

Draft Genome of the Soil Fungal Isolate *Fusarium chlamydosporum* DS 682



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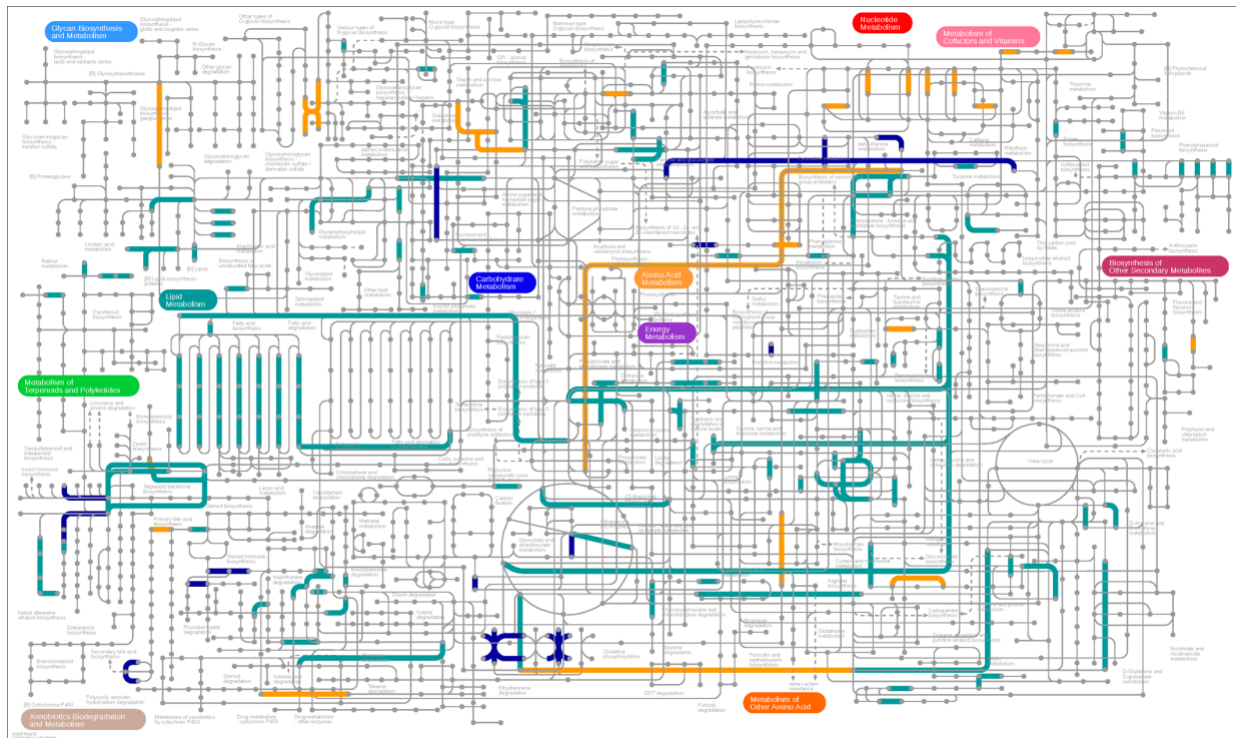
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ABSTRACT

Fusarium chlamydosporum DS 682 was isolated from Konza Prairie Biological Station, a region that experiences wide fluctuations in moisture, making it an ideal candidate for studying fungal dynamics under drought conditions. The draft genome is estimated to be 97.2% complete.



GENOME ACCESSION

KS4A-IsoG.1.0_FcDS682

DATA DOI

10.25584/KS4AlsoGFcDS682/1635527

PARENT METAGENOME

[KS-TmG.1.0](#)

FIELD SITE

Konza Prairie Biological Station Field Site 4A, Manhattan, KS, USA.

BIOSAMPLE RECORD

Identifiers:	BioSample Name: KS4A-IsoG.1.0_FcDS682 Assembly Name: SF-1-001 Pooled Lab IDs: SF-1_R1_001, SF-1_R2_001
Organism:	<i>Fusarium chlamydosporum</i> DS 682
Isolate Origin:	<i>Bouteloua gracilis</i>
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:	13,284 contigs (56.5 Mbp; avg=4253 bp, N50=24701 bp)
Predicted Proteins:	19,949 predicted proteins (8,849 assigned KO annotations)
Description:	Draft genome of the fungal soil isolate <i>Fusarium chlamydosporum</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 PACKAGE CONTENTS

MIGS Eukaryote/Soil Genome Standard Information (metadata)

- [KS4A-IsoG.1.0_FcDS682_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

- [RawReads_KS4A-IsoG.1.0_FcDS682 \(2 items\)](#)

Name format:

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

SF-1_R1_001.fastq.gz

SF-1_R2_001.fastq.gz

Genomic Assembly Files

- [Assembly_KS4A-IsoG.1.0_FcDS682 \(2 items\)](#)

SF-1-001_final_contigs.bbstats (assembly parameters)

SF-1-001_final_contigs.fasta (assembled contigs)

Functional Annotation Files

- [FunctionalAnnotations_KS4A-IsoG.1.0_FcDS682 \(2 items\)](#)

SF-1-001.genemark_KOfam.faa (predicted protein file)
KS4A-IsoG.1.0_FcDS682 Metabolism.pdf (phylogenetic predicted metabolic KO activities)

DATA TAGS

Draft genome, arid soil, soil microbiome, SFA, KS, KPBS, *Fusarium chlamydosporum*, fungal pathogens, grassland, earth systems science, biology, data package, Illumina HiSeq, KO, raw reads, assembly, protein sequence predictions, MIGS.eu.soil.5.0

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