



Genome Sequence of *Fusarium graminearum* Strain MDC_Fg1, Isolated from Bread Wheat Grown in France

Tarek Alouane,^{a,b} H  l  ne Rimberty,^{a,b} Francis Fabre,^{a,b} Florence Cambon,^{a,b} Thierry Langin,^{a,b}  Ludovic Bonhomme^{a,b}

^aINRA, UMR 1095, Genetics, Diversity and Ecophysiology of Cereals, Clermont-Ferrand, France

^bUniversit   Clermont Auvergne, INRA, Laboratoire de G  n  tique, Diversit   et Ecophysologie des C  r  ales, Clermont-Ferrand, France

ABSTRACT *Fusarium graminearum* is a major fungal pathogen that induces *Fusarium* head blight (FHB), a devastating disease of small-grain cereals worldwide. This announcement provides the whole-genome sequence of a highly virulent and toxin-producing French isolate, MDC_Fg1.

Fusarium graminearum (phylum *Ascomycota*, class *Sordariomycetes*, order *Hypocreales*) is the main causal agent of the *Fusarium* head blight (FHB) disease that threatens small-grain cereals, including three of the world's four most widely produced cereals (i.e., maize, wheat, and barley). FHB induces severe losses in yield and grain quality and is of upmost concern for human and animal health because of the production and accumulation of mycotoxins such as deoxynivalenol (DON) (1). This makes *F. graminearum* among the 10 most-studied fungal pathogens in molecular plant pathology (2). Its whole-genome sequence was primarily made available and annotated from the North American strain PH-1 (3, 4) and further supplemented by other genomes obtained from Australian or European strains (5–7). Here, we present the whole-genome sequence of the MDC_Fg1 strain, also known as Fg1. MDC_Fg1 was isolated during field prospecting in the North of France and was selected from among a dozen isolates for its severe aggressiveness and its ability to produce DON (8, 9).

The fungus was grown on potato dextrose broth and the genomic DNA was prepared from the mycelium using a NucleoBond kit (Macherey-Nagel, D  ren, Germany). Libraries were produced using a SMRTbell template prep kit 1.0 (Pacific Biosciences, Menlo Park, CA, USA). A size selection of 12 kb was realized by using the BluePippin system (Sage Scientific, Beverly, MA, USA) according to the protocol "20 kb Template Preparation Using BluePippin Size-Selection System" (Pacific Biosciences; see <https://www.pacb.com/wp-content/uploads/Procedure-Checklist-20-kb-Template-Preparation-Using-BluePippin-Size-Selection-System-15-20-kb-Cutoff-Sequel-Systems.pdf>). The genome of MDC_Fg1 was sequenced using the Sequel PacBio platform (Pacific Biosciences) and Sequel Sequencing kit 1.2. A total of 855,732 subreads were generated, with an N_{50} of 6,441 bp, which led to a total of 3,831,551,101 bases with a 74.37 \times mean coverage. The read sequences were filtered and assembled using the Hierarchical Genome Assembly Process (HGAP4) implemented in SMRT Link v5.0 (Pacific Biosciences) using default settings, which keeps only subreads with read quality (rq) of ≥ 0.7 . The assembly resulted in 96 contigs, with a genome size of 36,807,931 bp, a G+C content of 47.97%, an N_{50} value of 1,646,471 bp, and a maximum contig size of 3,411,897 bp. The completeness of the assembly was assessed using Benchmarking Universal Single-Copy Orthologs (BUSCO) v3.0.2 (10), which estimated the genome assembly to be 98.2% complete, with 3,660 single-copy orthologs out of the 3,725 expected groups from the lineage *Sordariomycetes* data set.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [UJHA00000000](https://www.ncbi.nlm.nih.gov/nuclink/UJHA00000000) (BioSample accession

Received 13 September 2018 **Accepted** 22 October 2018 **Published** 15 November 2018

Citation Alouane T, Rimberty H, Fabre F, Cambon F, Langin T, Bonhomme L. 2018. Genome sequence of *Fusarium graminearum* strain MDC_Fg1, isolated from bread wheat grown in France. *Microbiol Resour Announc* 7:e01260-18. <https://doi.org/10.1128/MRA.01260-18>.

Editor Antonis Rokas, Vanderbilt University

Copyright    2018 Alouane 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 Thierry Langin, thierry.langin@inra.fr, or Ludovic Bonhomme, ludovic.bonhomme@inra.fr.

number [SAMEA4778736](#) and BioProject accession number [PRJEB27611](#)). The PacBio reads are available in SRA under accession number [ERP109716](#). The version described in this paper is the first version, UIHA01000000.

