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Complete genome sequence of *Fusarium kyushuense* WFK101 isolated from *Vulpia myuros* near a rice field in Korea

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국내 논 주변 잡초 들묵새(*Vulpia myuros*)로부터 분리한 *Fusarium kyushuense* WFK101의 참조유전체 조립

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Fusarium kyushuense WFK101 was isolated from *Vulpia myuros* collected near a rice field in South Korea. Whole genome of *F. kyushuense* WFK101 was sequenced using the Illumina HiSeq 2500 platform and confirmed to consist of four chromosomes. As a result of the analysis of the average nucleotide identity between *F. kyushuense* WFK101 and the reference species of the *Fusarium sambucinum* species complex, it showed the highest similarity of 98.8% with *F. kyushuense* NRRL 25348. *Fusarium kyushuense* WFK101 has 47 secondary metabolite gene clusters, and the *Tri16* gene was found next to the *Tri1* gene on chromosome 1. The genomic information of *F. kyushuense* WFK101 provides in-depth genetic information about *F. kyushuense*, which synthesizes the most poisonous type A trichothecene.

Keywords: *Fusarium kyushuense*, complete genome sequence, Illumina HiSeq, phylogenetic analysis, type A trichothecene

Fusarium kyushuense, one of the *Fusarium sambucinum* species complex (FSSP), can cause plant diseases and produce type A trichothecene in kernels (Aoki and O'Donnell, 1998). Type A trichothecene is the most concerned *Fusarium* trichothecene due to its contamination of agricultural products and high toxicity to humans and animals (Mahato *et al.*, 2022). The genetic variations of the *Tri1* gene and *Tri16* gene of *Fusarium* strains are known to determine type A trichothecene production (Wang *et al.*, 2023). In our previous study, we obtained *F. kyushuense* WFK101 from gramineous weed *Vulpia myuros* collected near the rice field in Boseong, South Korea (Ahn *et al.*, 2022). Since *F. kyushuense* is a threatening fungal plant pathogen that can produce type A trichothecenes, the genome of *F. kyushuense* WFK101 was sequenced.

Fusarium kyushuense WFK101 was grown on 5 ml of potato dextrose broth at 25°C for 3 days under shaking condition (180 rpm). A modified CTAB method (Cota-Sánchez *et al.*, 2006) was used to get the genomic DNA of *F. kyushuense* WFK101 from the culture. The whole genome sequencing of *F. kyushuense* WFK101 was performed using an Illumina HiSeq 2500 platform and a paired-end strategy (Illumina). On average, 112 times as many Illumina reads were used, and 127 contigs were made using SPAdes assembler v3.14.1 (Prjibelski *et al.*, 2020) for *de novo* assembly. By using the reference sequence of *F. asiaticum* KCTC 16664 (GCA_025258505.1; Jeong *et al.*, 2023), 49 contigs were joined together to make 8 contigs. These were then aligned to four chromosomes of *F. asiaticum* KCTC 16664, with one gap near the centromeric region of each (Table 1, Fig. 1A). Among the remaining contigs, 101 were

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Table 1. Draft genome feature of *Fusarium kyushuense* WFK101 compared with *Fusarium kyushuense* NRRL 25348

Features	*Fusarium kyushuense*	
	WFK101	NRRL 25348*
Genome size, bp	36,557,249	36,015,118
GC content, %	47.4	47.7
Number of contigs	22	325
N_{50}, bp	7,019,575	251,145
Number of protein-coding genes	11,964	11,588
Number of InterPro	9,384	9,141
Number of secondary metabolite gene clusters	47	47
BUSCO completeness, %	99.02	97.49
GenBank accession number	JAWRWB000000000	JABCJU000000000

*Note: The genome sequence of *F. kyushuense* NRRL 25348 was obtained from GenBank.

