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Identification and Pathogenicity of *Dothiorella sarmentorum* Causing Lavender Leaf Blight Disease in Xinjiang, China

Mengyao Li [1,†], Chuli Liu [1,†], Wanbin Shi [1], Aifan Wang [2], Rong Ma [1,*] and Xiujuan Su [2,*]

[1] College of Forestry and Landscape Architecture, Xinjiang Agricultural University, Urumqi 830052, China; limengyao0306@163.com (M.L.); 15199065502@163.com (C.L.); 18097723209@163.com (W.S.)
[2] Agricultural College, Xinjiang Agricultural University, Urumqi 830052, China; wangaifantop@163.com
* Correspondence: xjaumr@xjau.edu.cn (R.M.); suxiujuan@xjau.edu.cn (X.S.)
† These authors contributed equally to this work.

Abstract: Lavender is an oil-bearing plant, which has long been cultivated for oil, fresh flowers, dried products, and food. Leaf blight disease was observed on 'Bandera Pink', which belongs to *Lavandula stoechas* in Yining County, Xinjiang Uygur Autonomous Region, China. The causal agent of this disease was isolated, and Koch's postulates were assessed to confirm its pathogenicity. The morphological characteristics of the pathogen were observed, and the LSU, ITS, *tef1*, and *tub2* loci were combined and analyzed. Based on morphological characterization and phylogenetic analyses, the causal agent was identified as a fungal species named *Dothiorella sarmentorum*. Pathogenicity tests revealed that *D. sarmentorum* can infect seven varieties of three lavender species. This is the first report of *D. sarmentorum* causing lavender leaf blight. This study provides a theoretical basis for the diagnosis of disease and the monitoring of disease occurrence and epidemics.

Keywords: Botryosphaeriaceae; leaf disease; morphology; phylogeny

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1. Introduction

Lavender (*Lavandula*, Lamiaceae) contains several commercial species that are cultivated extensively in temperate climates for the extraction of essential oils, as well as traditional medicine, culinary herbs, and ornamental plants [1–5]. Yili Prefecture of Xinjiang is the main cultivation area of lavender in China. At the present time, the lavender cultivation area in the Yili River Valley is 4900 hm^2, accounting for 98% of the national lavender cultivation area and more than 90% of the national essential oil production, making it the largest lavender cultivation base in China [6,7].

In field conditions, lavender can be affected by some potential disease factors like fungi and bacteria. The most recognizable root rot of lavender is caused by *Fusarium foetens*, *F. oxysporum*, and *Meloidogyne javanica* [8–10]. The Downy mildew disease of lavender is caused by *Peronospora belbahrii*, and net blotch is caused by *Rhizoctonia solani* [11,12]. Bacterial speck disease is caused by *Xanthomonas hortorum* in Korea [13]. In August 2023, lavender leaf blight occurred in Yining County, Xinjiang Uygur Autonomous Region, China.

Dothiorella species are known pathogens on a wide range of hosts, causing environmental or agricultural production losses and seriously affecting healthy tree growth. It caused severe decline of almond trees in orchards in Spain, with disease symptoms including branch collapse, chlorosis of leaves leading to sudden wilting, death, and shoot dieback [14,15]. It also caused the wilting and death of a large number of grapevines in Australia's wine regions, severely affecting local wine production [16]. Severe stem and branch diseases of hazelnut trees have been observed in several groves in Italy, leading to crown dieback and total tree mortality, with a significant impact on crop production [17]. *Dothiorella* panicle and shoot blight has been identified as one of the major threats to the Californian pistachio industry [18]. It also causes ulceration and wilting shoot disease in elms in Europe, severely affecting healthy tree growth [19].

The identification of fungal pathogens on the basis of morphological, physiological, and biochemical tests is not precise enough as it is mostly dependent on subtle differences in nutrients, pH, humidity, and environmental acclimatization [20,21]. Thus, polyphasic identification involving morphological characteristics and more than one gene sequence phylogenetic analysis is recommended to remove this predicament [22]. Based on morphology and molecular data, Phillips revived *Dothiorella* for species with conidia that become brown and 1-septate while they were still attached to the conidiogenous cells; sexual morphs of *Dothiorella* have pigmented, 1-septate ascospores [23,24]. The research confirmed the presence of *D. sarmentorum* (Fr.). Spore size and shape are important taxonomic features and valuable criteria for distinguishing the species [25].

The objective of this study was to identify the pathogen causing blight disease on 'Bandera Pink' in Xinjiang Uygur Autonomous Region based on morphological characterization and molecular analyses and to compare the differences in the pathogenicity of pathogenic fungi to different varieties of lavender. This study is fundamental for subsequent research on lavender leaf diseases.

