GENOME SEQUENCES

Chromosome-Level *Aspergillus flavus* Strain CA14 Genome Assembly

Mark A. Weaver,[a] Brian M. Mack,[b] Matthew K. Gilbert[b]

[a]Biological Control of Pests Research Unit, National Biological Control Laboratory, USDA ARS, Stoneville, Mississippi, USA
[b]Food and Feed Safety Unit, USDA ARS, New Orleans, Louisiana, USA

ABSTRACT We report here a chromosome-level genome assembly of the aflatoxigenic fungus *Aspergillus flavus* strain CA14. This strain is the basis for numerous studies in fungal physiology and secondary metabolism. This full-length assembly will aid in subsequent genomics research.

The filamentous fungus *Aspergillus flavus* is an opportunistic pathogen of several crops, including corn, cotton, and peanut, and colonizes many stored grains intended for food and feed. It may be best known as a producer of aflatoxins, the most potent carcinogens found in nature (1). Isolates of *A. flavus* within a field population vary greatly with regard to aflatoxin production and microsatellite-based haplotype (2, 3). Additionally, numerous species-specific genes and genomic rearrangements have been documented within the *A. flavus* clade of *Aspergillus* section Flavi (4). Until recently, the reference genome for *A. flavus* was the Sanger-sequenced assembly of strain 3357, with 5× coverage and 331 scaffolds (5) (Table 1). Presently, >100 sequenced genomes have been made publicly available for *A. flavus*, created using various sequencing technologies or combinations of available systems (https://www.ncbi.nlm.nih.gov/genome/browse#%21/overview/aspergillus%20flavus). A pseudomolecule-level assembly of strain 3357 and AF13 (6) and full chromosome-level assembly of strain 3357 (7) were also reported in 2020 (Table 1). We report here the sequence of strain CA14, assembled at the chromosome level. Strain CA14 is a wild-type, large-sclerotia-producing, aflatoxigenic strain isolated from pistachio at the Wolfskill Grant Experimental Farm of University of California, Davis (8), that has been used in numerous knockout and functional studies of *A. flavus* isolates (9, 10).

Genomic DNA (gDNA) was extracted from ~10^7 conidia of *A. flavus* strain CA14 by grinding in liquid nitrogen and extracting in hot cetyltrimethylammonium bromide buffer (11). After gDNA cleanup, creation of a PacBio Express library, and size selection,

TABLE 1 Assembly statistics of some representative *Aspergillus flavus* genomes

Aspergillus flavus strain	GenBank assembly accession no.	Genome size (mbp)	Fold coverage (×)	No. of contigs/ scaffolds	N_{50} (Mb)	No. of genes predicted
3357[a]	GCA_000006275.2	36.89	5	331	2.39	13,485
3357[b]	GCA_009017415.1	37.75	600	8		
3357[c]	GCA_014117465.1	37.0	70	8[e]	2.40	
AF13[c]	GCA_014117485.1	37.44	70	8[e]	2.39	
KuPG#1[d]	GCA_003709025.1	37.7	121	199	1.3	12,846
CA14	GCA_014784225.1	37.81	140	8	6.27	

[a] From reference 5.
[b] From reference 7.
[c] From reference 6.
[d] Chang et al. (12), derived from isolate CA14.
[e] Pseudochromosomes inferred from alignment to *Aspergillus oryzae* strain RIB40.

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Address correspondence to Mark A. Weaver, mark.weaver@usda.gov.

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6.75 Gb of sequence (140× coverage) was generated from a single 10-hour single-molecule real-time (SMRT) cell using PacBio Sequel. *De novo* genome assembly was done using Flye (version 2.5, settings at "genome size 37m -t 14") (https://github.com/fenderglass/Flye) followed by three rounds of polishing with Arrow (version 2.3.3, default settings) (https://github.com/PacificBiosciences/GenomicConsensus) yielding 8 full chromosome-length scaffolds with an N_{50} value of 6.27 Mb. Nine to 11 telomere repeat sequences were present on six of the contig ends.

Data availability. The GenBank accession number is GCA_014784225.1, and the SRA accession number is SRR12683076.

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