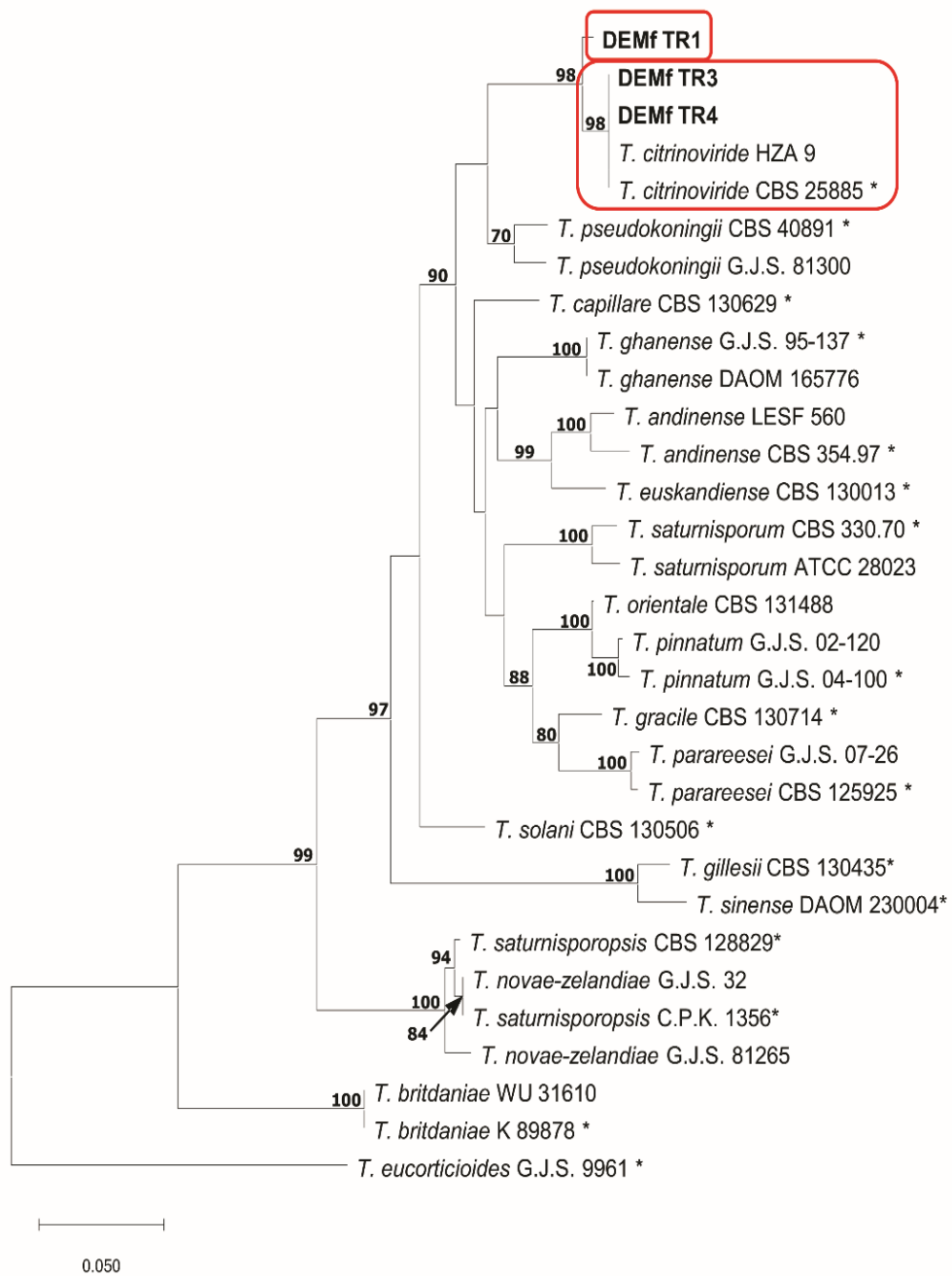
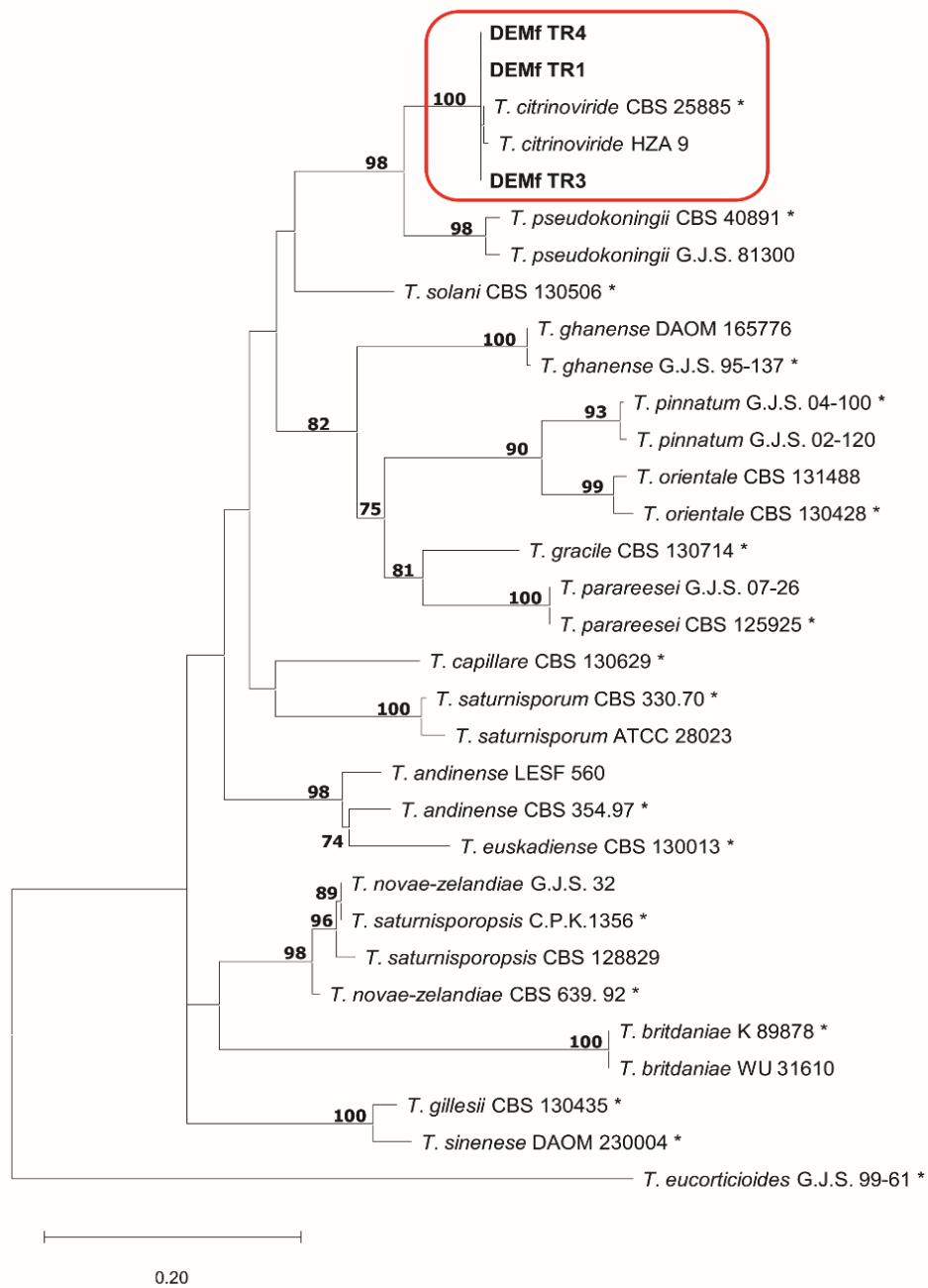