2. Materials and Methods

2.1. Sample Collection and Pathogen Isolation

The leaves of symptomatic lavender plants were collected in Yining County (43°94′35.49″ N 81°54′88.12″ E) Xinjiang Uygur Autonomous Region of China in August 2023. The symptomatic leaves were delivered to the laboratory and immersed in 75% ethanol for 30 s, then thoroughly washed in sterile distilled water. Small pieces (2 mm^2) with necrotic tissue and healthy parts of the collected leaves were cut using a sterilized blade. Tissue pieces were disinfected by placing them in 3% sodium hypochlorite solution for 3 min, then they were rinsed three times in sterile distilled water and dried naturally on sterilized filter paper. These tissue pieces were incubated on potato dextrose agar (PDA) at 28 °C under 12 h/12 h photoperiod conditions. After 3–4 days, the growing fungal colonies were sub-cultured onto fresh PDA, and pure cultures were obtained by subculturing hyphal tips. After the colony to be cultured had produced conidia, the conidia were gently scraped off the colony using sterile inoculation needles and suspended in 1 mL of sterile distilled water. The suspension of conidia was coated on a PDA culture dish and incubated at 25 °C for 24 h, individual germinated conidia were transferred to fresh PDA plates under a stereomicroscope, and incubation was continued at 25 °C for 36 h for mycelial development to obtain a pure culture strain. Isolates were maintained as a spore suspension in 25% glycerol at −80 °C until ready for use in further studies. Living cultures were deposited in the Pathology Laboratory of the College of forestry and landscape architecture (XJAU).

2.2. DNA Extraction, PCR Amplification, and Sequencing

Total genomic DNA was extracted from 5-day-old mycelium grown on PDA using the CTAB method [26]. The water solution of obtained DNA was kept at −20 °C for further experiments. PCR was run using a BIO-RAD T100TM Thermal Cycler(Bio-Rad Laboratories, Inc., Hercules, CA, USA) to amplify the internal transcribed spacer (ITS) region using primers ITS1/ITS4. The nuclear ribosomal large subunit (LSU), the translation elongation factor 1-alpha (*tef1*), and the β-tubulin gene (*tub2*) were amplified using primers LROR/LR5, EF-AF/EF-BR, and BT2A/BT2B (Table 1). All PCR reactions were performed in a 30 µL reaction volume containing 1.5 µL of DNA template, 1.5 µL of each forward and reverse primer, 15 µL of Taq PCR master mix (2×, with blue dye), and 10.5 µL of double-distilled water (dd H_2O). The cycling parameters were as follows: a first step of denaturation at 95 °C for 5 min followed by 35 cycles of (i) denaturation at 95 °C for 60 s, (ii) annealing at optimal temperature (55 °C for ITS, *tef1*, and LSU and 45 °C for *tub2*) for 80 s, (iii) elongation at 72 °C for 90 s, and a final elongation step of 5 min was applied. PCR products were detected using a 1% agarose gel under 120 V stable voltage, and the electrophoresis time was 25 min. PCR bands were observed in a gel imager to determine whether they were clear and to determine the size of the target bands. PCR products

were sent to Shanghai Sangon Bioengineering Co., Ltd. (Shanghai, China) for bidirectional sequencing.

Table 1. List of primer pair sets used for PCR and sequencing.

Gene Fragment	Primer	Primer Sequence	Reference
ITS	ITS1 ITS4	TCCGTAGGTGAACCTGCGG TCCTCCGCTTATTGATATGC	White et al., 1990 [27]
LSU	LROR LR5	GTACCCGCTGAACTTAAGC ATCCTGAGGGAAACTTC	Carbone & Kohn 1999 [28]
tub2	Bt-2a Bt-2b	GGTAACCAAATCGGTGCTGCTTTC ACCCTCAGTGTAGTGACCCTTGGC	Glass & Donaldson 1995 [29]
tef1-α	tef1-728F tef1-986R	CATCGAGAAGTTCGAGAAGG TACTTGAAGGAACCCTTACC	Rehner et al. 2005 [30]

2.3. Phylogenetic Analysis

The resulting sequences were edited and assembled by the SeqMan program within the DNASTAR software package (DNASTAR, Madison, WI, USA) and deposited in GenBank (Table 2). For molecular analysis, the ITS, LSU, *tef1*, and *tub2* sequences of the reference isolates of the *Dothiorella* species were retrieved from the NCBI database (Table 2) and aligned using MEGA 6 software. The phylogenetic analyses of the combined loci were performed using Maximum Likelihood (ML) implemented on the CIPRES Science Gateway portal using RAxML-HPC BlackBox 8.2.10, employing a GTRGAMMA substitution model with 1000 bootstrap replicates.

Table 2. Taxon names, strain or specimen numbers, and corresponding GenBank accession numbers of the taxa used for the phylogenetic studies. The newly generated sequences are indicated in bold.

