

## Supplementary information

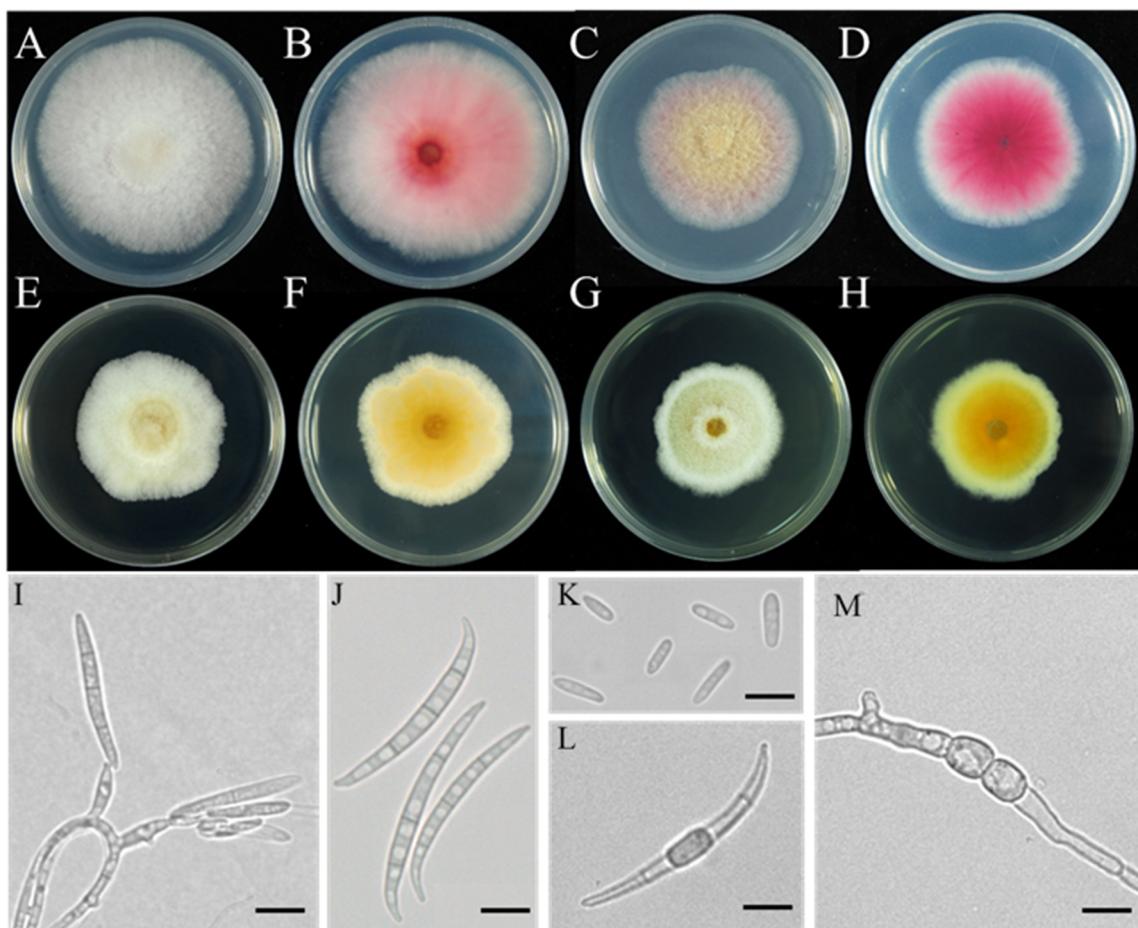


Figure S1. Effects of different culture media on phytopathogen-like endophytic *Fusarium* sp. isolates in this study. For colony morphology: Colony morphology of *Fusarium* sp. isolates cultured on potato sucrose agar (PSA) with 12 h light and dark (A and B), Colony morphology of *Fusarium* sp. isolates cultured on PSA in the dark (C and D), Colony morphology of *Fusarium* sp. isolates cultured on potato dextrose agar (PDA) with 12 h light and dark (E and F), Colony morphology of *Fusarium* sp. isolates cultured on PDA in the dark (G and H); I–M: Conidial morphology of *Fusarium* sp. isolates; I: Short and plump monopodial conidiophore; J: Macroconidia; K: Microconidia; L: Chlamydospore; M: Chlamydospore. Bar, 10  $\mu$ m.

