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# Whole-Genome Sequence of Phage-Resistant Strain *Escherichia coli* DH5 $\alpha$

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**ABSTRACT** The genomes of many strains of *Escherichia coli* have been sequenced, as this organism is a classic model bacterium. Here, we report the genome sequence of *Escherichia coli* DH5 $\alpha$ , which is resistant to a T4 bacteriophage (CCTCC AB 2015375), while its other homologous *E. coli* strains, such as *E. coli* BL21, DH10B, and MG1655, are not resistant to phage invasions. Thus, understanding of the genome of the DH5 $\alpha$  strain, along with comparative analysis of its genome sequence along with other sequences of *E. coli* strains, may help to reveal the bacteriophage resistance mechanism of *E. coli*.

*Escherichia coli*, generally known as *E. coli*, is the most common Gram-negative bacterium in warm-blooded animals (1). *E. coli* is recognized as one of the classic model creatures and is extensively used in various fields of the biological sciences (2, 3). *E. coli* is only one species of *Enterobacteriaceae*, although the physiological status of strains from different sources may vary dramatically. DH5 $\alpha$  is a typical engineered *E. coli* widely used in the laboratory, since it allows exogenous plasmid DNA to be amplified inside its body. More specifically, a strain of DH5 $\alpha$  preserved in our laboratory has resistance to a T4 phage (CCTCC AB 2015375). However, other *E. coli* strains such as BL21, DH10B, and MG1655, which are homologous to DH5 $\alpha$ , do not resist the invasion of that phage.

The single-molecule PacBio sequencing technique, belonging to the third-generation sequencing technology, was adopted to measure the complete genome map of the DH5 $\alpha$  strain. During sequencing, the Hierarchical Genome Assembly Process (HGAP) software was used to assemble the bacterial genome. After the sequencing, a total of 78,372 sequenced reads with an average length of 6,374.2 bp were obtained, and the sequencing depth reached 103.36 $\times$ . The remaining contig formed a framework sequence (scaffold) without gaps. The sequenced genes were predicted with the software Glimmer 3.02 (<http://ccb.jhu.edu/software/glimmer/index.shtml>). BLAST 2.2.28+ was applied to predict protein sequences in the NCBI nr, KEGG, STRING, and GO databases for BLAST comparative analysis to obtain the predicted gene annotation information. Gene analyses related to phage resistance, such as prophage and clustered regularly interspaced short palindromic repeat (CRISPR) sequences, were analyzed by PHAST (<http://phast.wishartlab.com/index.html>) and CRISPRFinder (<http://crispr.i2bc.paris-saclay.fr/>) respectively (4, 5). The software programs tRNAscan-SE v1.3.1 and Barrnap 0.4.2 were used for tRNA and rRNA determination (6, 7).

The size of the total genome is 4,833,062 bp, and the genome contains a circular chromosome but is without a plasmid. The 4,833,062 bp of the chromosome has 4,636 genes, including 22 rRNA genes and 89 tRNA genes with an average length of 919.23 bp. The GC content of the chromosome is 50.752% and is nearly identical to the GC content of other *E. coli* strains that can be found in NCBI. Moreover, a total of

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9 CRISPR sequences were found in the genes. Two of them are identified CRISPR sequences, and the remaining are questionable CRISPR sequences. In the whole genome, 5 prophage sequences were found, of which 4 are intact prophage sequences and the remaining 1 is an incomplete sequence. These prophage sequences correspond to the following phages: PHAGE\_Enterо\_Sf101\_NC\_027398, PHAGE\_Escher\_pro483\_NC\_028943, PHAGE\_Enterо\_lambda\_NC\_001416, PHAGE\_Shigel\_POCJ13\_NC\_025434, and PHAGE\_Salmon\_Fels\_2\_NC\_010463.

These CRISPR sequences, as well as the prophage sequences, may be involved in bacterial resistance to phage (8, 9). The full-genome sequence of the DH5 $\alpha$  strain may be employed to find phage resistance-related genes and determine the mechanisms at the molecular level of bacterial resistance to phages. Furthermore, the genome sequence information may also be utilized to evaluate the genetic diversity of various *E. coli* strains.

**Accession number(s).** The genome sequence of *E. coli* DH5 $\alpha$  is available in GenBank under accession number [CP026085](https://www.ncbi.nlm.nih.gov/nuclseq/CP026085).

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