Taxon Names	Strain/Specimen Numbers	GenBank Accession Numbers			
		ITS	**LSU**	***tef1-α***	***tub2***
Diplodia mutila	CBS 112553	AY259093	AY928049	AY573219	DQ458850
Diplodia mutila	CBS 112875	AY343484	–	AY343370	MT592509
Diplodia mutila	GZCC 23-0578	OR052057	OR020607	OR030454	OR030472
Diplodia neojuniperi	CBS 138652	KM006431	–	KM006462	MT592516
Diplodia sapinea	CBS 393.84	DQ458895	DQ377893	DQ458880	DQ458863
Diplodia scrobiculata	CBS 118110	AY253292	KF766326	AY624253	AY624258
Diplodia seriata	CBS 112555	AY259094	AY928050	AY573220	DQ458856
Diplodia seriata	CBS 112661	MT587378	–	MT592084	MT592541
Diplodia seriata	GZCC 23-0579	OR052058	OR052041	OR030455	OR030473
Diplodia subglobosa	CBS 124133	GQ923856	–	GQ923824	MT592576
Dothiorella acacicola	CBS 141295	KX228269	KX228320	KX228376	–
Dothiorella acericola	KUMCC 18-0137	MK359449	–	MK361182	–
Dothiorella albiziae	MFLUCC 22-0057	ON751762	ON751764	ON799588	ON799590
Dothiorella alpina	CGMCC 3.18001	KX499645	–	KX499651	–
Dothiorella baihuashanensis	CFCC 58549	–	–	OQ692933	OQ692927
Dothiorella baihuashanensis	CFCC 58788	–	–	OQ692934	OQ692928
Dothiorella brevicollis	CBS 130411	JQ239403	JQ239416	JQ239390	JQ239371
Dothiorella camelliae	CGMCC 3.24158	OQ190531	–	OQ241464	OQ275064
Dothiorella capri-amissi	CBS 121763	EU101323	KX464301	EU101368	KX464850
Dothiorella casuarinae	CBS 120688	DQ846773	MH874647	DQ875331	DQ875340
Dothiorella citricola	CBS 124728	EU673322	–	EU673289	KX464852
Dothiorella citrimurcotticola	CGMCC 3.20394	MW880661	–	MW884164	MW884193
Dothiorella citrimurcotticola	CGMCC 3.20395	MW880662	–	MW884165	MW884194
Dothiorella diospyricola	CBS 145972	MT587398	–	MT592110	MT592581
Dothiorella dulcispinae	CBS 130413	JQ239400	JQ239413	JQ239387	JQ239373
Dothiorella dulcispinae	CMW 36462	JQ239402	JQ239415	JQ239389	JQ239375
Dothiorella eriobotryae	CBS 140852	KT240287	–	KT240262	MT592582

Table 2. *Cont.*

Taxon Names	Strain/Specimen Numbers	GenBank Accession Numbers			
		ITS	**LSU**	***tef1-α***	***tub2***
Dothiorella heterophyllae	CMW46458	MN103794	–	MH548348	MH548324
Dothiorella iranica	CBS 124722	KC898231	–	KC898214	KX464856
Dothiorella koae	CMW 48017	MH447652	–	MH548338	MH548327
Dothiorella lampangensis	MFLUCC 18-0232	MK347758	–	MK340869	MK412874
Dothiorella longicollis	CBS 122068	EU144054	MH874718	EU144069	KF766130
Dothiorella magnoliae	CFCC 51563	KY111247	–	KY213686	–
Dothiorella mangifericola	IRAN 1584C	MT587407	–	MT592119	–
Dothiorella moneti	MUCC 505	EF591920	EF591937	EF591971	EF591954
Dothiorella obovata	MFLUCC 22-0058	ON751763	ON751765	ON799589	ON799591
Dothiorella ovata	MFLUCC 23-0035	OR052059	OR020691	OR030456	OR030474
Dothiorella ovata	MFLUCC 23-0036	OR052060	OR052042	OR030457	OR030475
Dothiorella plurivora	CBS 124724	KC898225	–	KC898208	KX464874
Dothiorella pretoriensis	CBS 130404	JQ239405	JQ239418	JQ239392	JQ239376
Dothiorella prunicola	CBS 124723	EU673313	EU673232	EU673280	EU673100
Dothiorella rosacearum	MFLUCC 23-0038	OR052061	OR052043	OR030458	OR030476
Dothiorella rosacearum	MFLUCC 23-0037	OR052062	OR052044	OR030459	OR030477
Dothiorella santali	WAC 13155	EF591924	EF591941	EF591975	EF591958
Dothiorella sarmentorum	CBS 115038	AY573206	DQ377860	AY573223	EU673101
Dothiorella sarmentorum	IMI 63581b	AY573212	AY928052	AY573235	–
Dothiorella sarmentorum	**XJAU XYC-1**	**OR947929**	**PP335474**	**PP335515**	**PP335512**
Dothiorella sarmentorum	**XJAU XYC-2**	**OR947930**	**PP335475**	**PP335516**	**PP335513**
Dothiorella sarmentorum	**XJAU XYC-3**	**OR947931**	**PP335476**	**PP335517**	**PP335514**
Dothiorella septata	MFLUCC 23-0039	OR020942	OR020695	OR030462	OR030480
Dothiorella septata	GZCC 23-0583	OR019776	OR052047	OR030463	OR030481
Dothiorella septata	GZCC 23-0584	OR019803	OR052048	OR030464	OR030482
Dothiorella striata	CBS 124731	EU673321	–	EU673288	EU673143
Dothiorella striata	CBS 124730	EU673320	EU673240	EU673287	EU673142
Dothiorella tectonae	MFLUCC 18-0382	KM396899	–	KM409637	KM510357
Dothiorella thailandica	MFLUCC 11-0438	JX646796	JX646813	JX646861	JX646844
Dothiorella thripsita	CBS 125445	FJ824738	–	KJ573639	KJ577550
Dothiorella ulmacea	CBS 138855	KR611881	KR611899	KR611910	KR611909
Dothiorella ulmacea	CBS 140005	KR611882	–	KR857697	MT592607
Dothiorella uruguayensis	CBS 124908	EU080923	MH874932	EU863180	KX464886
Dothiorella vinea-gemmae	DAR 81012	KJ573644	–	KJ573641	KJ577552
Dothiorella viticola	CBS 117009	AY905554	MH874565	AY905559	EU673104
Dothiorella yunnana	CGMCC 3.18000	KX499644	–	KX499650	–
Dothiorella zanthoxyli	CGMCC 3.24159	OQ190536	–	OQ241468	OQ275069

