

List of electronic supplementary materials

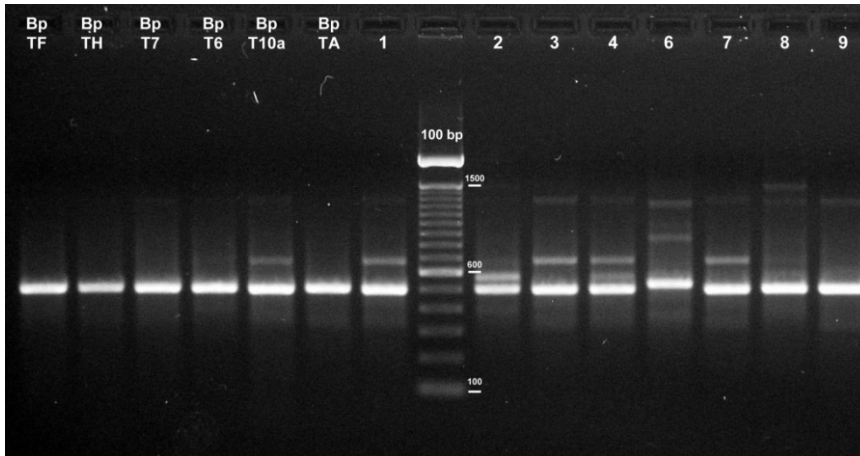


Fig. S1 Randomly amplified polymorphic DNA (RAPD) fingerprintings of *Trichoderma cf. harzianum*

Agarose gel showing the RAPD banding profile amplified from the genomic DNA of 14 *Trichoderma cf. harzianum* using the OPX02 primer. As a molecular weight marker the 100 bp ladder was used

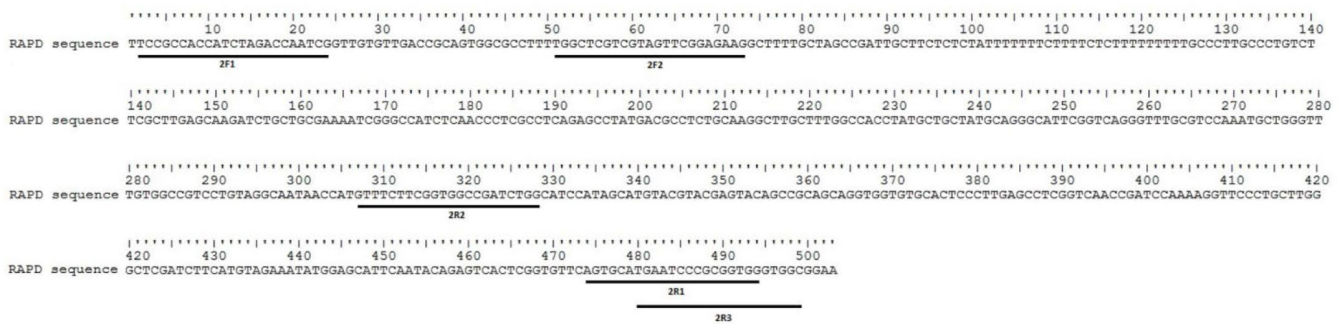


Fig. S2 Randomly amplified polymorphic DNA (RAPD) sequence used to design the SCAR primers

Five primers were developed (underlining regions)

