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GENOME ANNOUNCEMENT

# Genome of *Helicobacter pylori* Strain XZ274, an Isolate from a Tibetan Patient with Gastric Cancer in China

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**The infection rate of *Helicobacter pylori* is high all over the world, especially in the Chinese Tibetan Plateau. Here, we report the genome sequence of *Helicobacter pylori* strain XZ274 isolated from a Tibetan patient with gastric cancer. The strain contains 1,634,138 bp with 1,654 coding sequences and a pXZ274 plasmid of 22,406 bp with 26 coding sequences. This is the first complete genome sequence of *Helicobacter pylori* from the Tibetan Plateau in China.**

*Helicobacter pylori*, a spiral-shaped, Gram-negative bacterium that infects more than half of the world population, is a risk factor of gastric malignancies, including gastric noncardia adenocarcinoma and mucosa-associated lymphoid tissue lymphoma (7, 9, 11). It has been reported that the Tibet area has the highest rate of infection, with more than 73% of people infected (14). To discover the possible reasons for the high infection rate and pathogenicity in this area, we identified some unique characteristics in the genomes of *H. pylori* Tibet strains related to environmental adaptability and pathogenicity (4). Here, we first report the genome of an *H. pylori* Tibet strain, XZ274, isolated from the stomach of a female Tibetan patient with gastric cancer.

The XZ274 strain was identified and determined as *H. pylori* by the API CAMPY system (reference no. 20 800) (8). Then, the whole shotgun genome sequencing was performed with 454 Titanium. Totally, 177,978 454 reads with a length of 53,780,663 bp were generated. After trimming and removing low-quality reads, 175,326 reads (98.51% of the total) were assembled into 39 contigs, with a length of 1,620,727 bp. The $N_{50}$ contig and the largest length of the contig were 98,894 bp and 298,208 bp, respectively. The orders of contigs were determined by alignment with the published genome sequence of *H. pylori* strain 51. Gaps between contigs were closed by PCR and subsequent Sanger sequencing using an ABI 3730 capillary sequencer. The complete genome sequencing was carried out using Glimmer (1) and tRNAscan-SE 1.23 (6).

*H. pylori* strain XZ274 has one circular chromosome of 1,634,138 bp with a 38.66% G+C content and one plasmid of 22,406 bp with a 35.01% G+C content. The chromosome has 1,654 coding sequences, including 1,611 protein-coding genes, 36 tRNA genes, 3 16S rRNA genes, 2 23S rRNA genes, and 2 5s rRNA, with an average length of 911 bases that cover 92.23% of the chromosome. The plasmid has 26 coding sequences with an average length of 793 bases constituting 91.98% of plasmid. Genes annotated by the COG database were classified into 20 COG categories.

Comparison with other completed genome sequences of *H. pylori* showed that *H. pylori* B38 (12) was the closest neighbor. By performing GC skew analysis (2), 21 genomic islands were found. These region corresponded to the type IV secretory pathway (3, 5, 10), CAG pathogenicity island proteins, outer membrane receptor proteins, and transcription repair coupling factor(s). Strain XZ274 possesses complete general secretion machinery, which helps the secretion of outer membrane proteins to the extracellular environment from the inner membrane. In addition, it also contains an intact *cag* pathogenicity island, the genome island *tfs3*, and virulence-associated alleles of *vacA* (13).

The complete genome sequence would be helpful in understanding the evolution of the bacterium by comparative genome studies and help us to better understand the adaptation of this bacterium on high-altitude areas, as well as the reason for the high pathogenicity and infection rates in the Tibetan Plateau.

**Nucleotide sequence accession numbers.** The genome sequences of *H. pylori* strain XZ274 and the plasmid pXZ274 reported in this paper have been deposited in the GenBank database under accession numbers CP003419 and CP003420.

## ACKNOWLEDGMENTS

This work was supported by the State Key Development Program for Basic Research of China (973 Program) (no. 2009CB522606) and National Natural Science Foundation of China (no. 31170059).

We thank Huajun Zheng and Yongqiang Zhu (Chinese National Human Genome Center at Shanghai) for sequencing technical assistance.

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Received 10 May 2012 Accepted 21 May 2012

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doi:10.1128/JB.00804-12

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