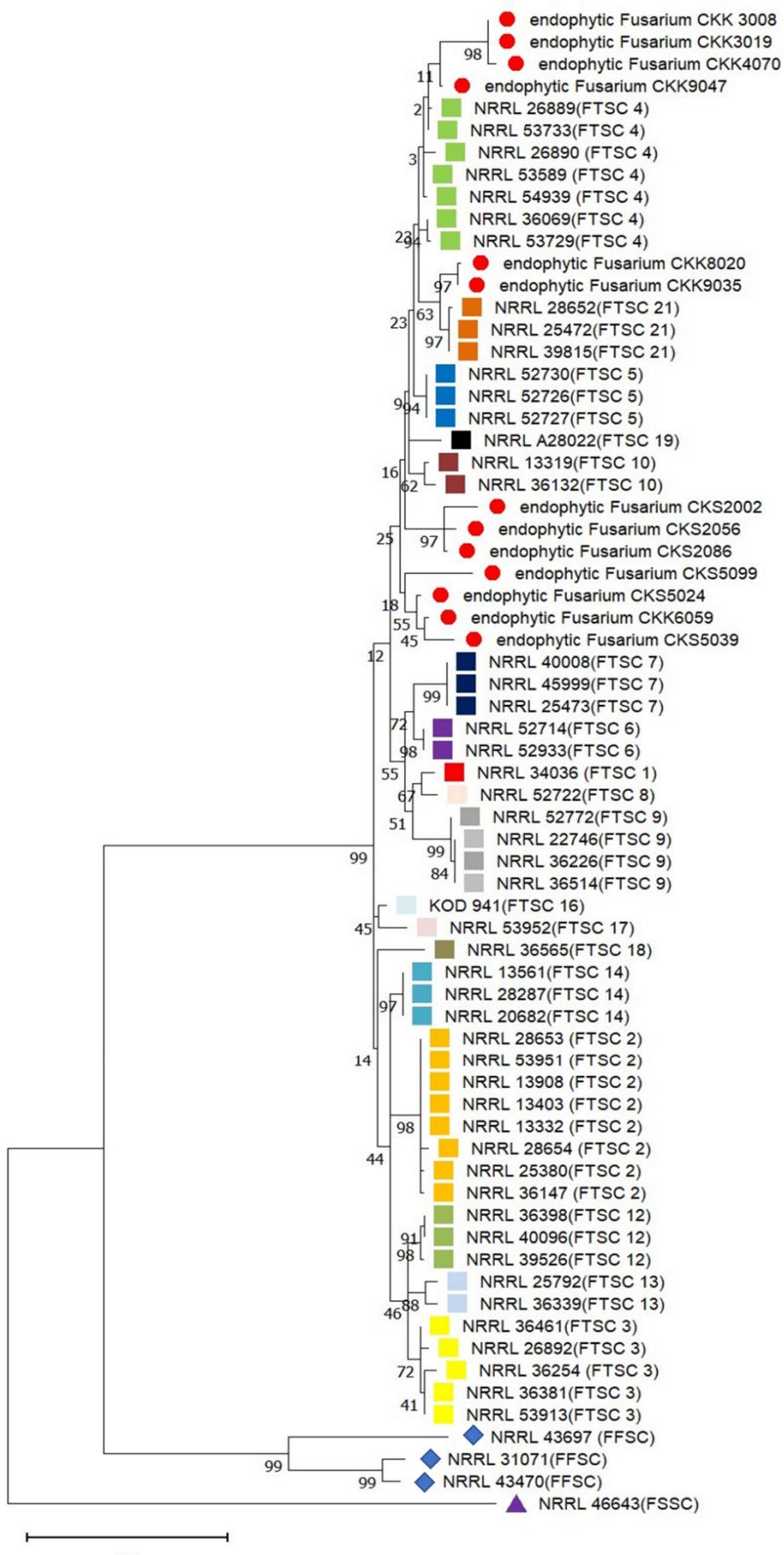


Figure S2. A phylogenetic tree was constructed using the maximum likelihood (ML) method, based on combined sequences of the internal transcribed spacer (ITS) sequence and translation elongation factor 1 alpha (EF-1 $\alpha$ ) gene of endophytic *Fusarium* isolates from *Cirsium kawakamii* in this study (●), related *Fusarium tricinctum* species complex (FTSC) isolates (▨), and *Fusarium fujikuroi* species complex (FFSC) isolates (◆) available at NCBI. The tree was rooted with *Fusarium solani* strain NRRL 46643 (▲) as the outgroup, and bootstrap values were determined using 1000 replicates. The scale bar indicates the nucleotide changes.