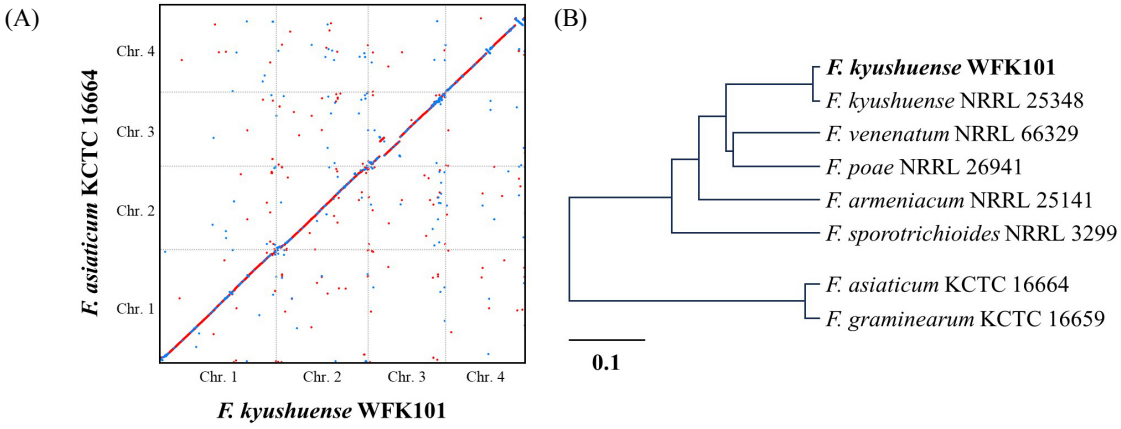

Fig. 1. Genome synteny and phylogenetic analysis of *F. kyushuense* WFK101. (A) Synteny plot of the chromosomes of *F. kyushuense* WFK101 and *F. asiaticum* KCTC 16664 was created using the MUMmer alignment. The red dots represent the synteny regions and the blue dots represent the rearrangement regions between the two strains. The lines connected by dots represent the high synteny regions. (B) Phylogenetic tree was constructed using hclust function in R package based on the average nucleotide identity (ANI) values of *F. kyushuense* WFK101 and other 7 strains of *Fusarium*. The whole genome sequences of 7 strains of *Fusarium* were obtained from GenBank and the ANI values were calculated using OrthoANI.

excluded from further analysis due to mitochondrial DNA, or a short size less than 500 bp. The remaining 14 unplaced contigs totaled around 64 kb.

For this study, we used OrthoANI (Lee *et al.*, 2016) to find the average ANI values between *F. kyushuense* WFK101 and 7 strains of FSSP (Laraba *et al.*, 2021). The genome of *F. kyushuense* WFK101 showed about 83.85–98.80% identity with seven representative strains of FSSP. Even though they are only 83.85% alike, the chromosome structures of *F. kyushuense* WFK101 and *F. asiaticum* KCTC 16664 are very similar (Fig. 1A). ANI-based phylogenetic tree showed that the genome of *F. kyushuense* WFK101 had 98.80% identity with *F. kyushuense* NRRL (Fig. 1B).

Funannotate pipeline v.1.8.9 (Palmer and Stajich, 2020) was used to annotate genes, and the results of *F. kyushuense* WFK101 and *F. kyushuense* NRRL 25348 were compared (Table 1). *Fusarium kyushuense* WFK101 and *F. kyushuense* NRRL 25348 were found to have 47 secondary metabolite gene clusters using antiSMASH analyses (Blin *et al.*, 2021). In the genomes of *F. kyushuense* WFK101 and *F. kyushuense* NRRL 25348, the trichothecene biosynthetic gene cluster was found on chromosome 2. The *Tri16* gene, a key gene for type A trichothecene biosynthesis, was found next to the *Tri1* gene on chromosome 1 (Wang *et al.*, 2023). The complete genome sequence of *F. kyushuense* WFK101 can provide basic information about the synthesis of type A trichothecene of *F. kyushuense*.

Strain and nucleotide sequence accession number

Fusarium kyushuense WFK101 has been deposited in the Korean Collection for Type Cultures (KCTC) under the number KCTC 56956. The complete genome sequence of *F. kyushuense* WFK101 has been deposited in the NCBI GenBank database under the accession number JAWRWB000000000. The genome sequence of *F. kyushuense* WFK101 was also deposited at the National Agricultural Biotechnology Information Center (NABIC) under the accession number NG-1860-000001–NG-1860-000018.

적 요

Fusarium kyushuense WFK101은 전라남도 보성의 논 주변에서 채집된 잡초, 들묵새에서 분리되었다. *Fusarium kyushuense*의 전장유전체는 Illumina HiSeq 2500 플랫폼을 사용하여 해독되었고 4개의 염색체가 확인되었다. *Fusarium kyushuense* WFK101와 *Fusarium sambucinum* species complex 내 대표 균주 간의 염기서열 평균 유사도 분석 결과, *F. kyushuense* NRRL 25348과 98.80%의 가장 높은 유사도를 보였다. 유전자 주석 분석 결과 *F. kyushuense* WFK101은 47개의 2차 대사산물 유전자 클러스터를 가지고 있으며, type A 트라이코세신 합성을 결정하는 *Tri16* 유전자는 1번 염색체 상의 *Tri1* 유전자 옆에 존재하는 것을 확인하였다. *Fusarium kyushuense* WFK101의 유전체 정보는 트라이코세신 중 가장 독성이 강한 type A 트라이코세신을 합성하는 *F. kyushuense*의 심층적인 유전정보를 제공한다.

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Conflict of Interest

The authors declare that there is no conflict of interest.

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