

Supplementary material

Effect of farnesol in *Trichoderma* physiology and in fungal-plant interaction

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Table S1. Oligonucleotides used in the current study.

Name		Sequence 5′-3′	
Construction of pTCdpp1-b1 to overexpress <i>T. harzianum dpp1</i> gene			
Th-dpp1 5F		ATGCCTTCTGTGCGCACCG	
Th-dpp1 3R		TCAGCTTCGTCGAGTTCCTA	
Analysis of <i>dpp1</i> overexpressed transformants, and to amplify a probe for Southern experiments			
Th-dpp1-E4-1F		ATCCCTCTAGGCGTCTCAT	
Th-dpp1-E4-3R		TACCTTGCTCTTCTTCGTCCC	
TADIR2		TGACCACTTCGCTGCCTATC	
Th-dpp1-E4-1R		GAGGACGTTGGGTTTGATGT	
Amplification of <i>ble</i> gene to be used as a probe in Southern experiments			
Phleo-3		GGTGTGGTCGGCGTCGG	
Phleo-4		TGGGTGTGGGTGCGCGG	
Oligos for qPCR analysis of <i>Trichoderma</i> terpene-related genes			
Gene	Oligo name	Sequence 5′-3′	Efficiency (%)
actin	aactinF	ACTGGGACGACATGGAGAAG	92
	aactinR	GGCCTGGATGGAGACATAGA	
<i>hmgR</i>	Th hmgR 1F	ACGAGGAGGTCGTTGAGCTA	101
	Th hmgR 1R	TAGTGCCTGTAGGGCAGCTT	
<i>erg1</i>	erg1-1F	CGTCGAGACAGAGGTTGTCA	90
	erg1-1R	GCTTTCGAAACTTGGAGTCG	
<i>erg7</i>	Th-erg7-F	ACTGGATCAGGACCAACCAG	107
	Th-erg7-R	GCTTTCAGACCAACCACCAT	
<i>erg9</i>	Th-erg9-1F	GGCAGACTACGCACAAAACA	101
	Th-erg9-1R	GTTAGGCCTTCACCAACCAA	
<i>dpp1</i>	Th-dpp1 1F	ATCCCTCTAGGCGTCTCAT	89
	Th-dpp1 1R	GAGGACGTTGGGTTTGATGT	
Oligos for qPCR analysis of <i>Trichoderma</i> genes related with regulation of circadian cycle			
Gene	Oligo name	Sequence 5′-3′	Efficiency (%)
<i>laeA</i>	Th-laeA 1F	AGAACAACAGGCGCTACCAT	90
	Th-laeA 1R	ATTCTGTGGGTTCTCCAACG	
<i>veA</i>	Th-vea 1F	CAGCTTGTACGAGACGACCA	102
	Th-vea 1R	ATGAGTCCGGGGAACCTTCTT	
<i>velB</i>	Th-velB-E1 4F	GTCAATCAGCAACCGCAGTA	106
	Th-velB-E1 4R	GGGGGTAGTTTGCAGTGTGT	
Oligos for qPCR analysis of tomato genes related with defense and growth			
Gene	Oligo name	Sequence 5′-3′	Efficiency (%)
<i>actin</i>	Actin-F	CACCACTGCTGAACGGGAA	114
	Actin-R	GGAGCTGCTCCTGGCAGTTT	
<i>PR1b1</i>	PR1b1F	GCACTAAACCTAAAGAAAAATGGG	112
	PR1b1R	AAGTTGGCATCCCAAGACATA	
<i>PR-P2</i>	PR-P2F	GGAACAGGAACACAAGAAACAGTGA	113
	PR-P2R	CCCAATCCATTAGTGTCCAATCG	
<i>PIN1</i>	PIN1F	TGAAACTCTCATGGCACGAAAAG	108
	PIN1R	GGCCACATTTGTTTTCTTCG	

