

Draft Genome Sequence of *Bacteroides faecis* MAJ27^T, a Strain Isolated from Human Feces

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Despite the ecological importance of the dominant gut bacteria *Bacteroides*, few genomes have been defined. The Gram-negative, strictly anaerobic intestinal bacterium *Bacteroides faecis* MAJ27^T was isolated from the feces of a healthy adult. Here, the draft genome sequence of the type strain *B. faecis* MAJ27 (6.11 Mbp) is reported.

The symbiotic intestinal bacteria *Bacteroides*, belonging to the phylum *Bacteroidetes*, account for up to 20% of colonic microbiota (11, 14) and are capable of utilizing a wide range of indigestible plant-derived polysaccharides and host-derived glycans (5, 10, 15). *Bacteroides* spp. contain several types of mobile elements within their genome, including plasmids, transposons, or prophage elements (3, 18), and frequent gene exchange (such as that of carbohydrate-active enzymes by horizontal gene transfer) in the *Bacteroides* population is observed (9, 16, 19). Functional redundancy may allow these bacteria to adapt to and dominate the complex intestinal ecosystem (7, 18). *Bacteroides thetaiotaomicron*, a prominent member of the intestinal microbiota, has been manipulated as a role model for understanding host-microbe relationships (1, 15, 18). The Gram-negative anaerobe *Bacteroides faecis* MAJ27^T is a colonic commensal microbe that was isolated from the feces of a healthy adult and is most closely related to *B. thetaiotaomicron* VPI-5482^T, with 98.7% 16S rRNA gene sequence similarity (6). The present study defined and characterized the genome of *Bacteroides faecis* MAJ27^T to determine its ecological role in the human intestine.

The genome sequence of *B. faecis* MAJ27^T was analyzed using a combination of 8-kbp paired-end libraries with a 454 GS FLX Titanium pyrosequencer (Roche) (178,425 reads; 7-fold coverage) and 100-bp paired-end libraries with an Illumina GA IIx genome analyzer (Solexa) (17,694,184 reads; 284-fold coverage). The sequence reads were assembled using CLC Genomics Workbench 4.7.2 (CLCbio) and GS Assembler v2.5.1 (Roche) software. The open reading frames (ORFs) of the assembled contigs were predicted using Glimmer 3.02 (4) and tRNAscan-SE 1.23 (8) software. The predicted ORFs were then compared with the NCBI RefSeq (13), NCBI COG (17), SEED (12), CatFam (20), and EzTaxon (2) databases for gene annotation.

The draft genome sequence of MAJ27^T was approximately 6.11 Mbp long (290-fold genome coverage) and comprised seven scaffolds containing 53 contigs. The N50 contig size was

approximately 211 kbp. The G+C content was 42.4 mol%. A total of 5,248 gene features containing three rRNA genes and 63 tRNA genes were predicted within the genome of *B. faecis* MAJ27^T. Of the 5,182 ORFs, 2,931 (56.6%) were identified as having putative functions based on homology to previously known proteins, and 207 (7.1%) of the predicted coding sequences shared homology with proteins of unknown function.

B. faecis MAJ27^T carried a wide range of predicted protein-coding genes involved in carbohydrate metabolism. In particular among the gene products, an abundance of glycosylhydrolases, including galactosidases, glucosidases, mannosidases, and xylanases, was predicted, along with several hydrolases that degrade a variety of host-derived glycans, such as arylsulfatases, hexosaminidases, fucosidases, and sialidases. The genome sequence also showed a number of mobile elements related to bacterial conjugation systems, such as transposons, suggesting that horizontal gene transfer occurs frequently within the genome of *B. faecis* MAJ27^T. Further genomic analysis and comparative studies using other symbionts will provide further insight into its symbiosis and contributions to host physiology.

Nucleotide sequence accession numbers. The data from this whole-genome shotgun project have been deposited in DDBJ/EMBL/GenBank under the accession number AGDG000000000. The version described in this paper is the first version, accession number AGDG01000000.

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