Genome Sequence of *Peptoniphilus rhinitidis* 1-13^T, an Anaerobic Coccus Strain Isolated from Clinical Specimens

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A new *Peptoniphilus* species has been isolated from samples from a patient who was scheduled for endoscopic sinus surgery for chronic rhinosinusitis. The isolate, *Peptoniphilus rhinitidis* 1-13^T (KCTC 5985^T), can use peptone as a sole carbon source and produce butyrate as a metabolic end product. This is the first report of the draft genome sequence of a novel species in the genus *Peptoniphilus* within the group of Gram-positive anaerobic cocci.

The Gram-positive anaerobic cocci (GPAC) are a major part of the normal flora and are isolated predominantly from the skin, mouths, and gastrointestinal, urinary, and vaginal tracts of humans (7). GPAC are associated with a variety of infections as opportunists, constituting about 20 to 40% of the anaerobes isolated from clinical specimens (3, 10). The seven genera of GPAC that have been characterized by biochemical methods are furthermore recovered from patients with chronic diseases (5, 6). Chronic rhinosinusitis (CRS) is an inflammatory disorder that commonly occurs after nasal bacterial infections.

Peptoniphilus rhinitidis 1-13^T was isolated from five male patients (40.2 ± 6.3 years old [mean ± standard deviation]) who were scheduled for endoscopic sinus surgery for CRS with nasal polyps. The samples were serially diluted in phosphate-buffered saline; spread onto brucella blood agar supplemented with 5% sheep blood, 1 mg/liter hemin stock solution (5mg/ml), and 1 ml/liter working vitamin K₁ stock solution (1mg/ml); and incubated at 37°C under anaerobic conditions (Forma Anaerobic System) using a gas phase of N₂-H₂-CO₂. According to the Genomes OnLine Database, sequencing of this organism's genome had not been completed or initiated when our project was proposed (9).

In this report, we present the draft genome sequence of *P. rhinitidis* 1-13^T, which consists of 56 contigs. Whole-genome shotgun sequencing, using a Roche 454 Titanium sequencer for pyrosequencing, was performed by the Genome Resource Center, Korea Research Institute of Bioscience and Biotechnology. Genome sequences from pyrosequencing were processed with Roche's software according to the manufacturer's instructions. Quality filtered reads were assembled *in silico* using the 454 Newbler 2.6 assembler, giving 56 contigs of >100 bp and 33 contigs of >2,000 bp. Open reading frames (ORFs) were predicted using the Glimmer 3.02 modeling software package (4) and RNAmmer 1.2 (8) and searched using the Clusters of Orthologous Groups databases (11). The draft genome sequence was also uploaded into the RAST (Rapid Annotation using Subsystem Technology) Server to check the annotated sequences and screen for noncoding rRNAs and tRNAs.

The percent GC content of all contigs was 30%. The predicted proteins were annotated by the Basic Local Alignment Search Tool (BLAST) (1) and the RAST Server (2). Seventy percent (1,309) of the ORFs were annotatable with known proteins. The genome contained 1,827 protein coding genes, one copy of the large-subunit rRNA gene,

37 tRNA genes, and one copy of the small-subunit rRNA gene. There were 1,866 possible ORFs in 56 contigs, with a size range of 71 to 13,416 bp. There were not many ORFs with lengths of >2,000 bp (only 111); in fact, most were <1,500 bp long.

The genome codes for a multiantimicrobial extrusion protein, a transcriptional regulator, IncP-type DNA topoisomerase III TraE, an ATP-binding protein, and LPXTG-specific sortase A. There were 24 subsystems represented in the genome, and we used this information to reconstruct the metabolic network. There are many protein metabolism and amino acid and derivative features, including genes involved in protein and methionine biosynthesis and polyamine metabolism.

Nucleotide sequence accession numbers. The draft genome sequence of *P. rhinitidis* 1-13^T is available in GenBank under accession numbers [BAEW01000001](#) to [BAEW01000056](#).

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