

# Draft Genome Sequence of *Fusarium fujikuroi* B14, the Causal Agent of the Bakanae Disease of Rice

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Here, we present the genome sequence of a Korean strain (B14) of *Fusarium fujikuroi*, a fungal rice pathogen. The final assembly consists of 455 contigs with 43,810,516 bp and 14,017 predicted genes. Comparison with the *F. verticillioides* 7600 genome revealed a reference coverage of 83% (66.3% of reads mapped).

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The genus *Fusarium*, a large group of filamentous ascomycetous fungi, includes a broad range of plant pathogens in many agricultural crops worldwide (1). Some species produce mycotoxins harmful to both humans and plants (2). Thus far, genomes of three species (*F. graminearum*, *F. oxysporum*, and *F. verticillioides*) have been sequenced (3–5). *F. fujikuroi* (teleomorph, *Gibberella fujikuroi*; synonym, *G. fujikuroi* mating population C) is a biologically and phylogenetically distinct species within the *G. fujikuroi* species complex and causes bakanae disease of rice (1, 6). This fungus also produces several toxic secondary metabolites in infected plants (1). Here, we present the genome sequence of *F. fujikuroi* (strain B14) isolated from rice in South Korea and confirm its pathogenicity in rice. This is the first available *F. fujikuroi* whole-genome sequence and the second, after the *F. verticillioides* 7600 strain, among the *G. fujikuroi* complex.

Genome sequencing of *F. fujikuroi* B14 was carried out using an Illumina HiSeq 2000-based whole-genome shotgun strategy. A total of 35,306,706 paired-end reads of ~3.57 Gb (101 nucleotide [nt] cycle, 486-bp average paired distance) were preprocessed and *de novo* assembled using CLC Genomics workbench 5.5. Initially, the assembly was 43,794,120 bp in length with 338 scaffolds (N<sub>50</sub> 678,621 bp, 48.3% G+C, 1,079 contigs). After automatic gap closing using GapFiller version 1.9 (<http://www.baseclear.com>) with the same reads, the final assembly consisted of 455 contigs in 333 scaffolds with a length of 43,810,516 bp exclusive of N's in remaining gaps. After masking repetitive sequences using a search against Repbase (<http://www.girinst.org/repbase>), 14,017 protein-coding genes were predicted using Augustus 2.5.5 (<http://augustus.gobics.de>) with *F. graminearum* parameters. Based on a BLASTP search against the UniRef90 database, significant matches (E value <10<sup>-5</sup>) were identified for 13,734 genes; 9,143 hits were derived from *F. oxysporum*. We also identified 576 tRNA genes using tRNAscan-SE (7). For comparative genomic analysis, the preprocessed Illumina reads were mapped to chromosomal reference sequences for the three known *Fusarium* species ([http://www.broadinstitute.org/annotation/genome/fusarium\\_group](http://www.broadinstitute.org/annotation/genome/fusarium_group)

[/MultiHome.html](#)). *F. verticillioides* 7600 was most similar to B14 in terms of reference coverage (83%; 66.3% of reads were mapped). The percent coverage values of *F. oxysporum* 4287 and *F. graminearum* PH-1 were 57% and 29%, respectively. BLASTP analysis showed that 46.2% and 42.1% of the B14 genes matched those of *F. oxysporum* (total, 17,701 genes) and *F. verticillioides* (14,188 genes), respectively. In the B14 genome, all conserved gene clusters for secondary metabolites previously characterized in *F. fujikuroi* were identified, including those for gibberellin, fumonisin, bikaverin, melanin, fusarin, fusaric acid, and carotenoids. Additionally, *F. fujikuroi* B14, confirmed as the *MAT1-2* mating type strain, carries 20 polyketide synthase (PKS) genes, including two nonreducing PKS and four PKS-NRPS (non-ribosomal peptide synthetase) hybrid genes.

In conclusion, the *F. fujikuroi* B14 genome will contribute to a greater understanding of the biology and evolution of the *G. fujikuroi* species complex, as well as the genus *Fusarium*.

**Nucleotide sequence accession number.** The sequence determined in this study was deposited in the GenBank database under accession number ANFV00000000.

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## REFERENCES

1. Leslie JF, Summerell BA. 2007. The *Fusarium* laboratory manual. Blackwell Publishing, Ames, OH.
2. Desjardins AE, Proctor RH. 2007. Molecular biology of *Fusarium* mycotoxins. *Int. J. Food Microbiol.* 119:47–50.
3. Cuomo CA, Güldener U, Xu JR, Trail F, Turgeon BG, Di Pietro A, Walton JD, Ma LJ, Baker SE, Rep M, Adam G, Antoniw J, Baldwin T, Calvo S, Chang YL, 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 HW, Mitterbauer R, Muehlbauer G, Münsterkötter M, Nelson D, O'Donnell K, Ouellet T, Qi

- W, Quesneville H, Roncero MI, Seong KY, 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.
4. Ma L-J, van der Does HC, Borkovich KA, Coleman JJ, Daboussi M-J, Di Pietro AD, Dufresne M, Freitag M, Grabherr M, Henrissat B, Houterman PM, Kang S, Shim W-B, Woloshuk C, Xie X, Xu J-R, Antoniw J, Baker SE, Bluhm BH, Breakspear A, Brown DW, Butchko RAE, Chapman S, Coulson R, Coutinho PM, Danchin EGJ, Diener A, Gale LR, Gardiner DM, Goff S, Hammond-Kosack KE, Hilburn K, Hua-Van A JW, Kazan K, Kodira CD, Koehrsen M, Kumar L, Lee Y-H, Li L, Manners JM, Miranda-Saavedra D, Mukherjee M, Park G, Park J, Park S-Y, Proctor RH, Regev A, Ruiz-Roldan MC, Sain D, Sakthikumar S, Sykes S, Schwartz DC, Turgeon BG, Wapinski I, Yoder O, Young S, Zeng Q, Zhou S, Galagan J, Cuomo CA, Kistler HC, Rep M, Rep M. 2010. Comparative genomics reveals mobile pathogenicity chromosomes in *Fusarium*. *Nature* 464:367–373.
  5. Rep M, Kistler HC. 2010. The genomic organization of plant pathogenicity in *Fusarium* species. *Curr. Opin. Plant Biol.* 13:420–426.
  6. O'Donnell K, Cigelnik E, Nirenberg HI. 1998. Molecular systematics and phylogeography of the *Gibberella fujikuroi* species complex. *Mycologia* 90:465.
  7. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25: 955–964.