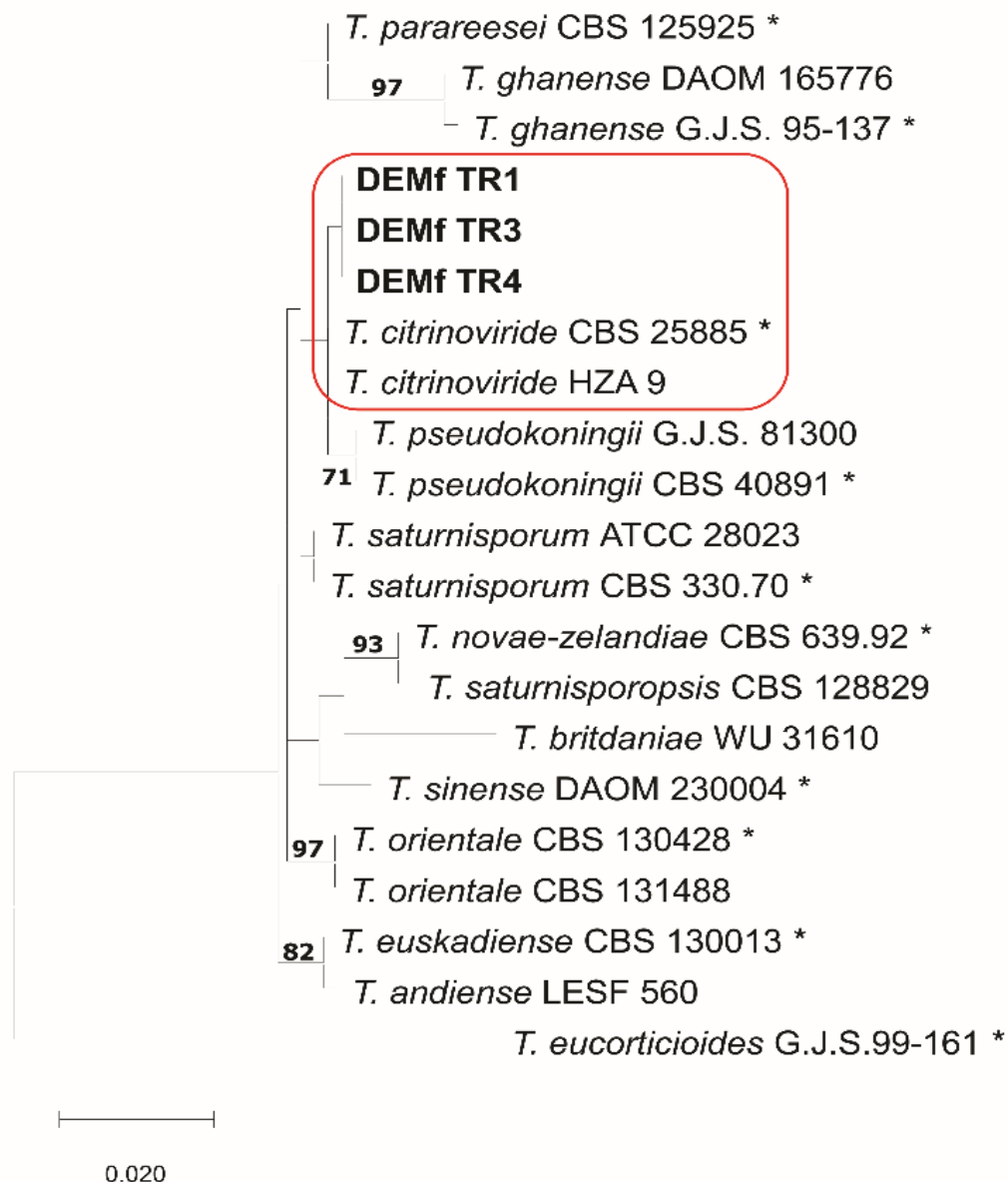
a)



