

# Complete Genome Sequences of *Helicobacter pylori* Clarithromycin-Resistant Strains

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**We report the complete genome sequences of two *Helicobacter pylori* clarithromycin-resistant strains. Clarithromycin (CLR)-resistant strains were obtained under the exposure of *H. pylori* strain 26695 on agar plates with low clarithromycin concentrations. The genome data provide insights into the genomic changes of *H. pylori* under selection by clarithromycin *in vitro*.**

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*Helicobacter pylori* is a spiral Gram-negative bacterium that infects more than half of the world's population and is currently accepted to play a causative role in the pathogenesis of chronic gastritis, peptic ulcer diseases, gastric cancer, and mucosa-associated lymphoid tissue (MALT) lymphoma (1, 2). The eradication of *H. pylori* not only improves peptic ulcer healing but also prevents its recurrence and reduces the risk of developing gastric cancer (3–6). However, the prevalence of antibiotic resistance in *H. pylori* is increasing worldwide and is a growing public health problem needing more attention (7–11). Especially, resistance to clarithromycin (CLR) is the most important factor causing treatment failure and is responsible for the decline of the *H. pylori* eradication rate (7, 12–14).

In the present report, we announce two genome sequences of CLR-resistant *H. pylori* strains (26695-1CL and 26695-1CH) obtained *in vitro*. The genomes of these strains provide insights into the genomic changes of *H. pylori* under CLR selection.

Two CLR-resistant strains were obtained under exposure to low concentrations of CLR *in vitro* (0.03 and 0.06  $\mu\text{g/ml}$  CLR agar plates), and whole-genome sequencing was performed using 90-base paired-end reads on the Illumina HiSeq 2000 genome sequencer (Illumina, Inc., San Diego, CA). The whole-genome sequences of the two strains were reconstructed by mapping the short-read sequences on the genome of *H. pylori* 26695 (GenBank accession no. NC\_000915) using the CLC Genomics Workbench version 4.0 (CLC bio, Aarhus, Denmark). The lengths of the 26695-1CL and 26695-1CH genomes are 1,667,239 bp and 1,667,302 bp, with coverage depths of 840 $\times$  and 1,257 $\times$ , respectively. The G+C content of both strains is 38.87%.

In the two CLR-resistant strains, 5 and 7 mutations (including the well-known mutations in the 23S rRNA gene) were found. Three mutations (C712T, T743A, and G160A in the genes *hp0190*, *hp0471*, and *hp1048*, respectively) were present in both strains. Two mutations were found only in the *H. pylori* 26695-1CL strain, without mutations in the 23S rRNA gene, and four mutations were found only in the *H. pylori* 26695-1CH strain, including the A2143G mutation in the 23S rRNA gene.

**Nucleotide sequence accession numbers.** The genome sequences of clarithromycin-resistant *H. pylori* strains 26695-1CL and 26695-1CH were deposited at GenBank under the accession no. [AP013356](https://www.ncbi.nlm.nih.gov/nuccore/AP013356) and [AP013355](https://www.ncbi.nlm.nih.gov/nuccore/AP013355), respectively.

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