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Genome Sequence of the Emerging Mycotoxin-Producing Filamentous Fungus *Fusarium tricinctum* Strain INRA104

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ABSTRACT The genome of the phytopathogenic fungus *Fusarium tricinctum* strain INRA104 was sequenced at a fold-coverage of more than 500×. This led to 23 scaffolds, including one scaffold for the mitochondrial genome, for a total genome size of 42.8 Mb, with an average GC content of 45% and 13,387 predicted genes.

Up to 15 *Fusarium* spp. can be found on cereal ears with *Fusarium* head blight (FHB) symptoms (1). Most of these fungal species are able to produce several types of mycotoxins that first accumulate in grains and then contaminate processed products in the food chain, representing both a health risk and an important economic stake. Some of these fusariotoxins are already subject to international regulation (deoxynivalenol, fumonisins, and zearalenone). In addition, other mycotoxins are considered emerging because they were recently found in crops in Europe and Asia (2) and, by their suspected toxicity, constitute subjects of interest for food security agencies. Regulations setting threshold values for contamination should be published shortly. Indeed, emerging mycotoxins, such as enniatins, beauvericin, and moniliformin, have been reported to possess genotoxic effects *in vitro* (3). Enniatin B1 and beauvericin could be more hepatotoxic than major and regulated toxins, such as aflatoxin B1 (4). Despite these significant potential health risks, there are still few data on enniatins, including the regulation of their biosynthesis and their secretion by the producing species. Enniatins are cyclohexadepsipeptides synthesized outside the ribosome by multifunctional enzymes, including enniatin synthase (ESyn1, 347 kDa) (5). However, the characterization of the different genes encoding and regulating the enzymes involved in the production of the 29 enniatins described to date is still a challenge (5). On cereals, the enniatins are produced by *Fusarium avenaceum*, for which three reference genomes are available (6), and *Fusarium tricinctum*. In this context, the genome of an enniatin- and other-mycotoxin-producing strain of *F. tricinctum* was sequenced.

The *F. tricinctum* strain INRA104 was isolated in 2001 from corn kernels collected in a French field from an agricultural region located roughly 150 km south of Paris (i.e., department number 45, Loiret). Genomic DNA was extracted from freeze-dried mycelia (1 week of liquid culture in glucose-yeast extract-neopeptone [GYEP] medium) using the cetyltrimethylammonium bromide (CTAB) method (7). A combination of third-generation sequencing (PacBio Sequel platform) and next-generation sequencing (Illumina HiSeq platform) produced more than 22 billion bases. After read correction (FALCON pipeline v1.8.8-1 [PacBio]), assembly (SMART *de novo*, for the nuclear genome), and an in-house modified version of CANU v1.7 [8] for the mitochondrial genome), and genome polishing (GenomicConsensus package [PacBio] and Pilon v1.22 [9]), we obtained 22 scaffolds for a genome size of 42.8 Mb (with sizes ranging from 7,333 bp to 5,080,745 bp; mean size, 1,782,168 bp; N_{50} value, 2,710,832 bp; N_{90} value, 1,246,557 bp; GC content, 45%) plus one unique scaffold (GenBank accession number CM009895) for the mitochondrial genome, consisting of 48,506 bp (GC content, 33%).

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De novo gene prediction using the genome of *Fusarium graminearum* PH-1 as a reference (AUGUSTUS v3.3 [10]) identified 13,387 protein-coding genes, with an average length of 1.7 kbp.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [QFZF00000000](https://doi.org/10.1093/bioinformatics/bty111). The version described in this paper is version QFZF01000000.

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