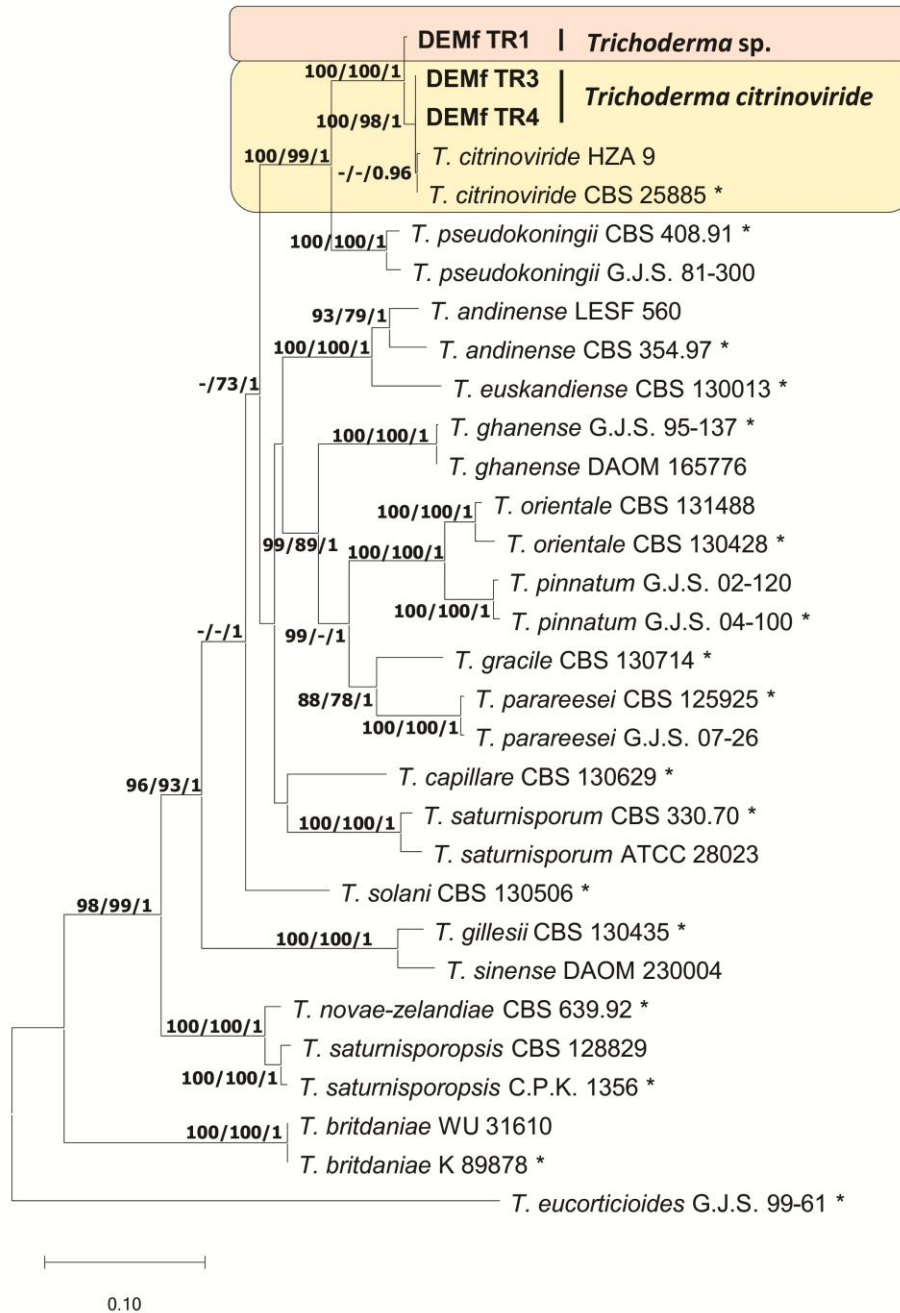
b)



