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GENOME SEQUENCES

Draft Genome Sequences of *Alternaria* Strains Isolated from Grapes and Apples

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ABSTRACT Here, we report the draft genome sequences of *Alternaria alternata*, isolated from seedless grapes, and *Alternaria arborescens* and *Alternaria atra*, isolated from Red Delicious apples, all from the Washington, DC, area.

Fungi belonging to the genus *Alternaria* are the primary molds contaminating cereal crops, rape seed, tomato, apples, citrus fruits, and fruit juices (1–3) and are of increasing environmental concern, as more than 70 *Alternaria* toxins have been reported (4–6). There is strong evidence that *Alternaria* mycotoxins may be mutagenic and carcinogenic to human and animals (4, 7, 8). Here, we present whole-genome sequences of isolate MOD1-FUNGI5 (*Alternaria alternata*) from seedless grape and isolates MOD1-FUNGI6 (*Alternaria arborescens*) and MOD1-FUNGI7 (*Alternaria atra*) from Red Delicious apples. Although limited data are available about the presence of *Alternaria* toxins in food and feed products, comparative genomics should allow us to catalog the biochemical pathways for mycotoxin synthesis and predict the pathogenic potential of these fungi.

Red Delicious apples and seedless grapes were purchased from local supermarkets in the Washington, DC, area at weekly intervals. The grapes and the apples were tested for fungal contamination as follows: they were placed in several sterilized beakers covered with a double layer of aluminum foil and incubated at room temperature (~21°C) for 2 to 4 weeks. Any visible growth was transferred and purified on peptone-dextrose agar (PDA) agar. Pure mold cultures were further subcultured on Czapek yeast extract agar (CYA), malt extract agar (MEA), and 25% glycerol nitrate agar (G25N) at 5°C, 25°C, and 37°C for microscopic examination and identification (9–13). DNA libraries were prepared with an Illumina Nextera XT DNA library preparation kit (Illumina, Inc., San Diego, CA) and were sequenced on the Illumina NextSeq platform with the NextSeq 500/550 v2 midoutput reagent cartridge (no. of samples, 8) and with 2 × 150-bp paired-end sequencing. The average insert size was 210 bp. Low-quality reads were trimmed with a quality threshold of $Q > 30$ using Trimmomatic (14) with the NexteraPE adapter file, and the trimmed reads were subjected to *de novo* assembly using the SPAdes assembler v3.12.0 (15). Quality assessment of the assembly was performed with QUAST (16) (Table 1). All software programs were run using default settings unless otherwise noted. The reads were assembled to 1,170 contigs for *Alternaria alternata*, 520 contigs for *Alternaria arborescens*, and 948 contigs for *Alternaria atra*, and the coverages were 27×, 115×, and 104×, respectively. The three genomes were analyzed using BUSCO for assessing genome assembly completeness (17) using the lineage data set fungi_odb9; MOD1-FUNGI5 had 3 missing and 3 fragmented benchmarked universal single-copy orthologs (BUSCOs) out of 290, MOD1-FUNGI6 had 2 missing and 2 fragmented, and MOD1-FUNGI7 had 3 missing and 4 fragmented.

Initial identification of the *Alternaria* species was performed by k-mer and BLAST

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TABLE 1 Quality assessment of assemblies using QUAST

Sample	No. of 150-bp reads	No. of contigs >500 bp long	Total no. of contigs	Length (bp) of:			GC content (%)	N_{50} (bp)	Coverage (×)
				Largest contig	Smallest contig	Total assembly			
MOD1-FUNGI5	35,876,557	1,170	1,170	315,762	500	33,510,320	51.2	71,241	27
MOD1-FUNGI6	56,961,781	520	664	1,990,081	200	33,792,118	51.1	319,518	115
MOD1-FUNGI7	52,878,830	948	1,862	815,703	200	34,791,487	51.0	161,367	104

matching of the contigs against whole-genome sequences available in GenBank. BLAST matching of the contigs to a collection of multilocus sequence typing (MLST) genes, which included elongation factor 1 alpha, calmodulin, glyceraldehyde 3-phosphate dehydrogenase, actin, and 18S rRNA genes from 141 *Alternaria* species, helped identify the sequence of MOD1-FUNGI7 as *Alternaria atra* and confirmed the identity of the other two isolates.

Data availability. The draft genome assemblies were deposited in DDBJ/ENA/GenBank under BioProject number PRJNA482816, and the complete genome sequences are available in GenBank under the accession numbers SJDQ00000000, SJDP00000000, and SJDO00000000. The FASTQ files are available in the SRA under the accession numbers SRS3811035, SRS3811040, and SRS3811041. The genome sequences reported in this announcement are the first versions.

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