2.4. Morphology and Culture Characteristics

To study the morphological characteristics of pure isolates, 5 mm (diameter) mycelial plugs from the edge of 5-day-old cultures were transferred to fresh PDA. The plates were incubated at 25 °C in a 12 h/12 h photoperiod. Morphological observation was conducted mainly based on the conidiomata naturally formed on the host tissues, including size, shape, and color. Macromorphological photographs were obtained using a Leica stereomicroscope (M205, Leica, Wetzlar, Germany). Micromorphological observations including the size and shape of conidiophores and conidia were performed using a Nikon Eclipse 80i microscope (Nikon, Tokyo, Japan). Twenty conidiomata were sectioned using a sterile scalpel, and then the lengths and widths of 50 randomly chosen conidia were measured. Colony morphology and growth rates were recorded [24].

2.5. Pathogenicity Test

The lavenders used in the experiment were all from the experimental base of the College of Agriculture, Xinjiang Agricultural University. The 'Bandera Pink' variety, belonging to *Lavandula stoechas*, was used to test Koch's hypothesis; the 'Blue Spear', 'Ellagance Sky',

'Avignon Early Blue', 'Taikonglan', and 'Faguolan' varieties belonging to *L. angustifolia*; the Spanish Eyes variety belonging to *L. multifida*; and the 'Bandera Pink' variety belonging to *L. stoechas* were the different varieties used for the pathogenicity difference test.

Pathogenicity assays were performed on the leaves of lavender seedlings. The strain XJAU XYC-1 was prepared into a spore suspension with a concentration of 1×10^5 cfu/mL for use (the spore concentration was determined using a blood cell counting plate). The spore suspension was sprayed evenly on healthy lavender plants, spraying about 30 mL per plant. Then, a black plastic bag was used for moisturizing for 36 h, and sterile water treatment was sprayed as a control. These seedlings were raised in a growth chamber with a 12 h/12 h photoperiod at a 28 ± 2 °C temperature regime. After 36 h, the black silk plastic bag was removed and the disease incidence was monitored and recorded using the incidence area proportion counting method, which was used to calculate the ratio of the affected area to the total area every 2 days until the 15th day. Furthermore, to confirm Koch's postulates, re-isolation was performed from lesions and identified based on morphological and molecular characteristics as described above.

2.6. Statistical Analysis

The means and standard errors of the data were calculated using Microsoft Excel formulas. Analysis of variance was used to detect differences among treatments using IBM SPSS Statistics 22.0 and Origin 9.5.

3. Results

3.1. Isolation of the Pathogen

A total of 19 strains of the fungal genus *Dothiorella* were obtained with similar colony morphology. Sequences of ITS, LSU, *tef1*, and *tub2* were compared and considered to be consistent among the 19 obtained strains. Three strains (XJAU XYC-1, XJAU XYC-2, and XJAU XYC-3) were then randomly selected for the following phylogenetic analysis for species identification.

3.2. Phylogenetic Analysis

The combined dataset of ITS, LSU, *tef1*, and *tub2* loci consisted of 45 strains, with *Diplodia subglobosa* (CBS 124133) as the outgroup taxon. The final alignment comprised 3152 characters including 512 characters in ITS, 801 characters in LSU, 242 characters in *tef1*, and 416 characters in *tub2*. The final ML optimization likelihood value of the best RAxML tree was −8740.98. The topology of our phylogenetic tree is nearly identical to previous publications. Three isolates from the present study formed a clade with CBS 115038 and IMI 63581b named *Dothiorella sarmentorum* (Figure 1).