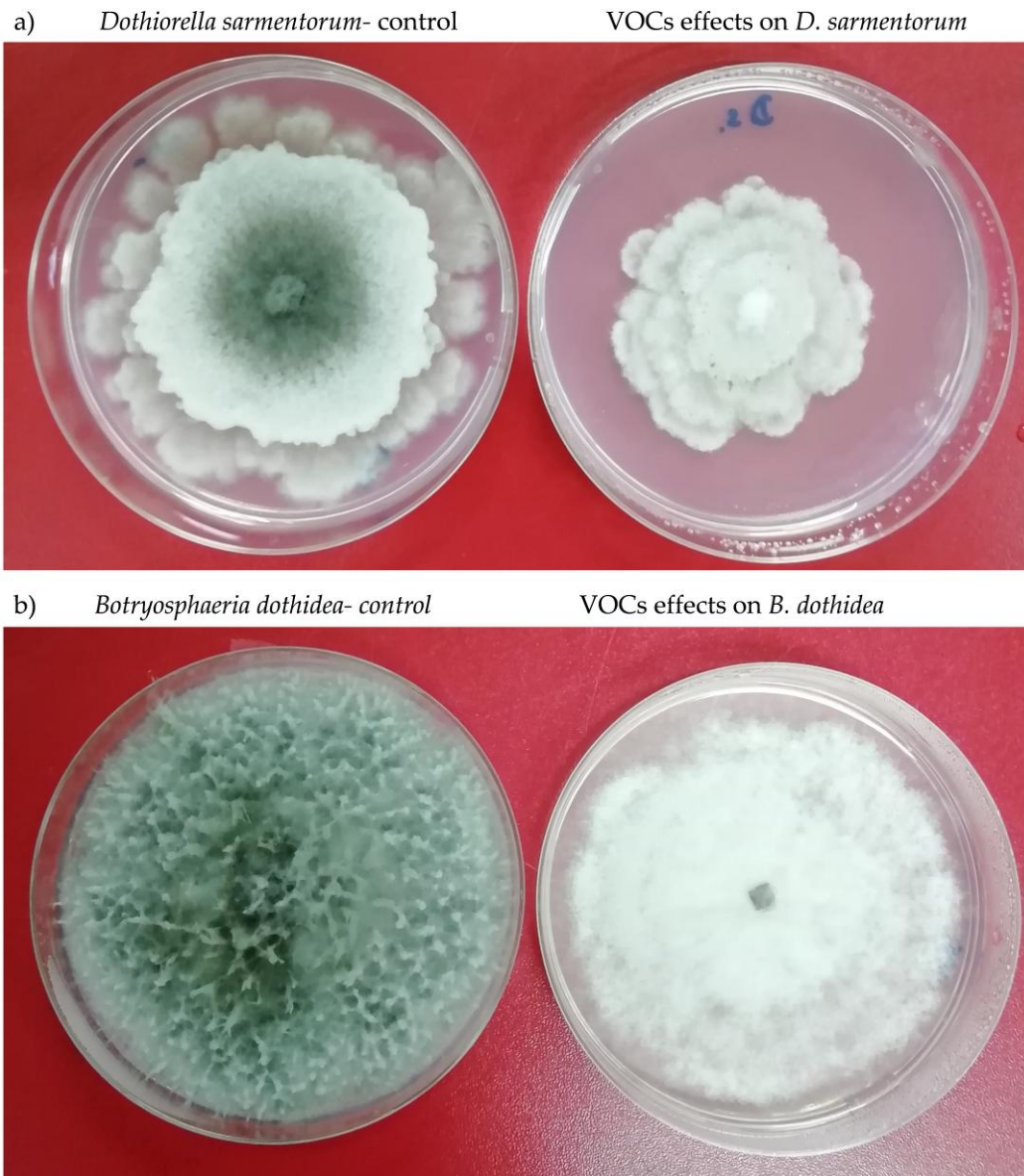
c)



