

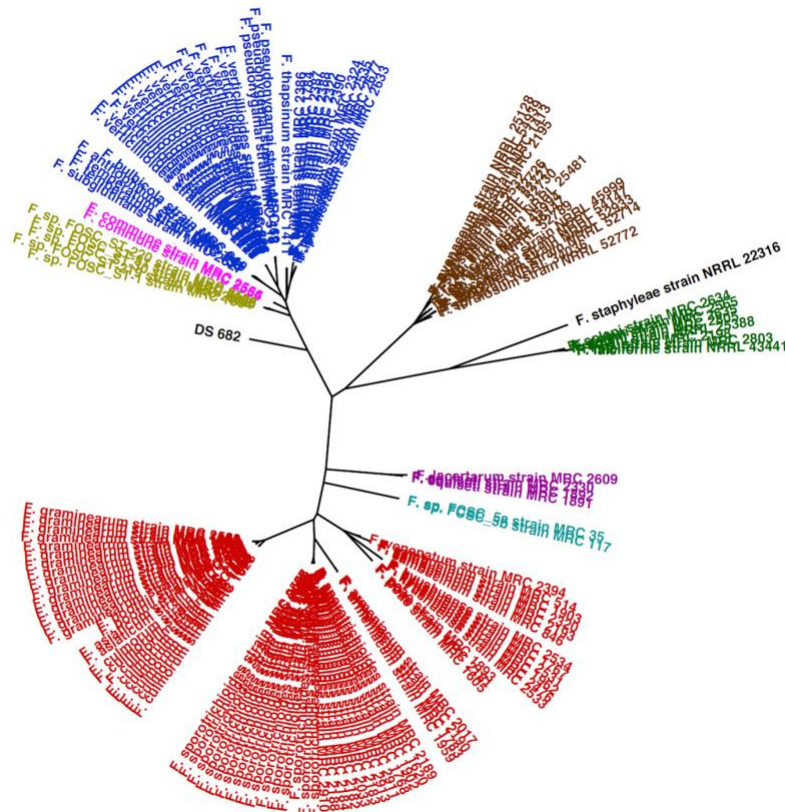
Draft Genome of *Fusarium* sp. strain DS 682, a novel Fungal isolate from the Grass Rhizosphere



Bhattacharjee A, Anderson LN, Alfaro T, Porras-Alfaro A, Jumpponen A, Hofmockel KS, Jansson JK, Anderton CR, Nelson WC. 2021. DOI: [10.1128/MRA.00884-20](https://doi.org/10.1128/MRA.00884-20)

ABSTRACT

The novel fungal strain, *Fusarium* sp. DS 682, was isolated from the rhizosphere of the perennial grass, *Bouteloua gracilis*, at the Konza Prairie Biological Station in Kansas. This fungal strain is common across North American grasslands and is resilient to environmental fluctuations. The draft genome is estimated to be 97.2% complete.



DATASET ACCESSION ID

KS4A-IsoG.1.0_FspDS682 ()

DATA PACKAGE DOI

Data DOI: [10.25584/KS4AIsoGFspDS682/1635527](https://doi.org/10.25584/KS4AIsoGFspDS682/1635527)

Data Download: https://release.datahub.pnnl.gov/released_data/1364

RELATED METAGENOME

[KS-TmG.1.0](#)

FIELD SITE

Konza Prairie Biological Station (KPBS), [Field Site 4A](#)
Manhattan, KS, USA.