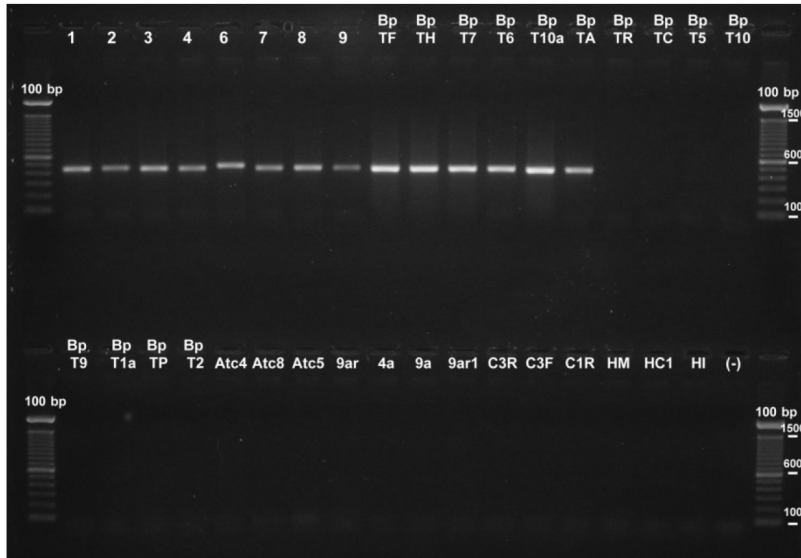


Fig. S3 Evaluation of the sequence-characterized amplified region (SCAR) marker primers by polymerase chain reaction

(PCR) The 448 bp fragments amplified from different *T. cf. harzianum* strains using the SCAR 2F2 and 2R3 primers are showed in the agarose gel together with the absence of amplification from other fungal species. Lanes labeled as 1, 2, 3, 4, 6, 7, 8, 9, BpTF, BpTH, BpT7, BpT6, BpT10a and BpTA correspond to gDNA from *T. cf. harzianum* isolates; BpTR, BpTC, BpT5, BpT10, BpT9 from *T. atroviride*; BpT1a from *T. novaезelandiae*; BpTP from *T. citrinoviride*; BpT2 from *Trichoderma* sp.; Atc4, Atc5, 9a, 9a1, C1R, and C3F from *Penicillium* spp.; HI, HC1 and 4a from *Aspergillus* spp.; HM from *Davidiella* sp.; 9ar from *Paecilomyces* sp.; Atc8 from *Monascus* sp. (see Table 1 for details); and C3R from a compost sample. As a molecular weight marker the 100 bp ladder was used; (-) is a negative control