**Figure S1.** Phylogenetic trees generated from Maximum likelihood (ML) analyses based on a single gene alignment of a) RPB2, b) TEF 1- $\alpha$ , and c) ITS sequence data. ML bootstrap support values greater than 70% are indicated at the tree nodes (ML). The type strains are marked with an asterisk. Isolates sequenced in this study are given in bold and highlighted. *Trichoderma euorticioides* (G.J.S. 99-161) was included as an outgroup. Scale bar indicates expected number of substitutions per site.



**Figure S2.** Phylogenetic tree generated from a maximum likelihood analysis (ML) based on a concatenated alignment of *tef* 1- $\alpha$  and *RPB2* sequence data showing the position of *Trichoderma citrinoviride* in relation to its closely related species belonging to the *Longibranchiatum* clade. ML and maximum parsimony (MP) bootstrap support values greater than 70% and Bayesian posterior probability values (PP) greater than 0.95 are indicated at the tree nodes (ML/MP/PP). The type strains are marked with an asterisk and isolates sequenced in this study are shown in bold. *T. eucorticioides* G.J.S. 99-61 (clade *Hypocreanum*) is included as an outgroup. Scale bar indicates expected number of substitutions per site.



**Figure S3.** Effects of VOCs of *Trichoderma citrinoviride* DEMf TR4 on mycelial growth of *D. sarmentorum* (a) and *B. dothidea* (b).

