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Title

Draft genome sequence of Phascolarctobacterium faecium DSM 14760 isolated from koala feces in Australia

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Running title

Genome Sequence

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Abstract

Phascolarctobacterium faecium was originally isolated from koala feces in 1992. Here, we sequence and analyze the type strain, with a length of 2,317,131 bp, 27 contigs, and average G+C content of 43.73%, and three virulence factors that are potential health hazards to humans..

Announcement

Introduction

Phascolarctobacterium faecium is a spiral-shaped, gram-negative, anaerobic bacterium (1) that produce short-chain fatty acids acetate and propionate (2) and are associated with hosts' metabolic state and mood (3), The bacteria can be used as a biomarker for colorectal cancers due to its high prevalence in patients (4). The 16S rRNA sequence can be found in NCBI under the accession number X72865. P. faecium is found in the gut microbiome of koalas (2) and humans (3). The type of strain was isolated feces in Australia in 1992 (5). Feces were emulsified in 0.25-strength Ringer solution serially diluted 10-

fold, plated onto Wilkins-Chalgren Anaerobe agar (Oxoid) with 5% defibrinated horse blood, incubated for 5 days at 37°C in 10% CO2, 10% H2, and 80% N2 by Bio-Bag (6). P. faecium was sequenced as part of the Genomic Encyclopedia of Type Strains, Phase IV, with the goal of sequencing genomes valuable for metagenomic binning, taxonomic classification, and comparative biology (7).

Methods and related outcomes

Details on organism growth and DNA isolation to be provided by DSMZ. Draft genome of Phascolarctobacterium faecium DSM 14760 was sequenced at the DOE Joint Genome Institute (JGI) using the Illumina HiSeq-2000 1TB platform, generated 8,845,394 raw reads totaling for 1,335,654,494 bp. Raw data was filtered using BBTools per SOP 1061, which removed about 200 bp from each contig. The final drafts had a total of 27 contigs in 21 scaffolds, totaling 2,317,131 bp in size. The sequencing FASTQ file, using the BZZZN library, showed 8,787,470 reads. Pair-end sequence processed 151 bp reads. The genome assembly was 100% complete with 0.23% contamination using the software, SPAdes, v3.10.1, with parameters —phred–offset 33 —cov–cutoff auto –t 16 –m 115 —careful –k 25,55,95 —12 (8). The Standard JGI Microbial Genome Annotation Pipeline was used for annotation (9).

Results

The genomic features of Phascolarctobacterium faecium are listed in Table 1. The highest similarity detected was draft type strain P. faecium JCM 14760 genome (Assembly accession number GCF_009719105.1; 23 contigs). Next closest relatives were Acidaminococcus fermentans DSM 20731 and Acidaminococcus massiliensis Marseille-P2828 T, with respective (dDDH-d4) similarities of 39.5% and 31.5%. These relationships are depicted in the phylogenetic tree in Figure 1.

The Comprehensive Antibiotic Resistance Database (CARD) website version 4.0.0 compares our bacterial genome sequences to determine their antibiotic resistance through their AMR genes (10). There is resistance to the disinfecting agents fluoroquinolones, tetracycline, and vancomycin, which are the van genes. The CRISPRCasFinder website version 1.12 identified two CRISPR localization regions in the genome with evidence (11). AntiSMASH 7.0 identified two secondary metabolite regions in the genome: NZ_QLTS01000002.1 (RiPP-like) and NZ_QLTS01000006.1 (ranthipeptide) (12). Using the Virulence Factor Database (VFDB) software version 2.0, there are three main virulence factors that can be a possible health hazard to humans (13). Factors are based on stress response, biofilm formation, and virulence gene activation.

Table 1: Genomic Features of *Phascolarctobacterium faecium* DSM 14760.

Feature:	Finding:
Length (bp)	2,317,131
No. of Scaffolds	21
No. of Genes	2248

No. of Protein coding genes	2176
No. of rRNA genes	8
No. of tRNA genes	54
GC content %	43.73
Scaffold N50 (bp)	195,470
Average fold coverage	576.43

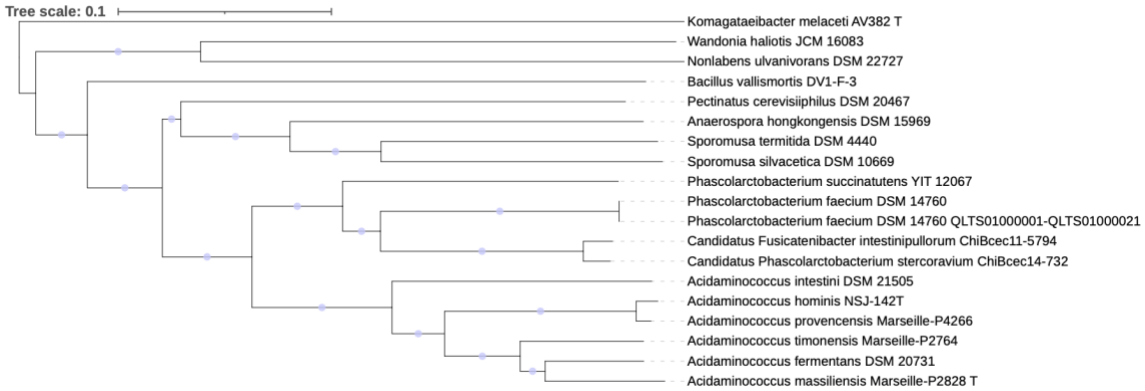

Figure 1. The tree above was inferred with FastME 2.1.6.1 [7] from whole-proteome-based GBDP distances. The branch lengths are scaled via GBDP distance formula *d5*. Branch values are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 100.0 %. The tree was midpoint-rooted [8].

Data availability statement

The raw reads have been deposited in the NCBI SRA under the accession number X72865.

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