Periodontopathic *Porphyromonas gingivalis* strain Ando abundantly expresses a 53-kDa-type Mfa1 fimbria. Here, we report the draft genome sequence of Ando, with a size of 2,229,994 bp, average G+C content of 48.4%, and 1,755 predicted protein-coding sequences.

**Porphyromonas gingivalis**, a Gram-negative anaerobe, is a major contributor to periodontal diseases (1, 2). *P. gingivalis* expresses two types of fimbriae, FamA and Mfa1 (3), and it is known that there are six genotypes in genes encoding the major fimbрин of FamA fimbriae (4). Recently, we reported that there were variants even in the major fimbрин of Mfa1 fimbriae, the Mfa1 (75-kDa) and 53-kDa types (5). The published complete genome sequences of *P. gingivalis* strains, including W83 (6), ATCC 33277 (7), TDC60 (8), and HG66 (9), show that they all possess a DNA sequence corresponding to the gene encoding a 75-kDa fimbрин. Here, we report the draft genome sequence of *P. gingivalis* strain Ando, which abundantly expresses a 53-kDa-type Mfa1 fimbria.

The genomic DNA of Ando was sequenced using the Illumina HiSeq 2000 (90- or 100-bp paired-end reads, with an average 186-bp insert size). After the raw sequences were trimmed and quality filtered (Sanger QV, 180 bp), for a total length of 2,229,994 bp (N50, 55,724 bp) and a G+C content of 48.4%. Protein-coding sequences (CDSs), tRNA genes, and clustered regularly interspaced short palindromic repeats (CRISPRs) were predicted by MetaGeneAnnotator (10), tRNAscan-SE 1.23 (11), and CRISPRFinder (12), respectively. Functional annotation of CDSs comes from BLASTP searches against NCBI’s nonredundant (NR) protein database (ftp://ftp.ncbi.nlm.nih.gov/blast/db/FASTA/nr.gz).

A total of 1,755 CDSs, 47 tRNA genes, 4 rRNA genes, and 3 CRISPRs were predicted in the Ando genome. PHAST (13) did not detect any prophage region. A comparative analysis of the CDSs among Ando and the other four *P. gingivalis* strains using CD-HIT 4.6.4 (14) (cutoff, 90% sequence similarity, 90 to 110% length coverage) showed significant similarities, with 87.7% similarity to TDC60, 86.2% similarity to HG66, 85.1% similarity to W83, and 85.1% similarity to ATCC 33277. A reciprocal best hit analysis of Ando chromosomal CDSs against W83 chromosomal CDSs (6) using BLASTP (E value cutoff, 10^-10) predicted potential virulence genes in Ando (described as numbers in Ando out of numbers in W83): 1 of 1 hemolysin, 9 of 13 adhesin (e.g., hemagglutinin), 62 of 67 evasion proteins (e.g., glycosyltransferase), 10 of 10 invasion proteins, 16 of 16 stress response proteins, 5 of 5 antibiotic resistance proteins, and 40 of 41 peptidases. The gene encoding the 53-kDa fimbрин (PGANDO_1061) in Ando was not found in the other four *P. gingivalis* strains. However, the PGANDO_1061 gene was located at the same locus of the mfa1 gene in other strains. We found several other genes that were specifically detected in Ando (e.g., plasmid-related proteins, CRISPR-associated proteins, and virulence-associated protein E). Further comparative genomic and functional analyses with other strains that express 53-kDa fimbрилиn will help understand the pathogenic mechanism of *P. gingivalis*.

**Nucleotide sequence accession numbers.** This genome sequence and raw sequence reads have been deposited, respectively, in DDBJ/ENA/GenBank and DDBJ Sequence Read Archive under the accession numbers BCBV01000001 to BCBV01000112 and DRA003978 (BioProject PRJDB4201).

**ACKNOWLEDGMENTS**

This work was supported by JSPS KAKENHI grant no. 25462880 to K.N. and by the Kazusa DNA Research Institute Foundation. These funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

We thank Filgen, Inc. for the Illumina technology sequencing services.

**REFERENCES**