3.3. Morphological Description of the Pathogen Dothiorella sarmentorum

On the PDA medium, the mycelium formed filamentous colonies. Initially, it was white (Figure 2A), subsequently forming small white colonies, within 4 days. Later, the mycelium turned leaden appressed and became smoke-grey to olivaceous grey at the surface, starting from the center (Figure 2B,C). The mycelium was immersed, consisting of septate, branched, brown, finely verruculose hyphae. Conidiomata that readily formed from the middle of colonies within 20 days were pycnidial, solitary, globose, dark brown to black, immersed in the medium, thick-walled, and up to 400 µm wide (Figure 2D). Conidiophores were hyaline, smooth, rarely branched, and aseptate (Figure 2G,H). The conidiogenous layer with developing conidia was thick and composed of dark brown 5–6-cell layers. Conidiogenous cells were cylindrical to fusiform, hyaline, thin-walled, smooth, and giving rise to periclinal thickenings (Figure 2E). Dark, oval to ovoid, often pigmented ellipsoid conidia were 18.9–24.9 × 8.8–12.1 µm (x = 22.2 × 8.7 µm, n = 60), hyaline, later brown, thick-walled, 1-septate prior to release from conidiogenous cells, and occasionally slightly constricted at the septum with a broadly rounded apex and truncate base (Figure 2F,K).

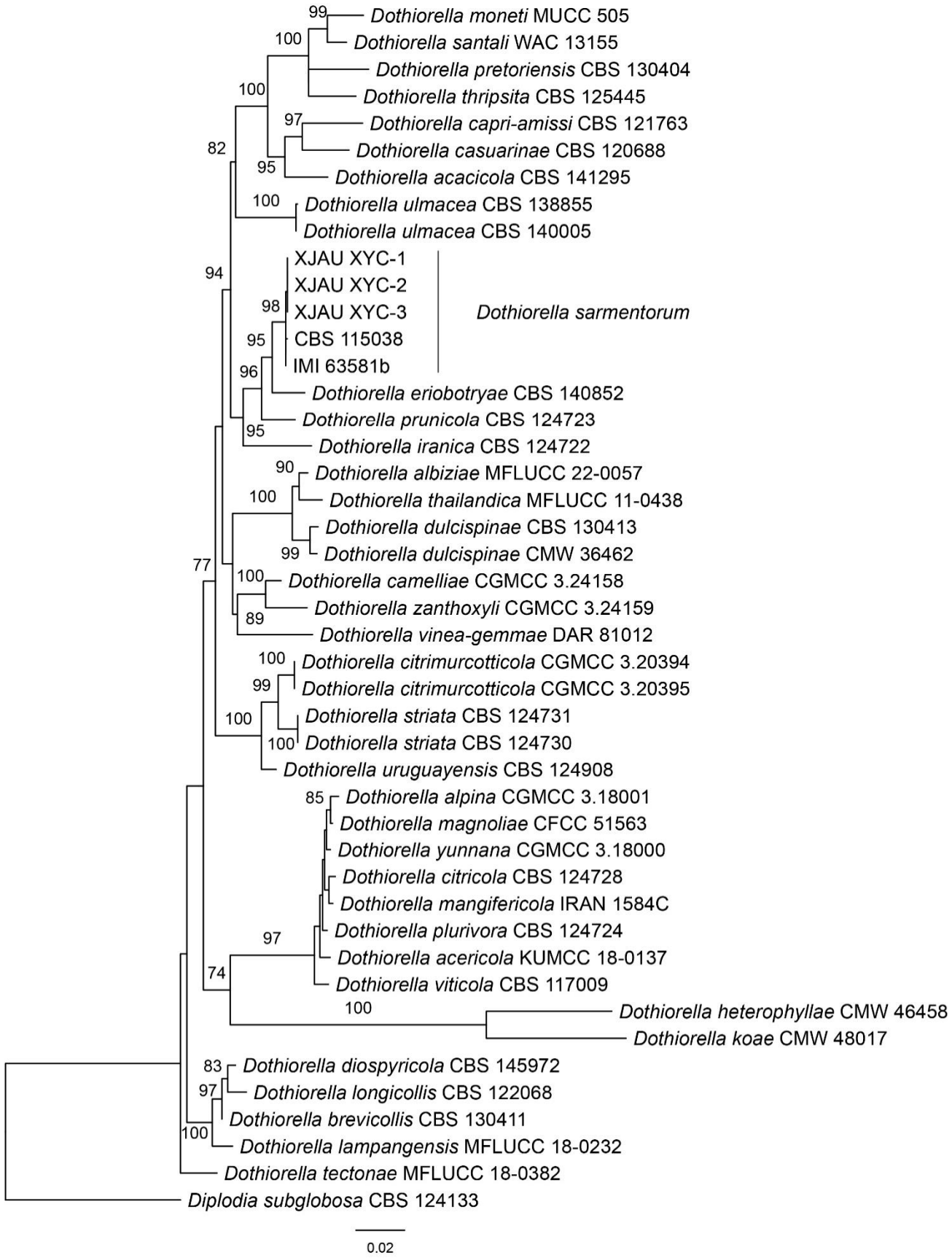

Figure 1. Phylogenetic tree of *Dothiorella* generated from the maximum likelihood (ML) analysis based on the combined loci of ITS, LSU, *tef1*-α, and *tub2* sequences.