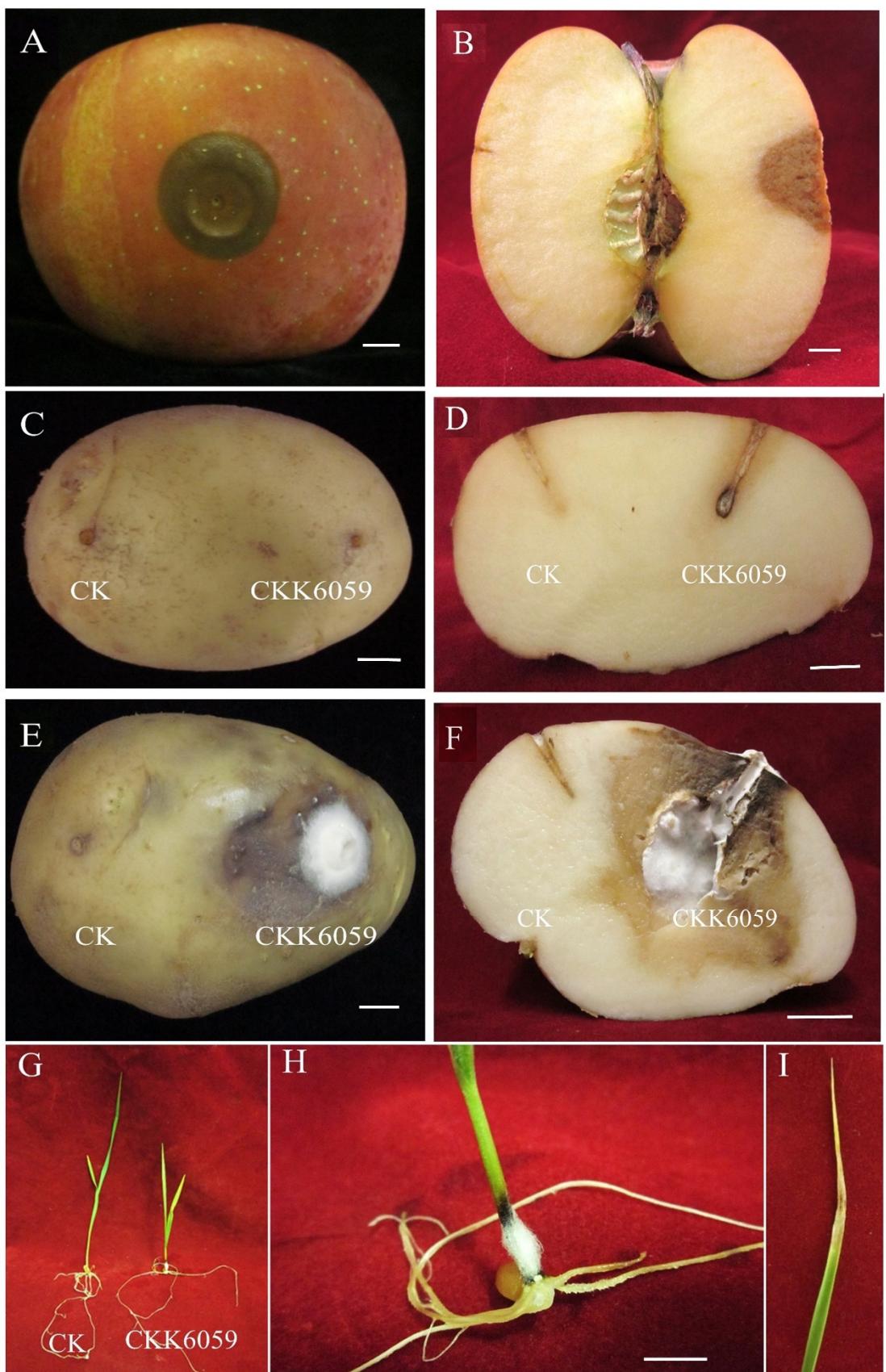


Figure S3. Symptoms of potato, apple, and wheat inoculated with *Fusarium* sp. CKK6059 spore suspension ( $10^6$  conidia/mL). A, B: Symptoms on apple ‘Fuji’; C, D: Potato inoculated with CKK6059, after 28 d of incubation at 4 °C; E, F: Potato inoculated with CKK6059, after 28 d of incubation at 20 °C. For wheat: Growth inhibition (G), Necrosis and root-rot of wheat (H), and Leaf blight of wheat (I). Control (CK): inoculation with sterile soil extract broth. (white bar = 1 cm)

Table S1. Endophytic *Fusarium tricinctum* species complex (FTSC)-like isolates collected from *Cirsium kawakamii* in this study

Collection area <sup>1</sup>	Collection site	Coordinates	Elevation (m)	Collection date	Fungal isolates
Tatachia	1	23°31'15.2"N 120°53'41.7"E	2,474	2013/10/11	CKK 3008、 CKK 3019、 CKK 4070
	2	23°28'29.1"N, 120°52'21.1"E	2,462	2013/10/11	CKK 6059
	3	23°28'34.4"N 120°51'55.8"E	2,461	2013/10/11	CKK 8020、 CKK 9035、 CKK 9047
Hehuanjian	1	24°06'51.4"N 121°13'8.6"E	2,776	2013/09/27	CKS 2002、 CKS 2056、 CKK 2086
	2	24°08'23.1"N 121°17'13.7"E	3,140	2013/09/27	CKS 5024、 CKS 5039、 CKK 5099

<sup>1</sup> The collection area of *Cirsium kawakamii* used for isolating endophytic fungi for this study.

Table S2. GenBank strain numbers for phylogenetic tree analysis of the internal transcribed spacer (ITS) and translation elongation factor subunit alpha (EF-1 $\alpha$ ) sequences in this study

