



HAL
open science

Genome sequence of the emerging mycotoxin-producing filamentous fungus *Fusarium tricinctum* strain INRA104

Nadia Ponts, Florence Richard-Forget, Honghai Zhang, Gérard Barroso, Chen Zhao

► To cite this version:

Nadia Ponts, Florence Richard-Forget, Honghai Zhang, Gérard Barroso, Chen Zhao. Genome sequence of the emerging mycotoxin-producing filamentous fungus *Fusarium tricinctum* strain INRA104. *Genome Announcements*, 2018, 6 (25), pp.1-2. 10.1128/genomeA.00509-18. hal-02620835

HAL Id: hal-02620835

<https://hal.inrae.fr/hal-02620835>

Submitted on 26 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



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

Nadia Ponts,^a Florence Richard-Forget,^a Honghai Zhang,^b Gérard Barroso,^{a,c} Chen Zhao^b

^aINRA UR1264, MycSA, Villenave d'Ornon, France

^bAcademy of State Administration of Grain, Beijing, China

^cBordeaux University, Bordeaux, France

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%).

Received 24 May 2018 Accepted 24 May 2018 Published 21 June 2018

Citation Ponts N, Richard-Forget F, Zhang H, Barroso G, Zhao C. 2018. Genome sequence of the emerging mycotoxin-producing filamentous fungus *Fusarium tricinctum* strain INRA104. *Genome Announc* 6:e00509-18. <https://doi.org/10.1128/genomeA.00509-18>.

Copyright © 2018 Ponts et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Gérard Barroso, gerard.barroso@u-bordeaux.fr, or Chen Zhao, zc@chinagrain.org.

G.B. and C.Z. contributed equally to this work.

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.

ACKNOWLEDGMENTS

This work was financially supported by grants from the National Key Research and Development Program of China (grant 2016YFD0501207) and the Department of Microbiology of the Food Chain (MICA) of the French National Institute for Agricultural Research (INRA).

REFERENCES

1. Beccari G, Prodi A, Tini F, Bonciarelli U, Onofri A, Oueslati S, Limayma M, Covarelli L. 2017. Changes in the *Fusarium* head blight complex of malting barley in a three-year field experiment in Italy. *Toxins* 9:120. <https://doi.org/10.3390/toxins9040120>.
2. Jestoi M. 2008. Emerging *Fusarium*-mycotoxins fusaproliferin, beauvericin, enniatins, and moniliformin—a review. *Crit Rev Food Sci Nutr* 48: 21–49. <https://doi.org/10.1080/10408390601062021>.
3. Fraeyman S, Croubels S, Devreese M, Antonissen G. 2017. Emerging *Fusarium* and *Alternaria* mycotoxins: occurrence, toxicity and toxicokinetics. *Toxins* 9:228. <https://doi.org/10.3390/toxins9070228>.
4. Svingen T, Lund Hansen N, Taxvig C, Vinggaard AM, Jensen U, Have Rasmussen P. 2017. Enniatin B and beauvericin are common in Danish cereals and show high hepatotoxicity on a high-content imaging platform. *Environ Toxicol* 32:1658–1664. <https://doi.org/10.1002/tox.22367>.
5. Sy-Cordero AA, Pearce CJ, Oberlies NH. 2012. Revisiting the enniatins: a review of their isolation, biosynthesis, structure determination and biological activities. *J Antibiot* 65:541–549. <https://doi.org/10.1038/ja.2012.71>.
6. Lysøe E, Harris LJ, Walkowiak S, Subramaniam R, Divon HH, Riiser ES, Llorens C, Gabaldón T, Kistler HC, Jonkers W, Kolseth A-K, Nielsen KF, Thrane U, Frandsen RJN. 2014. The genome of the generalist plant pathogen *Fusarium avenaceum* is enriched with genes involved in redox, signaling and secondary metabolism. *PLoS One* 9:e112703. <https://doi.org/10.1371/journal.pone.0112703>.
7. Noël T, Labarère J. 1989. Isolation of DNA from *Agrocybe aegerita* for the construction of a genomic library in *Escherichia coli*. *Mushroom Sci* 1:187–201.
8. Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. 2017. Canu: scalable and accurate long-read assembly via adaptive *k*-mer weighting and repeat separation. *Genome Res* 27:722–736. <https://doi.org/10.1101/gr.215087.116>.
9. Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. *PLoS One* 9:e112963. <https://doi.org/10.1371/journal.pone.0112963>.
10. Stanke M, Steinkamp R, Waack S, Morgenstern B. 2004. AUGUSTUS: a Web server for gene finding in eukaryotes. *Nucleic Acids Res* 32: W309–W312. <https://doi.org/10.1093/nar/gkh379>.