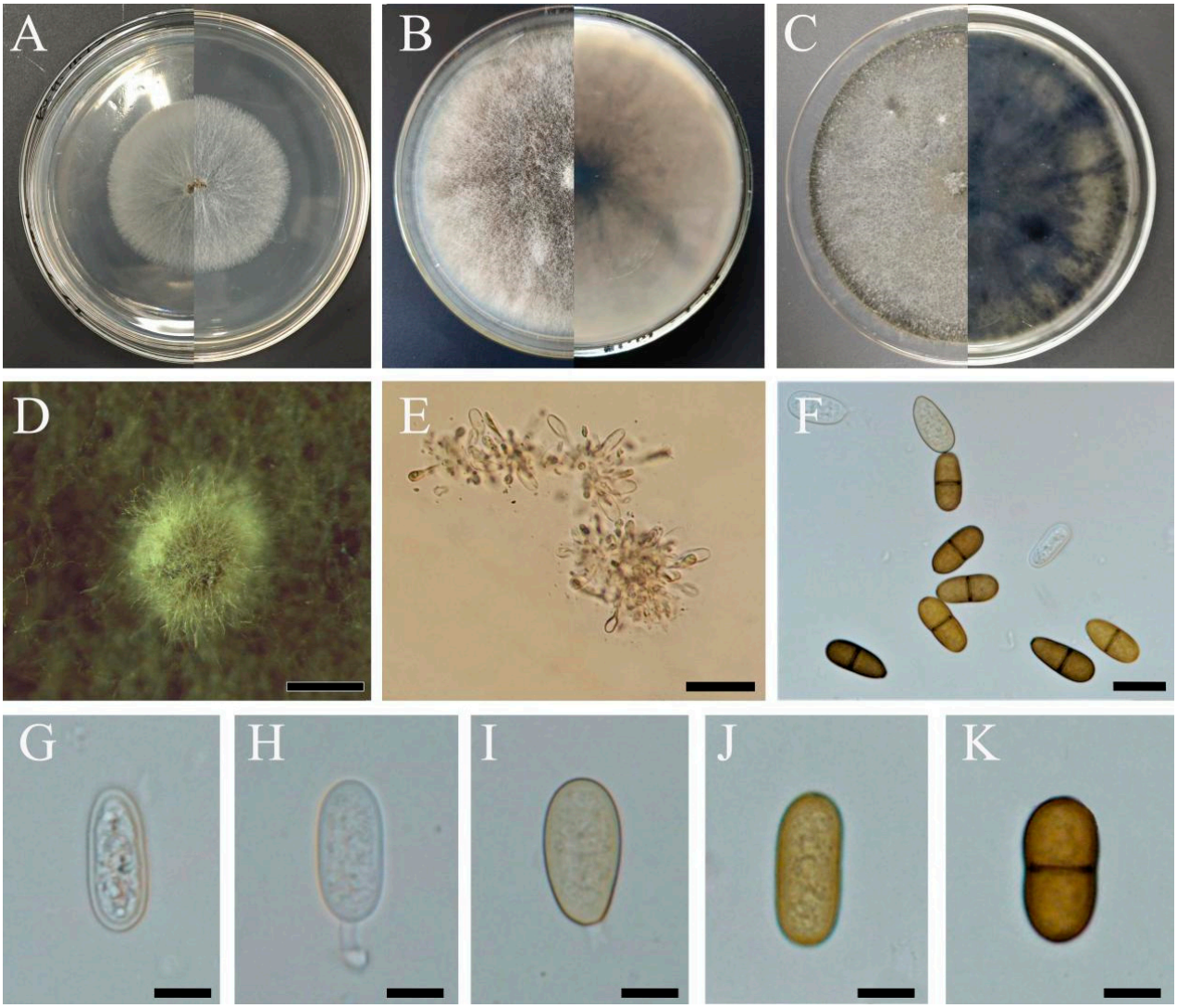

Figure 2. Morphological characteristics of *Dothiorella sarmentorum* (XIAU XYC-1). (**A**–**C**): colonies of white, later olivaceous grey mycelia after 2 (**A**), 6 (**B**), and 10 days (**C**) of incubation on PDA; (**D**): conidiomata; (**E**): conidiogenous cells; (**F**,**K**): dark, ovoid, diplodia-like conidia. (**G**–**J**): immature conidia. Scale bars: (**D**) = 2 mm, (**E**) = 50 μm, (**F**) = 20 μm, (**G**–**K**) = 10 μm.

3.4. Pathogenicity

Seedlings of 'Bandera Pink' inoculated with *Dothiorella sarmentorum* (XJAU XYC-1) developed symptoms that were the same as those observed in the field. The lavender leaves turned black and curled, and disease spots spread through the stems 4 d after inoculation (Figure 3D–F). The whole lavender plant was curled, withered, and necrotic, and the lavender roots were black 10 d after inoculation (Figure 3G–I,K,M). The negative control was sprayed with sterile water on healthy lavender plants and did not develop disease symptoms (Figure 3A–C,J,L). The fungus was reisolated from symptomatic leaves and identified as *D. sarmentorum* based on morphological characteristics and DNA sequence data, thus fulfilling Koch's postulates.

