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GENOME SEQUENCES

Draft Genome Sequence of *Kazachstania slooffiae*, Isolated from Postweaning Piglet Feces

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ABSTRACT *Kazachstania slooffiae* is a dimorphic fungus which colonizes the feces and gastrointestinal tract of postweaning pigs. This fungus persists in the gut environment of piglets into adulthood and is implicated in porcine health through microbe-microbe and microbe-host interactions. Here, we report a draft genome sequence for *K. slooffiae* ABBL.

Kazachstania slooffiae is a dimorphic fungus in the *Kazachstania* (*Arxiozyma*) *telluris* species complex and is a member of the family Saccharomycetaceae. *K. slooffiae* is the dominant fungus in the gastrointestinal tract of postweaning piglets, and this dominance persists in the long term (1–4) with positive inferred interactions with beneficial gut bacteria (4–8). Weaning is a period of stress and predisposition to infection, resulting in poor growth performance (9–11). The ability to alter microbiome members, including *K. slooffiae*, to enhance the host health and growth is of interest to industry to reduce financial losses.

Piglet feces were sterilely collected on day 24 of life (day 3 postweaning) at the Beltsville Agricultural Research Center in the Animal Biosciences and Biotechnology Laboratory. This animal study was reviewed and approved by the USDA–ARS Institutional Animal Care and Use Committee of the Beltsville Agricultural Research Center. The feces were diluted in sterile 1× phosphate-buffered saline and cultured on yeast potato dextrose (YPD) agar (BD Difco, Franklin Lakes, NJ) supplemented with 0.1 mg/ml cefoperazone sodium salt (Cef) (Sigma-Aldrich, St. Louis, MO) to prevent bacterial growth. Cultures were grown at 37°C and 5% CO_2 for up to 72 h. Colonies of strain ABBL were isolated by streaking onto YPD + Cef agar; the 18S region was amplified using the primers FF290F and FR-1R (12) and Sanger sequenced. *K. slooffiae* was maintained on YPD + Cef agar, and a single colony was inoculated into 4 ml of YPD + Cef broth. Cultures were grown at 37°C (200 rpm, 24 h) and then brought up to a volume of 15 ml and grown for another 24 h. Additional medium was provided daily until a total volume of 120 ml was obtained. On day 3 of incubation, cells were collected in 4 individual 30-ml aliquots and centrifuged at 100 × *g* for 5 min. Supernatants were removed, and the pellet dry weights were recorded (0.60 to 0.76 g). Each pellet was homogenized 3× in liquid N_2 with a tissue homogenizer (Omni International, Kennesaw, GA) and kept on dry ice until total genomic DNA was isolated using the DNeasy plant maxikit (Qiagen, Hilden, Germany). The DNA was quantified using the Qubit Flex fluorometer (Invitrogen, Carlsbad, CA) and visualized with a 0.7% agarose gel to check for high-quality, high-molecular-weight DNA. The isolate identification was confirmed by phylogenetic analysis of the assembled draft genome internal transcribed spacer (ITS) gene region (ITS1-5.8S-ITS2) (13).

Whole-genome sequencing of the *K. slooffiae* ABBL isolate was performed on the Pacific Biosciences Sequel II 18M SMRT Cell platform (Menlo Park, CA). The raw reads (154 Gb) were quality checked, and a draft genome sequence was assembled using FALCON version 1.8.0 at the University of Maryland Genomics Resource Center (14) with default parameters. The assembly totaled 50 Mb, with a G+C content of 30.84%, 157 contigs, and an N_{50} value of 531,052 bp. The genomes of other published *Kazachstania* spp. range from 12 to 14 Mb; therefore, this assembly is inflated in size, likely due to high heterozygosity levels (5.7 to 5.8%) as predicted by Genomescope2 (15). Highly heterozygous genomes can

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confound assemblers and may result in the inclusion of multiple haplotypes in the primary assembly (15). Thus, we removed haplotype contigs using the Purge Haplotigs program (16), which yielded a 25-Mb assembly with improved assembly statistics (37 contigs; N_{50}, 716,300 bp).

Data availability. The raw draft genome data were deposited in the NCBI Sequence Read Archive under accession number SRP310305, BioSample accession number SAMN17978627, and BioProject accession number PRJNA702779. The draft genome sequences were submitted to GenBank at JAFHAQ000000000. The 18S Sanger sequences were submitted to GenBank at MW575538.

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