

Draft Whole-Genome Sequence of *Trichoderma gamsii* T6085, a Promising Biocontrol Agent of *Fusarium* Head Blight on Wheat

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***Trichoderma gamsii* T6085 is a promising beneficial isolate whose effects consist of growth inhibition of the main agents causing *Fusarium* head blight, reduction of mycotoxin accumulation, competition for wheat debris, and reduction of the disease in both the lab and the field. Here, we present the first genome assembly of a *T. gamsii* isolate, providing a useful platform for the scientific community.**

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Fusarium head blight (FHB) is one of the most important diseases of wheat, caused by a complex of *Fusarium* species, including *F. graminearum* and *F. culmorum*. The most serious consequence of FHB is the contamination of grain and cereal products with mycotoxins, with deoxynivalenol (DON) and its acetylated derivatives, 3- and 15-acetyl-DON, as the most frequently encountered trichothecene in FHB of wheat throughout Europe (1). Different strategies are used to reduce the impact of FHB, such as crop rotation, tillage practices, fungicide application, and resistant cultivars, but none of these by itself is able to reduce the impact of the disease. In this context, biological control offers, by the use of beneficial fungi, such as *Trichoderma* spp., a promising alternative for the management of FHB (2–4).

Trichoderma gamsii T6085 has been studied for many years by our research group for its ability to control FHB on wheat. From experimental data collected since then, T6085 resulted in being effective against *F. graminearum* and *F. culmorum* by inhibiting their growth (5), reducing mycotoxin contamination, particularly that of DON, and controlling the disease in both the lab and the field (6, 7). T6085 also was a good competitor against *F. graminearum* for cultural debris (8).

T. gamsii T6085 was sequenced using Illumina mate-paired sequencing technology by the Génome Québec Innovation Centre, part of McGill University (Canada). Mate-paired reads of 250 bp (3.80 Gbp total; average coverage, 100×) were assembled using Velvet 1.2.08 (9). The draft genome of *T. gamsii* consists of 381 scaffolds, with a total assembly length of 37.97 Mbp (N_{50} , 417,961 bp; N_{90} , 106,959 bp), 49.00% G+C content, and a maximum scaffold size of 1,198,811 bp. The completeness of the assembly was assessed using CEGMA version 2.4 (10), which estimated the genome sequence to be 97.58% complete based on full and partial targets. The nuclear genome was annotated using the MAKER2 pipeline (11). Overall, 10,944 protein-coding genes were predicted. Analysis with WolfPSORT (9) revealed that 1,356 predicted proteins (12.39% of the proteome) contain secretion signal peptides; those values are comparable to what has been reported for other *Trichoderma* genomes (12). A first comparative

analysis within *Trichoderma* spp. (12, 13) and model organisms with publicly available genomes (*Fusarium* [14], *Neurospora* [15], *Colletotrichum* [16, 17], *Magnaporthe* [18], *Clonostachys* [19], and *Verticillium* (20)) suggested that *T. gamsii* T6085 contains a large number of specific carbohydrate-active enzymes (CAZy), such as GH30, GH2, GH13, and GH5, cerato-ulmin hydrophobin, proteinase inhibitor, peptidases, such as G1 and S53, and glucose/ribitol dehydrogenase enzymes. The genome sequence of *T. gamsii* T6085 represents a new resource that is useful for further research into the genetic bases of *Fusarium* head blight biological control by *Trichoderma* species.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in GenBank under the accession no. [JPDN000000000](https://ncbi.nlm.nih.gov/nucl/JPDN000000000) (BioProject PRJNA252048). The version described in this paper is JPDN000000000.1.

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