Figure 3. Leaf disease symptoms observed in lavender seedlings after *Dothiorella sarmentorum* fungal inoculation. (**A**–**C**): negative control—leaves sprayed with sterile water. (**D**–**F**): *Dothiorella sarmentorum* conidial suspension was spray-inoculated onto seedlings of lavender; (**G**–**I**): symptoms of disease 4 d after inoculation; (**G**–**I**): symptoms of disease 10 d after inoculation. (**J**): negative control—the whole plant is healthy; (**K**): treatment—the whole plant has withered; (**L**): negative control—the roots of plants are brown; (**M**): treatment: the roots of plants are black.

Dothiorella sarmentorum showed different degrees of pathogenicity on 'Blue Spear', 'Ellagance Sky', 'Spanish Eyes', 'Bandera Pink', 'Avignon Early Blue', 'Taikonglan', and 'Faguolan' seedlings (Figures 4 and 5). The average disease incidence that developed on inoculated 'Blue Spear', 'Ellagance Sky', 'Spanish Eyes', 'Bandera Pink', 'Avignon Early' Blue', 'Taikonglan', and 'Faguolan' seedlings were 38.96%, 41.46%, 16.38%, 31.78%, 11.62%, 7.99%, and 10.66%, respectively, 15 days after inoculation (Figure 4).

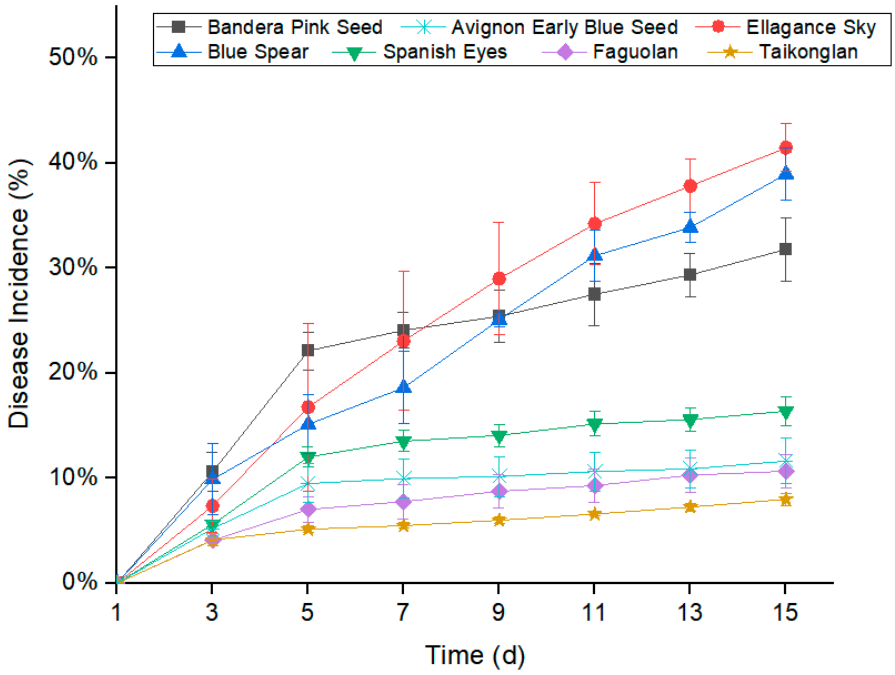

Figure 4. Disease incidence observed in different varieties of lavender after *Dothiorella sarmentorum* inoculation. Analysis of variance of disease incidence that developed on Blue Spear, Ellagance Sky, Spanish Eyes, Bandera Pink, Avignon Early Blue, Taikonglan, and Faguolan seedlings following inoculation with *Dothiorella sarmentorum*. Values shown are means ± the standard errors.

