Porphyromonas gingivalis is associated with oral and systemic diseases. Strain-specific P. gingivalis invasion phenotypes have been correlated with disease presentation in infected laboratory animals. Here, we present the genome sequence of AJW4, a minimally invasive strain, with a single contig of 2,372,492 bp and a G+C content of 48.27%.

Porphyromonas gingivalis is an anaerobic bacterium (1) found in the oral tissues of chronic periodontitis patients (2, 3) and selected nonoral tissues of systemic disease patients (4–6). Invasion of nonphagocytic host cells may be a mechanism by which P. gingivalis promotes oral and systemic disease (7). In vitro studies have shown variation among strain invasion phenotypes (8–10). Animals inoculated with highly invasive strains displayed oral components required for successful invasion by Porphyromonas gingivalis (7), including sequences linked to invasion capacity (17).

The availability of the AJW4 genome aids explorations of the genomic elements necessary for the invasion of host cells by P. gingivalis, a key aspect of its association with oral and systemic pathologies.

Nucleotide sequence accession number. This genome sequencing project was deposited in GenBank under the accession CP011996. The version described is the first version.
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We declare no conflicts of interest.

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