BIOSAMPLE RECORD

Identifiers:	BioSample Name: KS4A-IsoG.1.0_FspDS682 Assembly Name: SF-1-001 Pooled Lab IDs: SF-1_R1_001, SF-1_R2_001 Locus Tag: IL306
Organism:	Fusarium sp. (277345)
Isolate Strain:	<i>Fusarium sp.</i> DS 682
Isolate Source	Bouteloua gracilis
Metadata Package:	MIGS: eukaryote, soil; version 5.0 Package
Assembly method:	Megahit
Assembly version/date:	v1.1.2
Sequencing strategy:	Illumina HiSeq X
Data Repository:	DataHub
Full/Partial Genome:	Draft Genome; 97.2% complete
Assembly Size:	11, 597 contigs (see full sequence report)
Predicted Proteins:	15, 049 predicted proteins
Description:	Draft genome of the fungal soil isolate <i>Fusarium sp.</i> DS 682, from the rhizosphere of <i>Bouteloua gracilis</i> , a blue grama perennial grass grown at Konza Prairie Biological Station field site 4A in Manhattan, KS.
BioProject:	PNNL Soil Microbiome SFA 'Phenotypic Response of the Soil Microbiome to Environmental Perturbations'

FINAL ASSEMBLY STATISTICS

Minimum Scaffold Length	Number of Scaffolds	Number of Contigs	Total Scaffold Length	Total Contig Length	Contig Coverage
All	11,599	11,599	56,064,852	56,064,852	100.00%
250	11,599	11,599	56,064,852	56,064,852	100.00%
500	8,172	8,172	54,757,449	54,757,449	100.00%
1 KB	5,184	5,184	52,678,573	52,678,573	100.00%
2.5 KB	3,150	3,150	49,531,896	49,531,896	100.00%
5 KB	2,123	2,123	45,877,004	45,877,004	100.00%
10 KB	1,388	1,388	40,721,435	40,721,435	100.00%
25 KB	591	591	27,959,546	27,959,546	100.00%
50 KB	185	185	13,880,992	13,880,992	100.00%
100 KB	26	26	3,388,037	3,388,037	100.00%

DATA TAGS

draft genome, soil, soil microbiology, fungi, KS, isolate, *Fusarium*, grassland, rhizosphere, earth systems science, biology, data package, Illumina HiSeq, KO, raw reads, assembly, protein sequence predictions, MIGS.eu.soil.5.0

DATA PACKAGE CONTENTS

MIGS Eukaryote/Soil Genome Standard Information

- [KS4A-IsoG.1.0_FspDS682_MIGS.eu.soil.5.0 \(.xlsx\)](#)

Use for eukaryotic genomic sequences. Organism must have lineage Eukaryota. This package includes attributes defined by the Genome Standards Consortium (GSC) to formally describe and standardize sample metadata.

Raw Genomic Data [31.8 GB; 2 items]

- [RawReads_KS4A-IsoG.1.0_FspDS682](#)

Name format:

<field site>-<sequencing lane>_<paired ends (forward and reverse) 1/2>.fastq

1. SF-1_R1_001.fastq
2. SF-1_R2_001.fastq

Genomic Assembly Files [55.9 MB; 2 items]

- [Assembly_KS4A-IsoG.1.0_FspDS682](#)
 1. SF-1-001_final_contigs.bbstats (assembly parameters)
 2. Fusarium_sp._DS_682.v0.1.fsa (sequence file)

Functional Annotation Files [7.5 MB; 2 items]

- [FunctionalAnnotations_KS4A-IsoG.1.0_FspDS682](#)
 1. Fusarium_sp._DS_682.v0.1.pep (predicted protein file)
 2. KS4A-IsoG.1.0_FspDS682_Fig 1.pdf (phylogenetic tree)

Reference NCBI Deposit Information

- BioProject: [PRJNA664411](#)
- BioSample: [SAMN16214050](#)
- GenBank: [JACYFE000000000](#)
- Assembly: [GCA_014764975.1](#)
- WGS: [JACYFE01](#)
- SRA: [SRS7709489](#)

Reference GenBank Sequence (Other)

[Fusarium sp. isolate DS785 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence](#)

529 bp linear DNA
Accession: MK808907.1
GI: 1621556378

[> DS682 \(ITS1 partial\)](#)

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GAGGGATCATTACCGAGTTTACAACCTCCCAAACCCCTGTGAACATACCTTACTGTTGCCTCGGCGGATCAGCCCCGCG
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