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GENOME ANNOUNCEMENT

Complete Genome Sequence of the Bacteriophages ECBP1 and ECBP2 Isolated from Two Different *Escherichia coli* Strains

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***Escherichia coli* is recognized as one of the most abundant avian bacterial pathogens. In this study, we report the sequencing by the traditional Sanger method of ECBP1 and ECBP2: bacteriophages that infected two different *E. coli* strains which might be used as therapeutic agents in combination with alternative antibiotics.**

Escherichia coli is commonly found in the avian gastrointestinal tract and other mucosal surfaces. Although most of the *E. coli* strains are commensals, a separate group, avian pathogenic *E. coli* strains, have the ability to cause extraintestinal diseases in poultry (4, 8). Bacteriophages are the most abundant and diverse forms of life on Earth and exert a major influence over the microbial world (12). To date, numerous phage genomes have been sequenced that could supply important insights into the diversity and evolution of phage genomes and the functions of various phage genes (5, 10). Bacteriophage therapy is one of the biocontrol methods used to overcome bacterial infections without creating antibiotic resistance. Lytic bacteriophages are nonhazardous viruses that can be released from infected bacteria via degradation of the bacterial cell as they destroy the targeted bacteria (3, 7).

This study reports the complete genome sequences of two bacteriophages, ECBP1 and ECBP2, that infect *E. coli* strains KBP21 and KBP135 isolated from chicken farms located in Yesan, South Korea. Genomic DNA of bacteriophages was extracted as previously described (6) and sequenced by the shotgun sequencing method by NICEM, South Korea. Gaps between contigs were filled in by direct PCR sequencing using specific primers annealing to the ends of neighboring contigs. Open reading frames (ORFs) of ECBP1 and ECBP2 were predicted and annotated by the RAST server (2). The conserved protein domain analysis was performed using BLASTP (1), and to improve annotation results, the presence of tRNA sequences was determined using tRNA scan-SE (11).

The bacteriophage ECBP1 has a double-stranded DNA genome of 69,855 bp with GC contents of 42.73%. The genome showed 82 ORFs, of which 67 ORFs had a hypothetical function and 2 tRNA sequences could be determined. The protein was found to encode genes related to DNA metabolism and replication, including T7-like RNA polymerase, dCTP deaminase, helicase, polymerase, and endonuclease. Also, 1 structural protein could be encoded as a major coat protein.

The genomic sequence of ECBP2 was composed of 77,135 bp, with GC contents of 42.42%. The genome showed 120 ORFs, and 1 tRNA sequence could be determined. A total of 100 ORFs from the ECBP2 genome encode hypothetical/unknown proteins. The encoded morphogenesis-related proteins are the portal protein, major head protein, and tail fiber protein. The genome contains genes that encoded replication-related proteins and DNA manipulation proteins, such as endonuclease, serine/threonine protein phosphatase, exonuclease, two polymerases, phosphate starvation-inducible protein, thymidylate synthase, dCTP deaminase, and primase/helicase. Bacterophage ECBP2 also contained genes coding for lytic transglycosylase and phage lysozyme for host lysis.

The genome sequences of two bacteriophages had low similarity to each other and showed highly conserved synteny with *Escherichia* phage vB_EcoP_G7C (9) and *Enterobacteria* phage phiEco32 (12) for ECBP1 and ECBP2, respectively. The complete genomes of ECBP1 and ECBP2 can provide for understanding the interaction between bacteriophage and *E. coli* and contribute to the development of the biological control of pathogen.

Nucleotide sequence accession numbers. The complete genome sequences of ECBP1 and ECBP2 have been deposited in the GenBank database under accession no. JX415535 and JX415536, respectively.

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