Complex group <sup>a</sup>	Species	Strain number	Accession <sup>b</sup>	
			ITS	EF1- $\alpha$
--	<i>Fusarium</i> sp.	CKK 3008	OR540686	KT273977.1
--	<i>Fusarium</i> sp.	CKK 3019	OR540687	KT273978.1
--	<i>Fusarium</i> sp.	CKK 4070	OR540688	KT273979.1
--	<i>Fusarium</i> sp.	CKK 6059	OR540689	KT273976.1
--	<i>Fusarium</i> sp.	CKK 8020	OR540690	KT273983.1
--	<i>Fusarium</i> sp.	CKK 9035	OR540691	KT273984.1
--	<i>Fusarium</i> sp.	CKK 9047	OR540692	KT273985.1
--	<i>Fusarium</i> sp.	CKS 2002	OR540693	KT273986.1
--	<i>Fusarium</i> sp.	CKS 2056	OR540694	KT273987.1
--	<i>Fusarium</i> sp.	CKS 2086	OR540695	KT273988.1
--	<i>Fusarium</i> sp.	CKS 5024	OR540696	KT273989.1
--	<i>Fusarium</i> sp.	CKS 5039	OR540697	KT273990.1
--	<i>Fusarium</i> sp.	CKS 5099	OR540698	KT273991.1
FTSC 1	<i>F. gamsii</i>	NRRL 34036	GQ505451.1	OL772879.1
FTSC 2	<i>F. acuminatum</i>	NRRL 13332	OL832225.1	OL772797.1
FTSC 2	<i>F. acuminatum</i>	NRRL 13403	OL832175.1	OL772747.1
FTSC 2	<i>F. acuminatum</i>	NRRL 13908	OL832226.1	OL772798.1
FTSC 2	<i>F. acuminatum</i>	NRRL 25380	OL832242.1	OL772814.1
FTSC 2	<i>F. acuminatum</i>	NRRL 28653	OL832231.1	OL772803.1
FTSC 2	<i>F. acuminatum</i>	NRRL 28654	OL832249.1	OL772821.1
FTSC 2	<i>F. acuminatum</i>	NRRL 36147	OL832308.1	OL772880.1
FTSC 2	<i>F. acuminatum</i>	NRRL 53951	OL832232.1	OL772804.1
FTSC 3	<i>F. tricinctum</i>	NRRL 26892	OL832254.1	OL772826.1
FTSC 3	<i>F. tricinctum</i>	NRRL 36254	OL832262.1	OL772834.1
FTSC 3	<i>F. tricinctum</i>	NRRL 36381	OL832258.1	OL772830.1
FTSC 3	<i>F. tricinctum</i>	NRRL 36461	OL832255.1	OL772827.1
FTSC 3	<i>F. tricinctum</i>	NRRL 53913	OL832259.1	OL772831.1
FTSC 4	<i>F. avenaceum</i>	NRRL 26889	OL832176.1	OL772748.1
FTSC 4	<i>F. avenaceum</i>	NRRL 36069	OL832186.1	OL772758.1
FTSC 4	<i>F. avenaceum</i>	NRRL 36374	OL832183.1	OL772755.1

Complex group <sup>a</sup>	Species	Strain number	Accession <sup>b</sup>	
			ITS	EF1- $\alpha$
FTSC 4	<i>F. avenaceum</i>	NRRL 53589	OL832187.1	OL772759.1