BpT10a-SCAR	(1)	TGGCTCGTCGTAGTTCGGAGAAGGCTTTTGCTAG	CGATTGCTTCTCTCT
BpTA-SCAR	(1)	TGGCTCGTCGTAGTTCGGAGAAGGCTTTTGCTAG	CGATTGCTTCTCTCT
BpT6-SCAR	(1)	TGGCTCGTCGTAGTTCGGAGAAGGCTTTTGCTAG	CGATTGCTTCTCTCT
BpT7-SCAR	(1)	TGGCTCGTCGTAGTTCGGAGAAGGCTTTTGCTAG	CGATTGCTTCTCTCT
BpTF-SCAR	(1)	TGGCTCGTCGTAGTTCGGAGAAGGCTTTTGCTAG	CGATTGCTTCTCTCT
BpTH-SCAR	(1)	TGGCTCGTCGTAGTTCGGAGAAGGCTTTTGCTAG	CGATTGCTTCTCTCT
BpT10a-SCAR	(51)	ATTTTTCTCTTTCTCTTTTTTTT	GGCCCTGGCCCTGTCTCGCTTGAG
BpTA-SCAR	(51)	ATTTTTCTCTTTCTCTTTTTTTT	GGCCCTGGCCCTGTCTCGCTTGAG
BpT6-SCAR	(51)	ATTTTTCTCTTTCTCTTTTTTTT	GGCCCTGGCCCTGTCTCGCTTGAG
BpT7-SCAR	(51)	ATTTTTCTCTTTCTCTTTTTTTT	GGCCCTGGCCCTGTCTCGCTTGAG
BpTF-SCAR	(51)	ATTTTTCTCTTTCTCTTTTTTTT	GGCCCTGGCCCTGTCTCGCTTGAG
BpTH-SCAR	(51)	ATTTTTCTCTTTCTCTTTTTTTT	GGCCCTGGCCCTGTCTCGCTTGAG
BpT10a-SCAR	(100)	CAAGATCTGCTGCGAAAATCGGGCCATCTCAACCCTCGCCTCAGAGCCTA	
BpTA-SCAR	(98)	CAAGATCTGCTGCGAAAATCGGGCCATCTCAACCCTCGCCTCAGAGCCTA	
BpT6-SCAR	(99)	CAAGATCTGCTGCGAAAATCGGGCCATCTCAACCCTCGCCTCAGAGCCTA	
BpT7-SCAR	(99)	CAAGATCTGCTGCGAAAATCGGGCCATCTCAACCCTCGCCTCAGAGCCTA	
BpTF-SCAR	(99)	CAAGATCTGCTGCGAAAATCGGGCCATCTCAACCCTCGCCTCAGAGCCTA	
BpTH-SCAR	(99)	CAAGATCTGCTGCGAAAATCGGGCCATCTCAACCCTCGCCTCAGAGCCTA	
BpT10a-SCAR	(150)	TGACGCCTCTGCAAGGCTTGCTTTGGCCACCTATG	TGCTATGCAGGGCA
BpTA-SCAR	(148)	TGACGCCTCTGCAAGGCTTGCTTTGGCCACCTATG	TGCTATGCAGGGCA
BpT6-SCAR	(149)	TGACGCCTCTGCAAGGCTTGCTTTGGCCACCTATG	TGCTATGCAGGGCA
BpT7-SCAR	(149)	TGACGCCTCTGCAAGGCTTGCTTTGGCCACCTATG	TGCTATGCAGGGCA
BpTF-SCAR	(149)	TGACGCCTCTGCAAGGCTTGCTTTGGCCACCTATG	TGCTATGCAGGGCA
BpTH-SCAR	(149)	TGACGCCTCTGCAAGGCTTGCTTTGGCCACCTATG	TGCTATGCAGGGCA
BpT10a-SCAR	(200)	TTCGGTCAGGGTTTGGCTCCAAATGCTGG	TTGTGGCCGTCCTGTAGGCA
BpTA-SCAR	(198)	TTCGGTCAGGGTTTGGCTCCAAATGCTGG	TTGTGGCCGTCCTGTAGGCA
BpT6-SCAR	(199)	TTCGGTCAGGGTTTGGCTCCAAATGCTGG	TTGTGGCCGTCCTGTAGGCA
BpT7-SCAR	(199)	TTCGGTCAGGGTTTGGCTCCAAATGCTGG	TTGTGGCCGTCCTGTAGGCA
BpTF-SCAR	(199)	TTCGGTCAGGGTTTGGCTCCAAATGCTGG	TTGTGGCCGTCCTGTAGGCA
BpTH-SCAR	(199)	TTCGGTCAGGGTTTGGCTCCAAATGCTGG	TTGTGGCCGTCCTGTAGGCA
BpT10a-SCAR	(250)	AACCATGTTTCTTCGGTGGCCGATCTGG	
BpTA-SCAR	(248)	AACCATGTTTCTTCGGTGGCCGATCTGG	
BpT6-SCAR	(249)	AACCATGTTTCTTCGGTGGCCGATCTGG	
BpT7-SCAR	(249)	AACCATGTTTCTTCGGTGGCCGATCTGG	
BpTF-SCAR	(249)	AACCATGTTTCTTCGGTGGCCGATCTGG	
BpTH-SCAR	(249)	AACCATGTTTCTTCGGTGGCCGATCTGG	

Fig. S4 Sequence-characterized amplified region (SCAR) sequence analyses of the six *Trichoderma cf. harzianum* isolates

The alignment was performed on the Vector NTI advance[®] 11.5 software (Invitrogen). The polymorphic regions are shaded in green. Nucleotide positions 35, 59, 74, 186 and 230, represent transversions or transitions, and positions 51, 52, 77 and 252 correspond to INDELS

