

Draft Whole-Genome Sequence of the Biocontrol Agent *Trichoderma harzianum* T6776

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This article is dedicated to Maurizio Forti, friend and devoted technician at the University of Pisa, who passed away in December 2013.

***Trichoderma harzianum* T6776 is a promising beneficial isolate whose effects consist of growth promotion, positive response of photosynthetic activity, hormonal signaling, and carbon partitioning in tomato, coupled with biocontrol of plant pathogens. Here, we present the first genome assembly of T6776, providing a useful platform for the scientific community.**

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Trichoderma species are well-known beneficial fungi used as biocontrol agents. The capacity to produce antibiotics and enzymes, to induce systemic resistance in plants, and to parasitize phytopathogenic fungi, coupled with a high metabolic versatility and a strong competition ability, make many *Trichoderma* isolates useful microorganisms for commercial biofertilizers and biopesticides (1–3).

Trichoderma harzianum strain T6776 was isolated by the authors from soil in Tuscany, Italy, and it has been studied for many years as a bioactive principle in biostimulants and biopesticides.

The first evidence of its beneficial effects in terms of growth promotion and biocontrol activity against fungal plant pathogens of high economic impact was demonstrated on different tomato cultivars and against *Rhizoctonia solani*, *Fusarium oxysporum* f. sp. *lycopersici*, and *F. oxysporum* f. sp. *radicis-lycopersici* (4). The biostimulating effects of *T. harzianum* T6776, and its endophytic ability, have been further demonstrated under different tomato cultivation systems (soil and hydroponic). Recent data suggest the induction of resistance toward *Alternaria solani* by *T. harzianum*. In addition, significant positive responses of photosynthetic activity, hormonal signaling, and carbon partitioning have been obtained after inoculation of tomato with T6776 (5).

These results encouraged us to produce a complete sequence of *T. harzianum* T6776 as an efficient and powerful tool to investigate the molecular mechanisms controlling the interaction between the fungus and the tomato plant.

The genome of *T. harzianum* strain T6776 was sequenced using Illumina mate-paired sequencing technology by the McGill University and Genome, Quebec Innovation Centre (Canada). Mate-paired reads of 250 bp (3.26 Gbp; average coverage 85×) were assembled using Velvet version 1.2.08 (6). The draft nuclear genome of *T. harzianum* consists of 1,573 sequence scaffolds with a total assembly length 39.73 Mbp (N_{50} = 68,846 and N_{90} = 15,338), a GC content of 48.50%, and a maximum scaffold size of 330,970 bp. The completeness of the assembly was assessed using

CEGMA version 2.4 (7), which estimated the genome sequence to be 98.39% complete. The nuclear genome was annotated using the MAKER pipeline (8). Overall, 11,501 protein-coding gene models were predicted. Analysis with WoLF PSORT (9) revealed that 1,412 predicted proteins (12.28% of the proteome) contain a secretion signal peptide. Among those 63 are *Trichoderma*-specific proteins, of which 35 are strain specific as they do not have any sequence similarity to proteins in public databases, based on BLAST searches (E value threshold of $1E^{-3}$). Such characteristics are typical of fungal effectors, which modulate plant immunity and facilitate colonization (10, 11). A first comparative analysis within *Trichoderma* spp. (12) and model organisms with publicly available genomes (*Fusarium* [13], *Neurospora* [14], *Colletotrichum* [10, 15, 16], *Magnaporthe* [17], *Clonostachys* [18], and *Verticillium* [19]) suggested that *T. harzianum* T6776 contains a large number of carbohydrate-active enzymes (CAZy), such as α -L-fucosidase, chitosanases, α -galactosidase, and alginate lyase (three, five, eight, and three genes, respectively). The genome sequence reported here represents a new resource useful for further research into the biology, ecology, and evolution of biocontrol agents.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in GenBank under the accession number [JOKZ000000000](https://www.ncbi.nlm.nih.gov/nuccore/JOKZ000000000) (BioProject PRJNA252551). The version described in this paper is JOKZ000000000.1.

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