FTSC 4	<i>F. avenaceum</i>	NRRL 53729	OL832188.1	OL772760.1
FTSC 4	<i>F. avenaceum</i>	NRRL 53733	OL832184.1	OL772756.1
FTSC 4	<i>F. avenaceum</i>	NRRL 26890	OL832177.1	OL772749.1
FTSC 4	<i>F. avenaceum</i>	NRRL 54939	OL832320.1	OL772892.1
FTSC 5	<i>Fusarium</i> sp.	NRRL 52726	OL832312.1	OL772884.1
FTSC 5	<i>Fusarium</i> sp.	NRRL 52727	OL832313.1	OL772885.1
FTSC 5	<i>Fusarium</i> sp.	NRRL 52730	OL832314.1	OL772886.1
FTSC 6	<i>F. iranicum</i>	NRRL 52714	OL832311.1	OL772883.1
FTSC 6	<i>F. iranicum</i>	NRRL 52933	OL832317.1	OL772889.1
FTSC 7	<i>F. flocciferum</i>	NRRL 25473	OL832306.1	OL772878.1
FTSC 7	<i>F. flocciferum</i>	NRRL 40008	OL832325.1	OL772897.1
FTSC 7	<i>F. flocciferum</i>	NRRL 45999	OL832310.1	OL772882.1
FTSC 8	<i>Fusarium</i> sp.	NRRL 52722	OL832318.1	JF740804.1
FTSC 9	<i>F. torulosum</i>	NRRL 22746	OL832295.1	OL772867.1
FTSC 9	<i>F. torulosum</i>	NRRL 36514	OL832296.1	OL772868.1
FTSC 9	<i>F. torulosum</i>	NRRL 52772	OL832315.1	MH582397.1
FTSC 9	<i>F. torulosum</i>	NRRL 36226	OL832178.1	OL772750.1
FTSC 10	<i>Fusarium</i> sp.	NRRL 13319	OL832222.1	OL772794.1
FTSC 10	<i>Fusarium</i> sp.	NRRL 36132	OL832217.1	OL772789.1
FTSC 12	<i>Fusarium</i> sp.	NRRL 36398	OL832270.1	OL772842.1
FTSC 12	<i>Fusarium</i> sp.	NRRL 39526	OL832264.1	OL772836.1
FTSC 12	<i>Fusarium</i> sp.	NRRL 40096	OL832267.1	OL772839.1
FTSC 13	<i>F. reticulatum</i>	NRRL 36339	OL832280.1	OL772852.1
FTSC 13	<i>F. reticulatum</i>	NRRL 25792	OL832274.1	OL772846.1
FTSC 14	<i>F. negundinis</i>	NRRL 13561	OL832250.1	OL772822.1
FTSC 14	<i>F. negundinis</i>	NRRL 20682	OL832181.1	OL772753.1
FTSC 14	<i>F. negundinis</i>	NRRL 28287	OL832182.1	OL772754.1
FTSC 16	<i>F. sinensis</i>	KOD 941	OL832223.1	OL772795.1
FTSC 17	<i>Fusarium</i> sp.	NRRL 53952	OL832281.1	OL772853.1
FTSC 18	<i>Fusarium</i> sp.	NRRL 36565	OL832304.1	OL772876.1
FTSC 19	<i>Fusarium</i> sp.	NRRL A28022	OL832206.1	OL772778.1
FTSC 21	<i>Fusarium</i> sp.	NRRL 25472	OL832207.1	OL772779.1