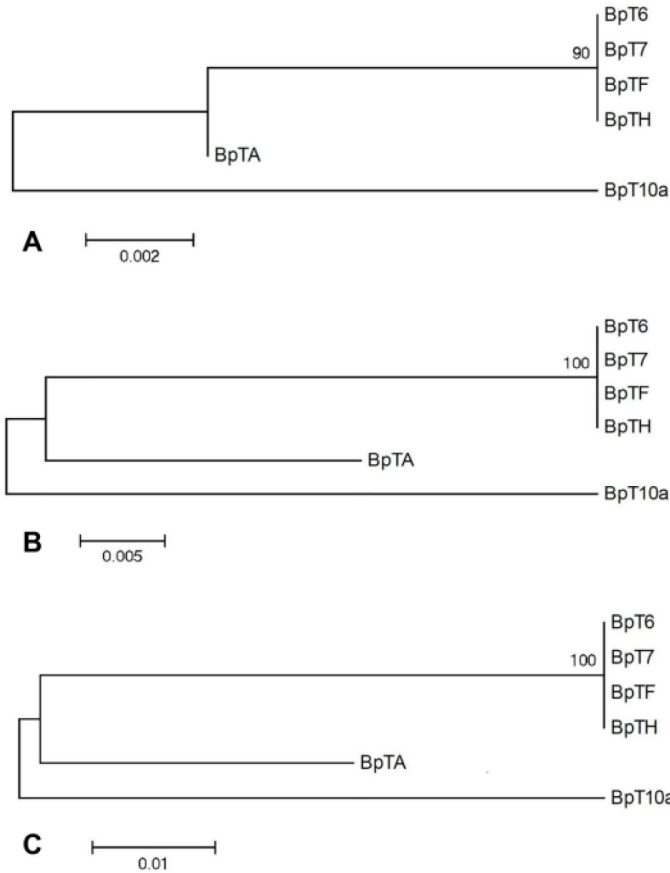


Fig. S5 Relationships between *Trichoderma cf. harzianum* isolates using different molecular markers

All analyses were performed on Mega 5.2 (Tamura *et al.*, 2011) based on the Neighbor Joining algorithm obtained with the *p*-distance method. Bootstrap values are indicated for the nodes that received significant support ($\geq 70\%$) with 1000 repetitions. A: dendrogram based on SCAR sequences. B: dendrogram based on calmodulin (*cal*) sequences. C: dendrogram based on translation elongation factor (*tef*) sequences.

Ref.: Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S., 2011. MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution*, **28**:2731-2739.

FASTA S1 Randomly amplified polymorphic DNA (RAPD) sequence based on which the sequence-characterized amplified region (SCAR) primers were designed

>RAPD sequence (BpTF clon)

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TTCCGCCACCATCTAGACCAATCGGTTGTGTTGACCGCAGTGGCGCCTTTTGGCTCGTCG
TAGTTCGGAGAAGGCTTTTGCTAGCCGATTGCTTCTCTCTATTTTTTCTTTTCTCTTTT
TTTTTGCCCTTGCCCTGTCTCGCTTGAGCAAGATCTGCTGCGAAAATCGGGCCATCTCAA
CCCTCGCCTCAGAGCCTATGACGCCTCTGCAAGGCTTGCTTTGGCCACCTATGCTGCTAT
GCAGGGCATTTCGGTCAGGGTTTGCCTCAAATGCTGGGTTGTGGCCGTCCTGTAGGCAAT
AACCATGTTTCTTCGGTGGCCGATCTGGCATCCATAGCATGTACGTACGAGTACAGCCGC
AGCAGGTGGTGTGCACTCCCTTGAGCCTCGGTCAACCGATCCAAAAGGTTCCCTGCTTGG
CTCGATCTTCATGTAGAAATATGGAGCATTCAATACAGAGTCACTCGGTGTTTCAGTGCAT
GAATCCC CGGTGGGTGGCGGAA

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FASTA S2 Sequence-characterized amplified region (SCAR) sequences of *Trichoderma cf. harzianum* isolates

>BpT6-SCAR

TGGCTCGTCGATGTTCCGAGAAGGCTTTTGCTAGCCGATTGCTTCTCTCT--ATTTTTTT
 CTTTTCTTTTTTTTTTGGCCCTGGCCCTGTCTCGCTTGAGCAAGATCTGCTGCGAAAATC
 GGGCCATCTCAACCCCTCGCCTCAGAGCCTATGACGCCTCTGCAAGGCTTGCTTTGGCCAC
 CTATGCTGCTATGCAGGGCATTTCGGTCAGGGTTTTCGTCCAAATGCTGGGTTGTGGCCGT
 CCTGTAGGCAATAACCATGTTTCTTCGGTGGCCGATCTGG

>BpT7-SCAR

TGGCTCGTCGATGTTCCGAGAAGGCTTTTGCTAGCCGATTGCTTCTCTCT--ATTTTTTT
 CTTTTCTTTTTTTTTTGGCCCTGGCCCTGTCTCGCTTGAGCAAGATCTGCTGCGAAAATC
 GGGCCATCTCAACCCCTCGCCTCAGAGCCTATGACGCCTCTGCAAGGCTTGCTTTGGCCAC
 CTATGCTGCTATGCAGGGCATTTCGGTCAGGGTTTTCGTCCAAATGCTGGGTTGTGGCCGT
 CCTGTAGGCAATAACCATGTTTCTTCGGTGGCCGATCTGG