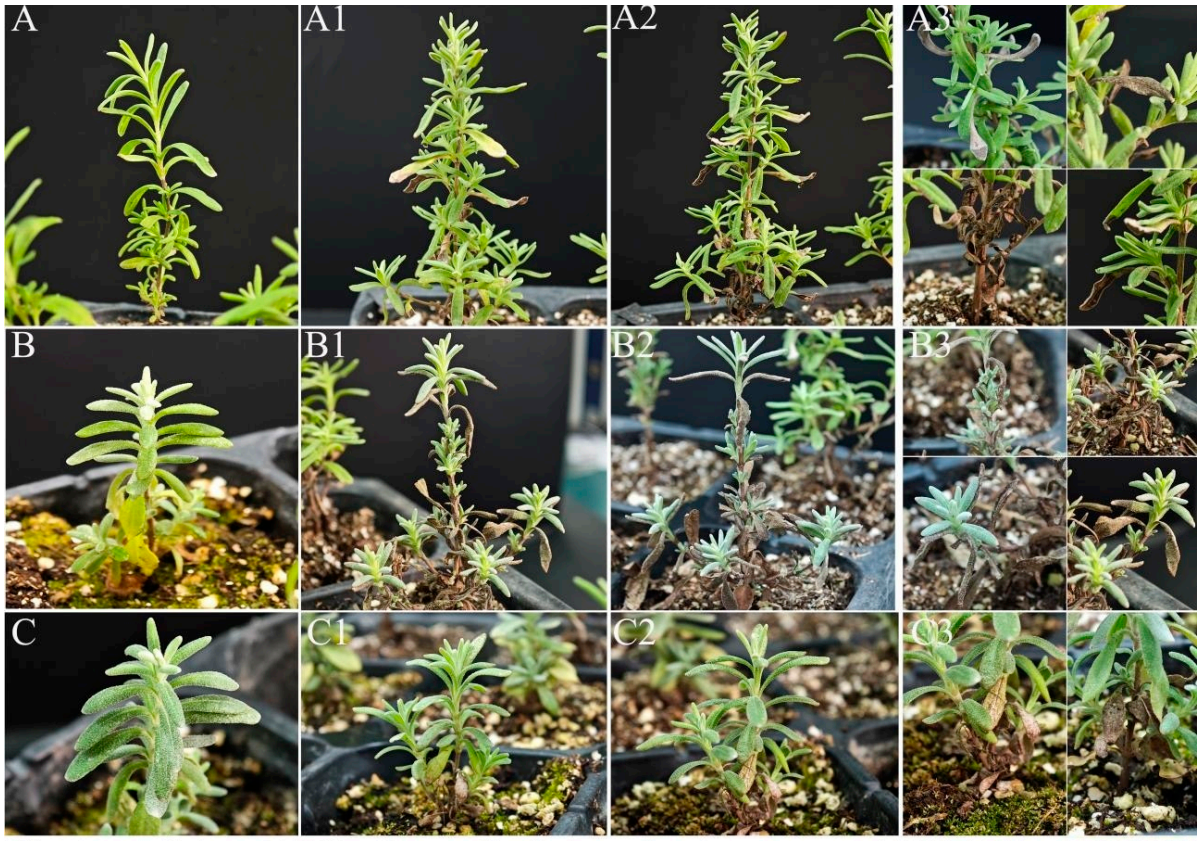

Figure 5. *Cont.*

Figure 5. Leaf disease symptoms observed in different varieties of lavender after *Dothiorella sarmentorum* inoculation. Leaf disease symptoms on (**A**–**A3**) Bandera Pink; (**B**–**B3**) Ellagance Sky; (**C**–**C3**) Blue Spear; (**D**–**D3**) Spanish Eyes; (**E**–**E3**) Faguolan; (**F**–**F3**) Taikonglan; and (**G**–**G3**) Avignon Early Blue lavender seedlings. (**A**–**G**) the negative control—leaves sprayed with sterile water (control—CK); the *Dothiorella sarmentorum* spore suspension was spray-inoculated onto seedlings of lavender. (**A1**–**G1**): 3 d after inoculation; (**A2**–**G2**): the overall image of 15 d after inoculation; (**A3**–**G3**): the partial image of 15 d after inoculation.

4. Discussion

According to morphological and molecular analyses as well as pathogenicity tests, we demonstrated that the dieback symptoms observed on lavender (*Lavandula stoechas*) plants in China are due to *D. sarmentorum*. To our knowledge, this is the first report of *D. sarmentorum* as a new pathogen of *L. stoechas*. The pathogenicity test confirmed that *D. sarmentorum* is a pathogenic fungus that can also infect *L. angustifolia* and *L. multifida*. There are variations in the pathogenicity of different varieties of lavender.

Dothiorella sarmentorum has been recorded in several countries around the world, and it can not only cause tree canker disease as a pathogenic bacterium but also parasitize 66 plant tissues such as Salicaceae and Rosaceae as endophytic fungi [24]. *D. sarmentorum* is a cosmopolitan species and has been isolated from 34 different host species including *Malus*, *Menispermum*, *Prunus*, *Pyrus*, and *Ulmus* genera. Molecular studies have described *D. sarmentorum* in 17 woody hosts [22,31]. However, there are relatively few reports on the diseases that *D. sarmentorum* causes in herbaceous plants. This study further confirms that lavender is a new host of *D. sarmentorum*, which is of great significance for understanding the source of this pathogen in nature. Considering that the lavender leaf spot disease caused by *D. sarmentorum* has the characteristics of a large lesion area, strong destructive power, and rapid development, it has the risk of widespread transmission and epidemics. Therefore, it is necessary to strengthen the knowledge about the ecology, epidemiology,

biogeography, and infection biology of this pathogen that represents a serious threat to the lavender industry.

5. Conclusions

Dothiorella sarmentorum is an emerging pathogen causing *L. angustifolia* leaf spot in Yining County, Xinjiang, China. The pathogenicity test confirmed that *D. sarmentorum* is a pathogenic fungus that can also infect *L. stoechas* and *L. pinnata*. The data obtained in this study should provide a theoretical basis for monitoring and preventing this disease. The potential impact of *D. sarmentorum* on lavender production in this area of China warrants further investigation to determine potential disease management strategies.

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