Genome Sequence of Oscillibacter ruminantium Strain GH1, Isolated from Rumen of Korean Native Cattle

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Oscillibacter ruminantium strain GH1 was isolated from the rumen of Korean native cattle (HanWoo; Bos taurus coreanae). Here, we present the 3.07-Mb draft genome of this strain, which could reveal the presence of certain fiber-specific glycoside hydrolases and butyric acid-producing genes.

Rumin microbes produce an array of fibrolytic enzymes; however, fiber digestion in the rumen is not optimal (4), which leads to low energy production and thus low animal productivity. To address the problem of poor fiber degradation, focus on a better understanding of glycosyl hydrolases of rumen microbes is warranted. Genus Oscillibacter was previously isolated from the alimentary canal of a Japanese corbicula clam and reported to produce valeric acid (3). However, many environmental sequences similar to that of Oscillibacter have been found in cow and goat fecal samples (3, 6). Oscillibacter ruminantium strain GH1 was isolated from the rumen of Korean native cattle, and this is the first example of pure isolation of a novel strict anaerobe, Oscillibacter species, from cattle. In contrast to O. valericigenes Sm18-20T, O. ruminantium strain GH1 does not produce valeric acid. Instead, butyric acid is a major end product from xylose, glucose, and ribose in strain GH1. Therefore, the genome sequence of strain GH1 will provide a better insight into the genes and the key proteins involved in butyric acid production and fiber degradation.

The genome of strain GH1 was analyzed by a whole-genome shotgun approach using the Roche 454 Titanium sequencer for pyrosequencing. Generated quality-filtered reads were assembled into contigs using the 454 Newbler 2.6 assembler, and 46 contigs of >500 bp and 39 contigs of >2,000 bp in size were obtained. The gene prediction was accomplished and verified using Glimmer-3.02 modeling software (2) and the RNAmer-1.2 (5) and NCBI COG (7) databases. The RAST server (1) was used for gene annotation and screening for noncoding rRNAs and transfer RNAs.

The draft genome sequence of O. ruminantium GH1 includes 3,078,743 bases and comprises 3,225 predicted coding sequences. It consists of 46 contigs (N50 contig size, approximately 138 kb), which can be assembled into 10 scaffolds (N50 scaffold size, approximately 699 kb). The G+C content was 54.6 mol%. Additionally, 40 tRNA genes, one 23S rRNA gene, and one 16S rRNA gene were predicted in the draft genome.

The genome sequence analysis of strain GH1 showed the presence of several glycosyl hydrolase genes. The genome also revealed the presence of genes ack and pta, for acetate kinase and phospho- transacetylase enzymes, respectively. These enzymes are involved in acetate formation in butyrate fermentation. Deletion of these genes can lead to improved butyrate production. Besides this, GH1 also harbors genes for penicillin binding proteins, beta-lactamases, and bacitracin-resistant proteins. With the known sequence, it is possible to perform various comparative genome analyses with other rumen bacteria for a better understanding of the genes related to fiber degradation and butyric acid production. Also, additional information about antibiotic resistance genes may be of clinical significance.

Nucleotide sequence accession numbers. The draft genome of Oscillibacter ruminantium strain GH1 was deposited in DDBJ/EMBL/GenBank under accession numbers BAGW01000001 to BAGW01000058.

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REFERENCES


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