>BpT10a-SCAR

TGGCTCGTCGATGTTCCGAGAAGGCTTTTGCTAGTCGATTGCTTCTCTCTATTTTTTCT
 CTTTTCTTTTTTCTT-GCCCTTGCCCTGTCTCGCTTGAGCAAGATCTGCTGCGAAAATC
 GGGCCATCTCAACCCCTCGCCTCAGAGCCTATGACGCCTCTGCAAGGCTTGCTTTGGCCAC
 CTATGTTGCTATGCAGGGCATTTCGGTCAGGGTTTTCGTCCAAATGCTGGCTTGTTGGCCGT
 CCTGTAGGCAAG-AACCATGTTTCTTCGGTGGCCGATCTGG

>BpTA-SCAR

TGGCTCGTCGATGTTCCGAGAAGGCTTTTGCTAGCCGATTGCTTCTCTCT--ATTTTTTT
 CTTTTCTTTTTTTTT-GCCCTTGCCCTGTCTCGCTTGAGCAAGATCTGCTGCGAAAATC
 GGGCCATCTCAACCCCTCGCCTCAGAGCCTATGACGCCTCTGCAAGGCTTGCTTTGGCCAC
 CTATGCTGCTATGCAGGGCATTTCGGTCAGGGTTTTCGTCCAAATGCTGGCTTGTTGGCCGT
 CCTGTAGGCAATAACCATGTTTCTTCGGTGGCCGATCTGG

>BpTF-SCAR

TGGCTCGTCGATGTTCCGAGAAGGCTTTTGCTAGCCGATTGCTTCTCTCT--ATTTTTTT
 CTTTTCTTTTTTTTTTGGCCCTGGCCCTGTCTCGCTTGAGCAAGATCTGCTGCGAAAATC
 GGGCCATCTCAACCCCTCGCCTCAGAGCCTATGACGCCTCTGCAAGGCTTGCTTTGGCCAC
 CTATGCTGCTATGCAGGGCATTTCGGTCAGGGTTTTCGTCCAAATGCTGGGTTGTGGCCGT
 CCTGTAGGCAATAACCATGTTTCTTCGGTGGCCGATCTGG

>BpTH-SCAR

TGGCTCGTCGATGTTCCGAGAAGGCTTTTGCTAGCCGATTGCTTCTCTCT--ATTTTTTT
 CTTTTCTTTTTTTTTTGGCCCTGGCCCTGTCTCGCTTGAGCAAGATCTGCTGCGAAAATC
 GGGCCATCTCAACCCCTCGCCTCAGAGCCTATGACGCCTCTGCAAGGCTTGCTTTGGCCAC
 CTATGCTGCTATGCAGGGCATTTCGGTCAGGGTTTTCGTCCAAATGCTGGGTTGTGGCCGT
 CCTGTAGGCAATAACCATGTTTCTTCGGTGGCCGATCTGG

Table S1 BLAST analysis performed to align Sequence-characterized amplified region (SCAR) sequence with different fungal genomes

Species	Strain	Scaffold	Position	Score	E-value	Hit
<i>Trichoderma harzianum</i>	CBS 226.95	Scaffold 2	3607433-3607694	220	3.84E-99	1
<i>Trichoderma reesei</i>		Scaffold 4	317388-317419	28	2.43E-7	1
<i>Trichoderma reesei</i>	RUT C-30	Scaffold 9	308436-308467	28	2.37E-7	1
<i>Trichoderma virens</i>	Gv29-8	Scaffold 90	348930-349108	99	1.35E-33	1

The blast was done using the 366 genomes available on the data base of the web site <http://genome.jgi.doe.gov/>. In the table is shown the species which present a positive alignment with the SCAR sequence, the position in the genome where the hit was found (scaffold, position), the number of coincident nucleotides (score) between the SCAR sequence and the genome, the E-value, and the number of times the SCAR was found in the genome (hit)