<i>PINII</i>	PINIIF	GGCCAAATGCTTGACCTTT	114
	PINIIR	CGTGGTACATCCGGTGGGATA	
<i>TomLoxA</i>	TomLoxAF	TGAACCATGGTGGGCTGAAA	95
	TomLoxAR	CTGCCCCGAAATTGACTGCTG	
<i>ACCS</i>	ACCSF	TGAGTTGGTGAACCATGGAA	104
	ACCSR	GCTTGAACAGCCTCAAGTCC	
<i>SUCS</i>	SUCSF	ATGAACCGAGTGAGGAATGG	106
	SUCSR	GCTGGACCACCGTGATTAGT	
<i>GAI</i>	GAIF	ACCTCCGGTGAACAATCAAG	92
	GAIR	GAACGCATTTGAACCCAGAT	

Table S2. Genomic sequences of *Trichoderma* spp. that were retrieved from the National Center for Biotechnology Information (NCBI) database for their use in the phylogenetic analysis carried out in the current study [31].

Species	GenBank accession number	Reference
<i>Trichoderma asperellum</i> CBS 433.97	GCF_003025105.1	Druzhinina, I.S.; Chenthamara, K.; Zhang, J.; et al. Massive lateral transfer of genes encoding plant cell wall-degrading enzymes to the mycoparasitic fungus <i>Trichoderma</i> from its plant-associated hosts. <i>PLoS Genet.</i> 2018. 14, e1007322. doi: 10.1371/journal.pgen.1007322.
<i>Trichoderma citrinoviride</i> TUCIM 6016	GCF_003025115.1	
<i>Trichoderma guizhouense</i> NJAU 4742	GCA_002022785.1	
<i>Trichoderma atroviride</i> IMI 206040	GCF_000171015.1	Kubicek, C.P.; Herrera-Estrella, A.; Seidl-Seiboth, V.; et al.. Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biol.</i> 2011. 12, R40. doi: 10.1186/gb-2011-12-4-r40
<i>Trichoderma virens</i> Gv29-8	GCF_000170995.1	
<i>Trichoderma hamatum</i> GD12	GCA_000331835.2	Studholme, D.J.; Harris, B.; Le Cocq, K.; et al. Investigating the beneficial traits of <i>Trichoderma hamatum</i> GD12 for sustainable agriculture-insights from genomics. <i>Front. Plant Sci.</i> 2013. 4,258. doi: 10.3389/fpls.2013.00258.
<i>Trichoderma arundinaceum</i> IBT 40837	GCA_003012105.1	Proctor, R.H.; McCormick, S.P.; Kim, H.S.; et al. Evolution of structural diversity of trichothecenes, a family of toxins produced by plant pathogenic and entomopathogenic fungi. <i>PLoS Pathog.</i> 2018. 14, e1006946. doi: 10.1371/journal.ppat.1006946
<i>Trichoderma brevicompactum</i> IBT 40841	GCA_003012085.1	
<i>Trichoderma atrobrunneum</i> ITEM 908	GCA_003439915.1	Fanelli, F.; Liuzzi, V.C.; Logrieco, A.F.; et al. Genomic characterization of <i>Trichoderma atrobrunneum</i> (<i>T. harzianum</i> species complex) ITEM 908: insight into the genetic endowment of a multi-target biocontrol strain. <i>BMC Genomics.</i> 2018. 19: 662. doi: 10.1186/s12864-018-5049-3
<i>Trichoderma koningii</i> JCM 1883	GCA_001950475.1	Manabe, R.; Endoh, R.; Uzuhashi, S.; et al. <i>Trichoderma koningii</i> strain JCM 1883, whole genome shotgun sequencing project. 2016. Direct submission.
<i>Trichoderma koningiopsis</i> POS7	GCA_002246995.1	Castrillo, M.L.; Bich, G.A.; Modenutti, C.P.; et al. First whole-genome shotgun sequence of a promising cellulase secretor, <i>Trichoderma koningiopsis</i> strain POS7. <i>Genome Announc.</i> 2017. 5: e00823-17. doi: 10.1128/genomeA.00823-17
<i>Trichoderma lentiforme</i> CFAM-422	GCA_011066345.1	Steindorff, A.S.; Formighieri, E.F.; Midorikawa, G.E.O.; et al.. <i>Trichoderma lentiforme</i> strain CFAM-422, whole genome shotgun sequence project. 2018. Direct submission.
<i>Trichoderma oligosporum</i> CGMCC 3.17527	GCA_015266385.1	Wang, C.; Zeng, Z.; Zhuang, W.; Comparative molecular evolution of chitinases in Ascomycota with emphasis on mycoparasitism lifestyle. 2020. Direct submission.
<i>Trichoderma parareesei</i> CBS125925	GCA_001050175.1	Yang, D.; Pomraning, K.; Kopchinskiy, A.; et al. Genome sequence and annotation of <i>Trichoderma parareesei</i> , the ancestor of the cellulase producer <i>Trichoderma reesei</i> . <i>Genome Announc.</i> 2017. 3, e00885. doi: 10.1128/genomeA.00885-15
<i>Trichoderma reesei</i> QM6a	GCF_000167675.1	Li, W.C.; Huang, C.H.; Chen, C.L.; et al. <i>Trichoderma reesei</i> complete genome sequence, repeat-induced point mutation, and partitioning of CAZyme gene clusters. <i>Biotechnol Biofuels.</i> 2017. 10, 170. doi: 10.1186/s13068-017-0825-x