**Table S1.** Sequences used in the phylogenetic analyses.

Isolate no. <sup>1,2</sup>	Identity	Country	GenBank accession no. <sup>3,4</sup>		
			ITS	tef 1- $\alpha$	RPB2
DEMf TR1	<i>Trichoderma</i> sp.	Serbia	OK384601	OK422203	OK422200
DEMf TR3	<i>Trichoderma citrinoviride</i>	Serbia	OK384602	OK422204	OK422201
DEMf TR4	<i>T. citrinoviride</i>	Serbia	OK384603	OK422205	OK422202
CBS 258.85	<i>T. citrinoviride</i>	USA	MH861877	AY865637	KJ842210
HZA 9	<i>T. citrinoviride</i>	China	MH624144	MK850831	MK962804
CBS 408.91	<i>T. pseudokoningii</i>	Australia	MH862258	JN175588	JN175535
G.J.S. 81-300	<i>T. pseudokoningii</i>	New Zealand	Z82908	AY937429	JN175534
CBS 330.70	<i>T. saturnisporum</i>	Italy	NR_103704	EU280044	DQ087243
ATCC 28023	<i>T. saturnisporum</i>	USA	X93977	JN388897	JN175524
LESF 560	<i>T. andinense</i>	Brazil	KT278909	KT279038	KT278980
CBS 354.97	<i>T. andinense</i>	Venezuela	-	AY956321	JN175531
CBS 130013	<i>T. euskandiense</i>	Spain	MH865626	KJ665492	KJ665269
DAOM 165776	<i>T. ghanense</i>	Ghana	Z48936	JN175610	JN175560
G.J.S. 95-137	<i>T. ghanense</i>	Ghana	Z69588	AY937423	JN175559
CBS 125925	<i>T. parareesei</i>	Argentina	MH863773	GQ354353	HM182963
G.J.S. 07-26	<i>T. parareesei</i>	Ghana	-	GQ354373	HM182966
CBS 130714	<i>T. gracile</i>	Malaysia	-	JN175598	JN175547
CBS 131488	<i>T. orientale</i>	Spain	JQ685873	JQ685868	JQ685884
CBS 130428	<i>T. orientale</i>	China	EU401550	EU401550	-
G.J.S. 02-120	<i>T. pinnatum</i>	Vietnam	-	JN175572	JN175516
G.J.S. 04-100	<i>T. pinnatum</i>	Vietnam	-	JN175571	JN175515
CBS 130629	<i>T. capillare</i>	Hungary	-	JN182283	JN182312
CBS 130506	<i>T. solani</i>	Mexico	-	JN175597	JN175546
CBS 130435	<i>T. gillesii</i>	France	-	JN175583	JN175527
DAOM 230004	<i>T. sinense</i>	Taiwan	-	AY750889	JN175528
C.P.K. 1356	<i>T. saturnisporopsis</i>	USA	-	JN182281	DQ857348
CBS 128829	<i>T. saturnisporopsis</i>	Italy	JQ685874	JQ685874	JQ685885
CBS 639.92	<i>T. novae-zelandiae</i>	New Zealand	DQ083019	AY937448	JN133563
WU 31610	<i>T. britdaniae</i>	Denmark	NR_138454	JQ685866	JQ685880
K 89878	<i>T. britdaniae</i>	UK: England	-	JQ685865	JQ685881
G.J.S. 99-61	<i>T. eucorticoides</i>	Costa Rica	NR_134431	DQ835502	DQ835518

<sup>1</sup> Ex-type or ex-epitype strains are shown in italic.

<sup>2</sup> Strains sequenced in this study are shown in bold.

<sup>3</sup> ITS: Internal Transcribed Spacer; tef 1- $\alpha$ : partial translation elongation factor 1-alpha gene; RPB2: RNA polymerase II gene.

<sup>4</sup> Dashes indicate that the corresponding sequence was not available from GenBank.

ATCC: American Type Culture Collection, USA; CBS: Culture Collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; culture collection of Christian P. Kubicek, Institute of Chemical Engineering, Vienna University of Technology, Vienna, Austria; DAOM: Canadian Collection of Fungal Cultures, Ottawa, Canada; DEMf: Collection of Microorganisms of the Department of Ecological Microbiology: Fungi (University of Belgrade, Faculty of Agriculture); G.J.S.: Culture Collection of G.J. Samuels, Systematic Botany and Mycology Laboratory, US Dept of Agriculture, Beltsville, MD, USA.

**Table S2.** Nucleotide differences between *Trichoderma* sp. and its closest phylogenetic relative *T. citrinoviride*.

Isolates	Locus															
	ITS	tef 1- $\alpha$				RPB2										
	595	49	68	479	285	294	372	393	426	447	733	750	792	801	804	855
<i>Trichoderma</i> sp. DEMf TR1	-	A	T	G	A	T	T	T	A	A	G	T	C	G	C	A
<i>T. citrinoviride</i> DEMf TR3	-	A	T	G	G	C	C	A	G	G	C	C	T	A	T	G
<i>T. citrinoviride</i> DEMf TR4	-	A	T	G	G	C	C	A	G	G	C	C	T	A	T	G
<i>T. citrinoviride</i> CBS 25885 *	T	A	C	G	G	C	C	A	G	G	C	C	T	A	T	G
<i>T. citrinoviride</i> HZA 9	T	C	C	C	G	C	C	A	G	G	C	C	T	A	T	G

Shared polymorphisms between *Trichoderma* sp. and *T. citrinoviride* are highlighted in grey, whereas fixed polymorphisms at which *Trichoderma* sp. differs from *T. citrinoviride* are highlighted in orange. The *T. citrinoviride* type strain is marked with an asterisk.