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GENOME ANNOUNCEMENT

# Complete Genome Sequences of Two *Helicobacter pylori* Bacteriophages Isolated from Japanese Patients

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***Helicobacter pylori*** **causes peptic ulcers and gastric cancer, which lead to significantly higher morbidity in Japan than elsewhere in the world. As bacteriophage (phage) and host bacteria coevolve, the study of *H. pylori* phages is important to extend understanding of the evolution and pathogenesis of *H. pylori*. Here we report two complete genome sequences of *H. pylori* phages KHP30 and KHP40, which were released spontaneously from the most pathogenic East Asian-type isolates from Japanese patients.**

*Helicobacter pylori*, a Gram-negative spiral bacterium, colonizes the human stomach and infects approximately 50% of the global population (2, 10). Infection can cause chronic inflammation, which may progress to peptic ulceration, atrophic gastritis, or gastric cancer (8). There is a significant correlation between the *H. pylori* strain type and the incidence of gastric cancer. In particular, the East Asian-type strain of *H. pylori* is the individual strain most likely to cause gastric cancer (10).

Several bacteriophages (phages) of *H. pylori* have been reported (4, 5, 9, 12). In general, phages are considered to contribute to bacterial evolution and may affect host features, such as biological behavior, pathogenesis, or adaptation, via their possible roles in horizontal gene transfer and bacteria-phage antagonistic coevolution (4, 5, 7). In this study, to extend our understanding not only of the *H. pylori* phages themselves but also of the process of coevolution of *H. pylori* and its phages, phages KHP30 and KHP40 were isolated from the culture supernatants of East Asian-type isolates from Japanese patients living in distinct geographic regions, and their complete genomic sequences were determined.

The genomic DNA of the phages was isolated from phage particles that had been purified by CsCl density gradient ultracentrifugation, essentially as described elsewhere (11). The genomic sequences were determined with a primer walking method using an ABI Prism 3100-Avant genetic analyzer (Applied Biosystems, Foster City, CA), and both strands were sequenced. The genome sequences of phages KHP30 and KHP40 were circularly connected. Whole-genome PCR scanning also validated our sequencing results. A BLASTN analysis was conducted between the genome sequences of phages KHP30 and KHP40. Open reading frames (ORFs) were predicted using Prodigal and GeneMark.hmm with heuristic models (1, 3) and were then manually confirmed with reference to the ribosomal binding site sequences. The conserved protein domains were analyzed using the NCBI Conserved Domain Database (6).

The complete DNA sequencing of phages KHP30 and KHP40 revealed that their genomes consist of 26,215 bp (G+C, 35.8%) and 26,449 bp (G+C, 35.8%), respectively. A comparison of the genomic sequences of KHP30 and KHP40 with BLASTN indicated a high level of sequence similarity (total score, 3.540e − 04; query coverage, 96%; E value, 0.0). Moreover, 30 and 32 ORFs were inferred in phages KHP30 and KHP40, respectively. A genomic analysis of KHP30 and KHP40 predicted an integrase (ORF2 in both phages), primases (ORF9 in phage KHP30, and ORFs 8 and 9 in phage KHP40), and other DNA-associated ORFs (ORFs 4 and 5 in both phages). However, the functions encoded by most ORFs could not be predicted.

These genomic data, and the similar genetic traits of phages KHP30 and KHP40, will promote investigation not only of the molecular characteristics of *H. pylori* phages, but also of the coevolution process of East Asian-type *H. pylori* strains and their phages.

**Nucleotide sequence accession numbers.** The complete genomic sequences of *H. pylori* phages KHP30 and KHP40 have been submitted to DDBJ/EMBL/GenBank under the accession numbers AB647160 and AB731695, respectively.

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