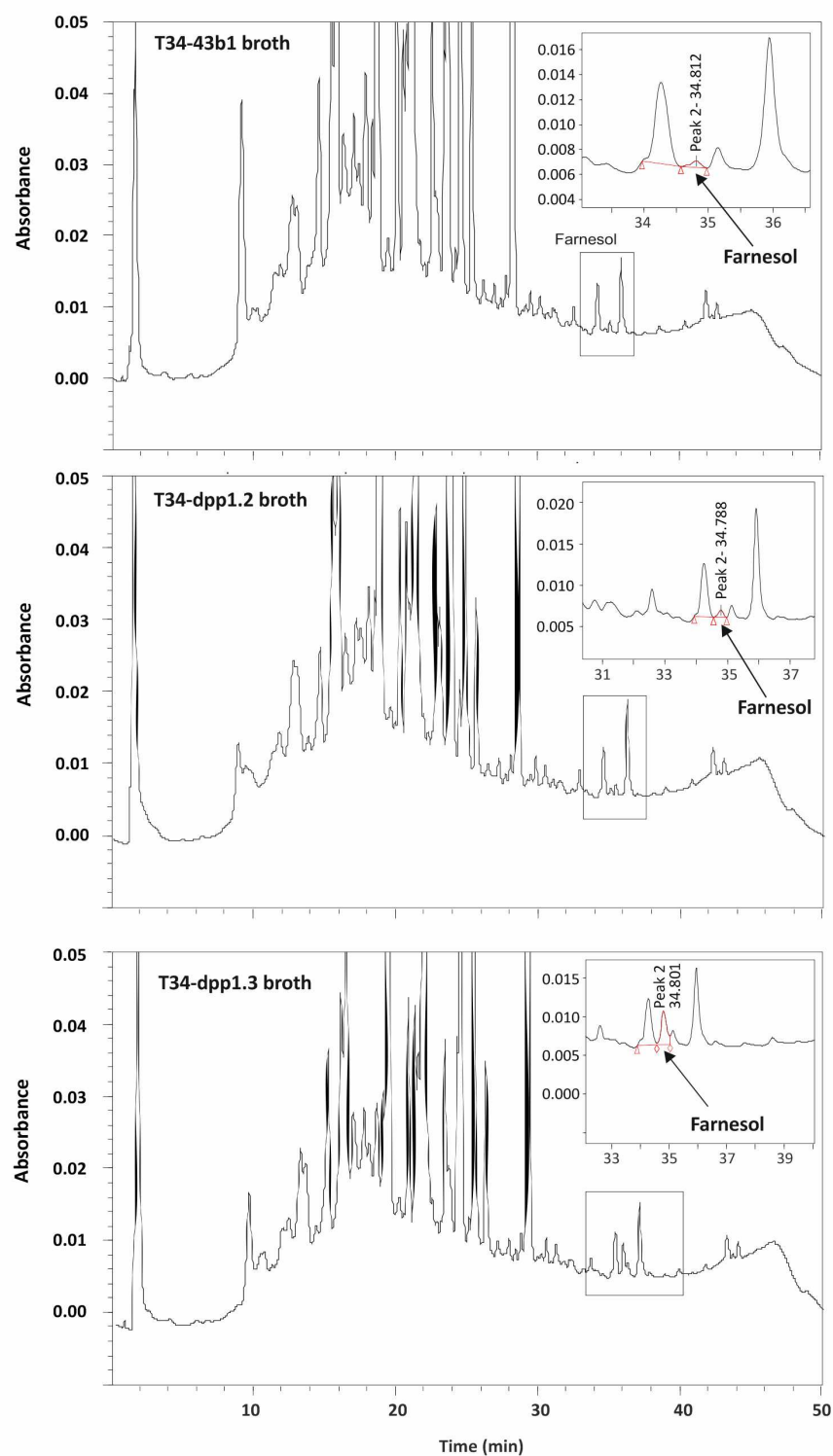


Figure S1. HPLC chromatograms showing the peaks corresponding to the farnesol production detected in 96 h culture broths of T34-43b.1 (**upper panel**), T34-dpp1.2 (**middle panel**) and T34-dpp1.3 (**bottom panel**) strains. Production of farnesol was deduced from the area of the farnesol peak using a calibration curve performed with different known concentrations of pure farnesol.

