




Complete Genome Sequence of *Escherichia coli* Siphophage BRET

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ABSTRACT The lytic *Escherichia coli* siphophage BRET was isolated from a chicken obtained at a local market in Abidjan, Côte d'Ivoire. Its linear genome sequence consists of 59,550 bp (43.4% GC content) and contains 88 predicted genes, including 4 involved in archaeosine biosynthesis. Phage BRET is related (95% nucleotide identity) to *Enterobacteria* phage JenK1.

Phages are being reconsidered as complements to antibiotics in many countries (1–3). Here, a new virulent phage was isolated from the gastrointestinal tract of a chicken collected at a local market in Abidjan, Côte d'Ivoire. A 2-cm intestine sample was suspended in 2 ml saline and filtered (0.45 μ m). The filtrate was added to *Escherichia coli* HER1036 in LB medium and incubated overnight at 37°C with shaking (4). A phage plaque was purified three times from LB plates and designated BRET. The lysate was observed under a transmission electron microscope, and BRET, with a slightly elongated capsid of 67 ± 2 nm \times 51 ± 1 nm and a noncontractile tail of 176 ± 8 nm \times 10 ± 1 nm (Fig. 1), belongs to the *Siphoviridae* family (5).

Phage genomic DNA was isolated from the lysate (6), and a DNA library was prepared (Nextera XT DNA library preparation kit). Sequencing was performed with an Illumina MiSeq system (250-nucleotide [nt] paired-end reads). The 557,108 reads were assembled with Ray v3.0.0 (7) using a k-mer length of 31, which led to a single contig with a coverage of 1,384 \times . Redundant contig ends were removed to produce the final complete genome. Functional genes were predicted with GeneMarkS (<http://topaz.gatech.edu/genemark/genemarks.cgi>), PECAAN Auto Annotation Tool (<https://discover.kbrinsgd.org/autoannotate/>), Geneious v11.0.5, and Glimmer v1.5 (plugin of Geneious v11.0.5) using the following principles: genes started with ATG, GTG, or TTG codons and were preceded with a Shine-Dalgarno (SD) sequence similar to AGGAGGU (5' to 3'). Only coding sequences (CDS) with more than 30 amino acids were annotated with Blast2GO v5.2.1 (8) and the deduced proteins were searched for function using the NCBI nonredundant protein database and a cutoff *E* value of 0.001. tRNAs were searched using tRNAscan-SE v2.0 (<http://lowelab.ucsc.edu/tRNAscan-SE/>).

The phage BRET genome consists of 59,550 bp with a GC content of 43.4%. The average nucleotide identity between phage BRET and *Enterobacteria* phage JenK1 was 95.15% according to MUMmer analysis in JSpeciesWS (<http://jspecies.ribohost.com/jspeciesws/#analyse>). BRET is also related to *Enterobacteria* phages 9g (94.06% identity), JenP1 (93.07%), and JenP2 (93.73%), as well as to *Salmonella* phage SE1 (93.75%).

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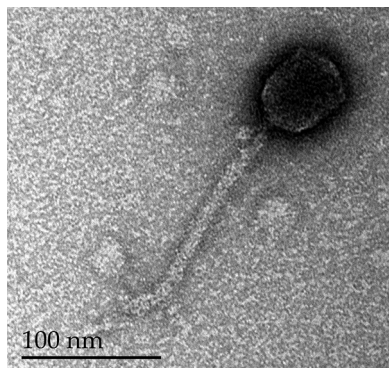


FIG 1 Micrograph of phage BRET stained with uranyl acetate (2%). Bar, 100 nm.

A total of 88 CDS were predicted, with sizes ranging from 138 bp to 3,261 bp. A majority of CDS started with ATG (94.32%), while start codons of GTG (3.41%) and TTG (2.27%) were also identified. ORF1 was designated based upon the annotation of phage JenK1 (9). Only 26 CDS were assigned a function, including terminase (ORF1 and ORF2), capsid protein (ORF6), and tail-related proteins (ORF12, ORF14, ORF16, ORF20, ORF23 and ORF25). Over 70% of the deduced BRET proteins have unknown functions.

tRNAs were not found, but genes involved in archaeosine DNA modification were identified in the BRET genome (10–13). ORF29 is likely a DpdA (proposed DNA ribosyltransferase), while ORF30 is similar to FoIE (GTP cyclohydrolase), ORF31 to QueD (6-carboxytetrahydropterin synthase), ORF33 to QueC (7-cyano-7-deazaguanine synthase), and ORF35 to QueE (5-carboxy-deazaguanine synthase). These enzymes probably lead to DNA modifications, which may protect the phage genome from host endonucleases (12).

Phage BRET was deposited in the Félix d'Hérelle Reference Center for Bacterial Viruses (www.phage.ulaval.ca) under the number HER589.

Data availability. The complete genome sequence of *E. coli* phage BRET is available in GenBank under the accession number [MK165087](https://doi.org/10.1093/nar/gkx176), and the raw data are in the SRA database under accession number [PRJNA508515](https://doi.org/10.1093/bioinformatics/btq006).

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