$  (BS/PP) are highlighted by arrows. The new coffee isolates included in the current study are in oblique and bold.

Hawaii, Mexico and Puerto Rico (52). *Diaporthe liquidambaris* (C.Q. Chang, Z.D. Jiang & P.K. Chi) Udayanga & Castl., and *D. phaseolorum* (Cooke & Ellis) Sacc. are endophytic fungi which have been isolated from mature healthy leaves of *Coffea Arabica*, in both conventional and organic coffee production systems, in the municipality of Garanhuns, Pernambuco, Brazil (36). *Diaporthe acutispora* Y.H. Gao & L. Cai and *Diaporthe yunnanensis* Y.H. Gao & L. Cai were also isolated from healthy leaves of *Coffea* sp. in Yunnan Province of China (10). It is not entirely clear whether *Diaporthe* spp. play a role as latent pathogens in *Coffea* spp., but species in these genera are known as endophytes and pathogens (13).

Although CBD caused by *C. kahawae* is so far restricted to Africa, in 1986 and 1994 isolates similar to *C. gloeosporioides* that cause coffee berry diseases were reported in the states of Lara, Portuguesa and Trujillo States, Venezuela, based on morphological identification. This species has been reported as the cause of anthracnose on leaves and branches, fruit diseases and dieback in coffee crops (29, 30, 51). In the current study, both morphological and molecular species identification detected absence of *C. gloeosporioides* but presence of other *Colletotrichum* species, including *C. siamense* and *C. alienum*. These reported *Colletotrichum* species are capable of and known for causing berry diseases and anthracnose on *Coffea* spp. shoots. Thus, appropriate management measures for pathogen control must be adopted to prevent the introduction of this disease to other coffee growing areas, specially to neighboring regions in South America. The current study is the first report of *D. pseudomangiferae* associated with anthracnose in coffee plantations in Venezuela. The pathogen can be considered an endophyte or a latent pathogen together with *Fusarium* species in the global trade market.

## DECLARATION OF COMPETING INTEREST

The authors declare no potential conflict of interest for this study, and the present research has not been published previously.

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