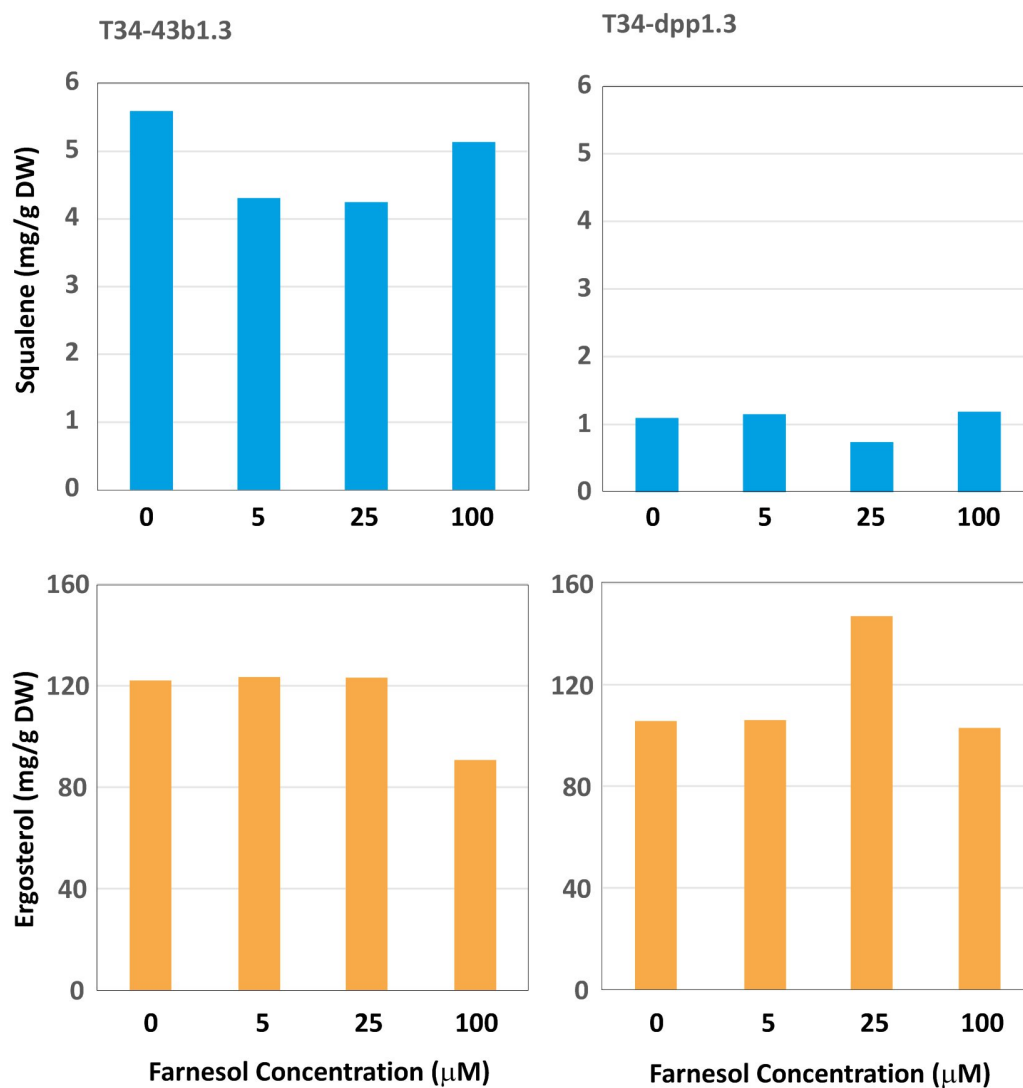


Figure S2. Level of squalene (**upper panels**) and ergosterol (**bottom panels**) produced in mycelia of strains T34-43b1.3 (**left panels**) and T34-dpp1.3 (**right panels**) grown for 96 h at 28 °C in minimal medium amended with farnesol at 0, 5, 25 or 100 μM. mg/g DW= milligrams of squalene or ergosterol per gram of freeze-dried mycelia.

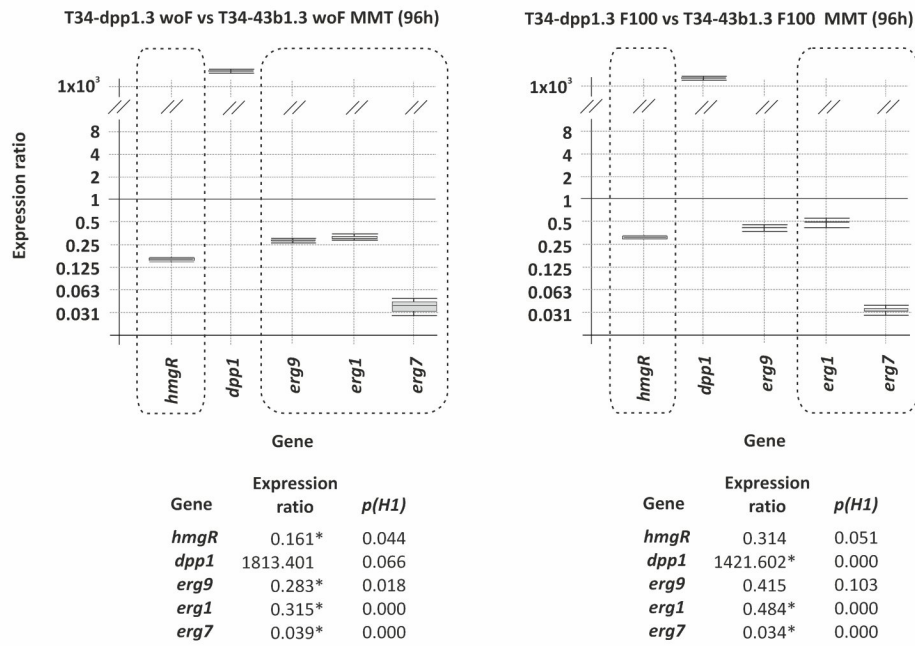


Figure S3. Analysis by qPCR of relative expression levels of five genes involved in ergosterol biosynthetic pathway in the transformant T34-dpp1.3 versus expression in the control strain T34-43b1.3. The study was carried out from mycelia grown for 96 h in minimal medium (MMT) without farnesol (**left panel**) and amended with farnesol 100 μ M (F100) (**right panel**). The data analysis and the graphic representation were performed as described in the legend to **Fig. 3**.

