

# Genome Sequence of *Plesiomonas shigelloides* Strain 302-73 (Serotype O1)

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This paper is dedicated to the memory of Spanish microbiologist Miquel Regué.

***Plesiomonas shigelloides*, the only species of the genus, is an emergent pathogenic bacterium associated with human diarrheal and extraintestinal disease. We present the whole-genome sequence analysis of the representative strain for the O1 serotype (strain 302-73), providing a tool for studying bacterial outbreaks, virulence factors, and accurate diagnostic methods.**

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*Plesiomonas shigelloides*, the only species of the genus, is a Gram-negative, flagellated, rod-shaped, ubiquitous, and facultative anaerobic bacterium that has been isolated from sources, such as freshwater, surface water, and many wild and domestic animals (1). *P. shigelloides* is associated with diarrheal disease in humans (2), as found in several types of gastroenteritis, including acute secretory gastroenteritis (3), an invasive shigellosis-like disease (4), and a cholera-like illness (5). Extraintestinal infections, such as meningitis, bacteremia (6), and pseudoappendicitis (7), are also associated with *P. shigelloides* infection.

It is considered an emergent bacterial pathogen, as there has been an increasing number of reports describing *P. shigelloides* infections in recent years (8) (about 5% of traveler's diarrhea is produced by *P. shigelloides* infection). To date, however, the lack of routine analysis for *P. shigelloides* in cases of gastroenteritis leads to only sporadic and occasional identification of this bacterium (8, 9). Therefore, the greatest challenge is to develop a rapid, early, and accurate diagnostic method for the detection of *P. shigelloides* (8).

The bacterium remained within the family *Vibrionaceae* until molecular studies carried out by Martínez-Murcia et al. (10) indicated that *P. shigelloides* is phylogenetically related to the genus *Proteus*, although it lately has been reported to be more related to the organism *Edwardsiella tarda* (11). The genus *Plesiomonas* has been reclassified under the family *Enterobacteriaceae* and is the only oxidase-positive member of this family (12). Compared to other phenotypic methods, serology has been used more successfully for distinguishing different strains of *P. shigelloides*. There are mainly two major serotyping schemes, which are based on somatic (O) and flagellar (H) antigens. At the present moment, 102 somatic antigens and 51 flagellar antigens have been recognized (13).

*P. shigelloides* strain 302-73, isolated in Japan (14), is the representative strain for the O1 serotype, whose complete lipopolysaccharide (LPS) has been chemically characterized (15, 16). For

the first time, we have obtained the whole-genome sequence of *P. shigelloides* 302-73. We think this information will contribute to the study of virulence factors and in the development of new accurate diagnostic methods.

For whole-genome sequencing, two runs of 8-kb paired-end sequencing using the GS FLX system (Roche Diagnostics) produced 80× genome coverage. Read assembly with the Newbler software (Roche Diagnostics) resulted in 13 large scaffolds, two of which account for >90% of the assembly ( $N_{90}$ , 1.76 Gb), and a total of 389 contigs >250 bp in length ( $N_{50}$ , 86.6 kb;  $N_{90}$ , 13.5 kb). Genome annotation was performed automatically via the Rapid Annotations using Subsystems Technology (RAST) server (17) and also by the NCBI Prokaryotic Genomes Annotation Pipeline (PGAAP). The assembled genome of *P. shigelloides* comprises a single circular chromosome (3.9 Mbp, 51.2% G+C content), with 3,285 coding DNA sequences (CDSs), 7 rRNAs, and 96 tRNA sequences (according to the RAST annotation).

**Nucleotide sequence accession numbers.** The draft genome sequences for *P. shigelloides* 302-73 have been deposited at DDBJ/EMBL/GenBank under the accession no. [AQ000000000](http://www.ncbi.nlm.nih.gov/nuccore/AQ000000000) (BioProject PRJNA196338). The version described in this paper is the first version, accession no. [AQ001000000](http://www.ncbi.nlm.nih.gov/nuccore/AQ001000000).

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