ACKNOWLEDGMENTS

We thank Philippe Lecomte for preparing *Fusarium graminearum* DNA samples and the GENTYANE INRA platform for the Sequel sequencing (Pacific Biosciences). We also acknowledge Antoine Mahul and the Mesocentre Clermont-Auvergne for providing the computer calculation and storage facilities.

This work is supported by the Agence Nationale de la Recherche (NewMyco project, ANR-15-CE21-0010).

REFERENCES

1. Kazan K, Gardiner DM, Manners JM. 2012. On the trail of a cereal killer: recent advances in *Fusarium graminearum* pathogenomics and host resistance. *Mol Plant Pathol* 13:399–413. <https://doi.org/10.1111/j.1364-3703.2011.00762.x>.
2. Dean R, Van Kan JAL, Pretorius ZA, Hammond-Kosack KE, Di Pietro A, Spanu PD, Rudd JJ, Dickman M, Kahmann R, Ellis J, Foster GD. 2012. The top 10 fungal pathogens in molecular plant pathology. *Mol Plant Pathol* 13:414–430. <https://doi.org/10.1111/j.1364-3703.2011.00783.x>.
3. Cuomo CA, Guldener U, Xu J-R, Trail F, Turgeon BG, Di Pietro A, Walton JD, Ma L-J, Baker SE, Rep M, Adam G, Antoniw J, Baldwin T, Calvo S, Chang Y-L, DeCaprio D, Gale LR, Gnerre S, Goswami RS, Hammond-Kosack K, Harris LJ, Hilburn K, Kennell JC, Kroken S, Magnuson JK, Mannhaupt G, Mauceli E, Mewes H-W, Mitterbauer R, Muehlbauer G, Munsterkotter M, Nelson D, O'Donnell K, Ouellet T, Qi W, Quesneville H, Roncero MIG, Seong K-Y, Tetko IV, Urban M, Waalwijk C, Ward TJ, Yao J, Birren BW, Kistler HC. 2007. The *Fusarium graminearum* genome reveals a link between localized polymorphism and pathogen specialization. *Science* 317:1400–1402. <https://doi.org/10.1126/science.1143708>.
4. King R, Urban M, Hammond-Kosack MCU, Hassani-Pak K, Hammond-Kosack KE. 2015. The completed genome sequence of the pathogenic ascomycete fungus *Fusarium graminearum*. *BMC Genomics* 16:544. <https://doi.org/10.1186/s12864-015-1756-1>.
5. Gardiner DM, Stiller J, Kazan K. 2014. Genome sequence of *Fusarium graminearum* isolate CS3005. *Genome Announc* 2:e00227-14. <https://doi.org/10.1128/genomeA.00227-14>.
6. Zapparata A, Lio D, Somma S, Muñoz V, Malfatti L, Vannacci G, Moretti A, Baroncelli R, Sarrocco S. 2017. Genome sequence of *Fusarium graminearum* ITEM 124 (ATCC 56091), a mycotoxigenic plant pathogen. *Genome Announc* 5:12–13. <https://doi.org/10.1128/genomeA.01209-17>.
7. Laurent B, Moinard M, Spataro C, Ponts N, Barreau C, Foulongne-Oriol M. 2017. Landscape of genomic diversity and host adaptation in *Fusarium graminearum*. *BMC Genomics* 18:203. <https://doi.org/10.1186/s12864-017-3524-x>.
8. Chetouhi C, Bonhomme L, Lecomte P, Cambon F, Merlino M, Biron DG, Langin T. 2015. A proteomics survey on wheat susceptibility to *Fusarium* head blight during grain development. *Eur J Plant Pathol* 141:407–418. <https://doi.org/10.1007/s10658-014-0552-0>.
9. Chetouhi C, Bonhomme L, Lasserre-Zuber P, Cambon F, Pelletier S, Renou J-P, Langin T. 2016. Transcriptome dynamics of a susceptible wheat upon *Fusarium* head blight reveals that molecular responses to *Fusarium graminearum* infection fit over the grain development processes. *Funct Integr Genomics* 16:183–201. <https://doi.org/10.1007/s10142-016-0476-1>.
10. Simão FA, Waterhouse RM, Ioannidis P, Kriventseva EV, Zdobnov EM. 2015. BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. *Bioinformatics* 31:3210–3212. <https://doi.org/10.1093/bioinformatics/btv351>.