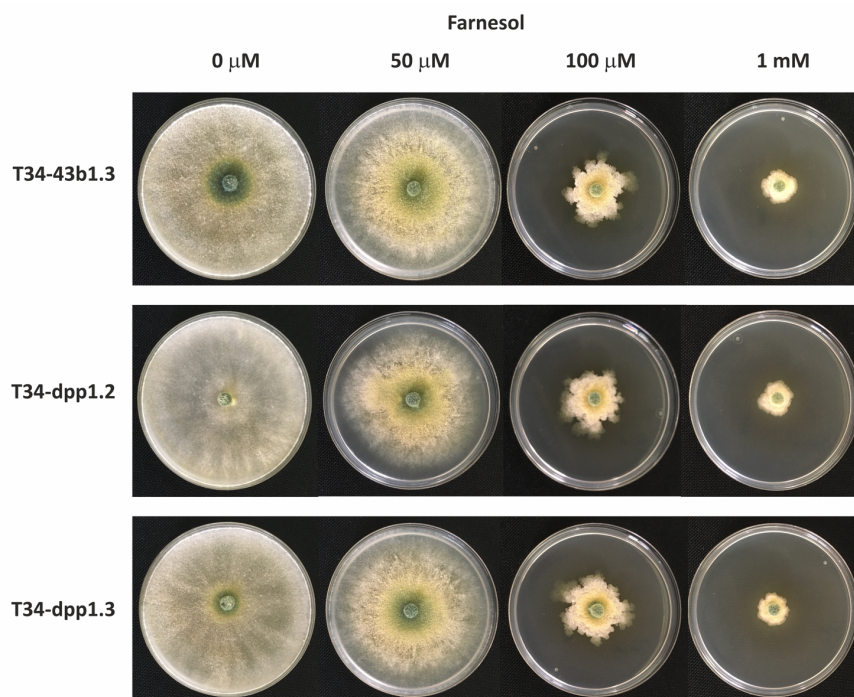
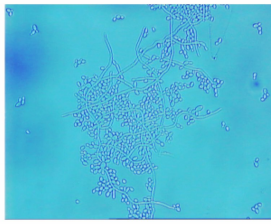


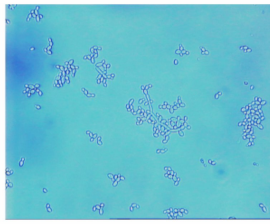
Figure S4. Effect of farnesol on growth of wild-type strain (T34-43b1.3) and the two *dpp1*-overexpressing transformants selected in the present work (T34-dpp1.2 and T34-dpp1.3). The plates were incubated for 7 days at 28 °C. Left panels correspond to the control condition without external addition of farnesol.

Candida albicans

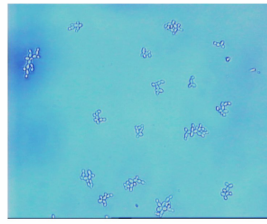
0 μ M farnesol



0.063 μ M farnesol

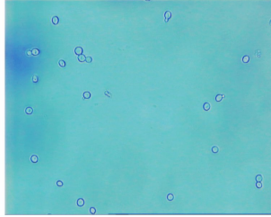


0.63 μ M farnesol

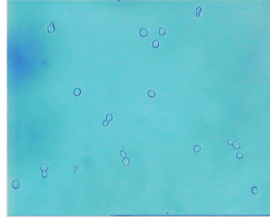


Saccharomyces cerevisiae

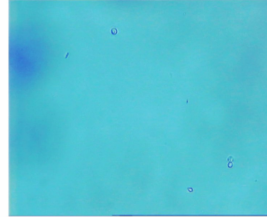
0 μ M farnesol



0.63 μ M farnesol



6.33 μ M farnesol



63.3 μ M farnesol



Figure S5. Toxicity of farnesol against *Candida albicans* (upper panel), and *Saccharomyces cerevisiae* (bottom panel).

