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GENOME SEQUENCES

Genome Sequence of an *Aspergillus flavus* CA14 Strain That Is Widely Used in Gene Function Studies

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ABSTRACT *Aspergillus flavus* produces aflatoxins that adversely impact human health and the economy. We report the genome sequence of *A. flavus* CA14 that has been widely used in gene function studies. The information will benefit *A. flavus* functional genomics studies on fungal development, secondary metabolite production, and fungus-host plant interactions.

Aspergillus flavus, a member of the Ascomycota, produces mycotoxins and infects corn, cotton, peanuts, and tree nuts. It is also the second most common causal agent of invasive aspergillosis in humans (1). Wild-type *A. flavus* CA14 was originally isolated from pistachios in the Wolfskill Grant Experimental Farm of University of California, Davis (2). Two versions of transformation recipients that are defective in the nonhomologous end-joining (NHEJ) pathway have been created from CA14, i.e., ATCC MYA-4921 (Δ*ku70* Δ*pyrG*) and SRRC1709 (PTSΔ*ku70* Δ*pyrG*) (3). While the ATCC MYA-4921 strain allows only gene knockout experiments to be performed, the SRRC1709 strain has been used satisfactorily in gene knockout and subsequent genetic complementation experiments. Other NHEJ-deficient strains from NRRL3357 and AF70 are available, but the majority (>90%) of gene function studies have been carried out with CA14. Until now, over 100 *A. flavus* genes have been disrupted, and the functions of most of these genes have been characterized (4, 5). The genome-sequenced strain CA14 KuPG#1 is derived directly from ATCC MYA-4921 and is the immediate parental strain of SRRC1709.

The CA14 strain was grown in potato dextrose broth, and genomic DNA was purified using a Quick-DNA fungal/bacterial kit (Zymo Research, Irvine, CA). DNA libraries were prepared with a NEBNext Ultra II DNA library prep kit for Illumina (New England BioLabs, Ipswich, MA), and sequencing was performed on an Illumina MiSeq v2 machine with 250-bp paired-end reads (North Carolina State University, Genomic Sciences Laboratory). A total of 9.2 million paired reads were obtained. Adapters and low-quality sequences were removed from the reads using BBDuk (version 3/30/17). Genome assembly of high-quality sequence reads (8.8 million) was carried out using SPAdes (version 3.10.1) with k-mer sizes of 21, 33, 55, 77, 99, and 127. The assembled genome had a total size of 37.7 Mb, with a G+C content of 47.4%. The total number of contigs is 199, with an N_{50} value of 1.3 Mb and an L_{50} of 8.

antiSMASH fungal version 5.0 (6) was used to identify secondary metabolite gene clusters in the CA14 genome; 76 regions were detected, including 28 that were homologous or similar to known gene clusters. Analysis with SMURF (version 2010) (7) identified a total of 77 secondary metabolite biosynthesis backbone genes, including eight for dimethylallyl tryptophan synthase, 32 for polyketide synthase (PKS), 34 for nonribosomal peptide synthase (NRPS), and three for hybrid PKS-NRPS. Alignment of the CA14 and NRRL3357 (8) genome sequences with Mauve (version 20150226) (9) showed that a large 1.5-Mb segment of the NRRL3357 genome was split into 277 kb,

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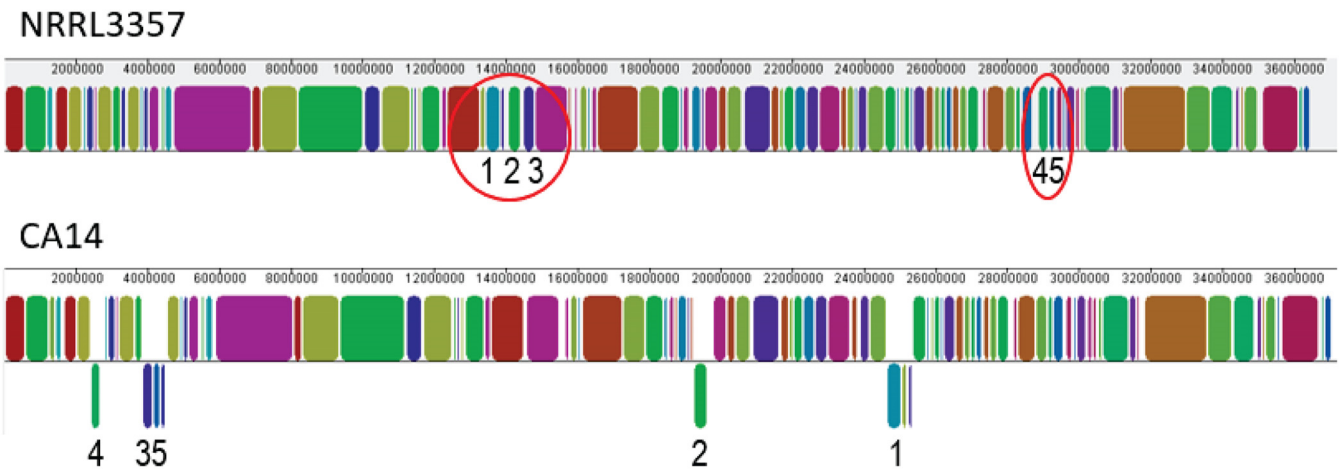

FIG 1 Alignment of genome sequences of *A. flavus* NRRL3357 and *A. flavus* CA14. Colored blocks are locally colinear blocks (LCBs), which indicate homologous regions between the two genomes. Two continuous regions (123 and 45) on the chromosomes of NRRL3357 that were split and translocated in the CA14 genome are shown as inverted segments with the corresponding numbers.

433 kb, and 716 kb and translocated to three locations in the CA14 genome (Fig. 1). Another 478-kb genome segment of NRRL3357 corresponding to two split segments of 290 kb and 196 kb was also translocated.

Data availability. This genome sequence has been deposited at the NCBI under the accession number QQZZ00000000. The accession number for the raw sequence read is PRJNA483051.

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