Complex group <sup>a</sup>	Species	Strain number	Accession <sup>b</sup>	
			ITS	EF1- $\alpha$
FTSC 21	<i>Fusarium</i> sp.	NRRL 28652	OL832209.1	OL772781.1
FTSC 21	<i>Fusarium</i> sp.	NRRL 39815	OL832214.1	OL772786.1
FFSC	<i>F. proliferatum</i>	NRRL 31071	AF291061.1	AF291058.1
FFSC	<i>F. fujikuroi</i>	NRRL 43470	DQ790538.1	DQ790494.1
FFSC	<i>F. verticillioides</i>	NRRL 43697	EF453174.1	EF453022.1
FSSC	<i>F. solani</i>	NRRL 46643	GU250667.1	GU250544.1
FSSC	<i>F. falciforme</i>	NRRL 43441	DQ790522.1	DQ790478.1
FOSC	<i>F. oxysporum</i>	NRRL 43542	DQ790553.1	DQ790509.1

<sup>a</sup> FTSC: *Fusarium tricinctum* species complex; FFSC: *Fusarium fujikuroi* species complex; FSSC: *Fusarium solani* species complex; FOSC: *Fusarium oxysporum* species complex.

<sup>b</sup> *Fusarium* internal transcribed spacer (ITS) and translation elongation factor 1 alpha (EF-1 $\alpha$ ) sequences accession in GenBank.

Table S3. Morphological characteristics of the endophytic *Fusarium tricinctum* species complex (FTSC)-like isolates collected from *Cirsium kawakamii* in this study

Spore	Shape	Media	Size(μm)		Characters on PSA
			Length (mean)	Width (mean)	
Chlamydospore	Globose to subglobose	Soil broth <sup>1</sup>	04.3 – 14.8 (7.8)	0.4 – 3.9 (6.1)	Aerial mycelium abundant and cottony above the agar surface.
Macroconidia	Sickle, slight curved, 1-5 septates (most 1 or 3 septate) hooked apical cell and foot-shaped basal cell	SNA <sup>2</sup>	18.7 – 72.5 (35.8)	2.1 – 4.8 (3.7)	Produces red pigments. Rare orange sporodochial conidial masses observed.
Microconidia	Fusiform, nonseptate	SNA	06.5 – 16.7 (12.0)	1.8 – 4.1 (2.9)	

<sup>1</sup> Soil broth promotes *Fusarium* chlamydospore formation [70].

<sup>2</sup> Synthetic nutrient agar (SNA) is the medium for the classification of *Fusarium* species [71].