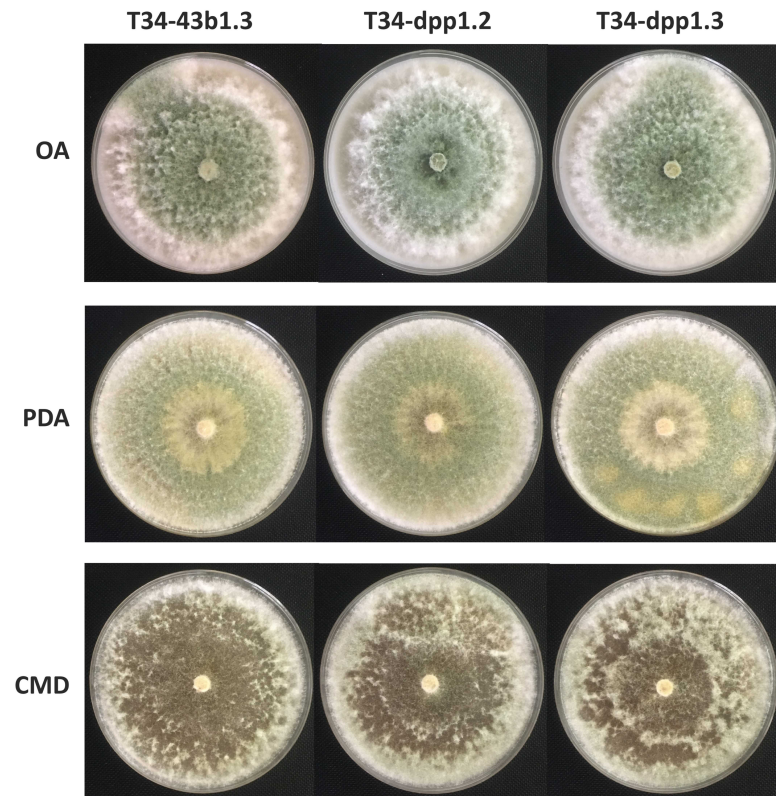


Figure S6. Effect of *dpp1* overexpression on growth in different media. Strains were grown for 14 days at 28 °C.



Figure S7. Antifungal assay on tomato leaves of 96 h PDB culture broths from T34-43b1.3 (control strain) and two *dpp1*-overexpressing transformants, against *Botrytis cinerea* B05.10.

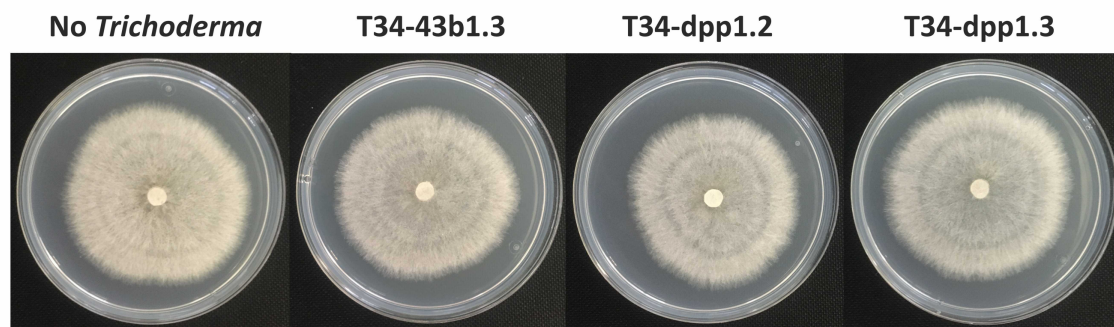


Figure S8. Effect of *T. harzianum* strains T34-43b1.3 (control strain), T34-dpp1.2 and T34-dpp1.3 (*dpp1*-overexpressing transformants) on growth of *R. solani* strain R43 in an antifungal membrane assay. Plate at the left corresponds to a control experiment in which no *Trichoderma* plug was placed on the plate before removal the cellophane membrane. Plates were incubated at 28 °C for four days after placement of the *R. solani* plug.