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GENOME SEQUENCES

Complete Genome Sequence of *Burkholderia cenocepacia* Phage Magia

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ABSTRACT *Burkholderia cenocepacia* is a Gram-negative bacterium that is implicated in respiratory infections. The 44,942-bp genome of Magia, a phage infecting *B. cenocepacia*, does not appear to have strong overall similarity to other known phages. The Magia genome encodes a Cro-like transcriptional regulator, a C2-like immunity repressor, and an integrase, suggesting that it is a temperate phage.

Burkholderia cenocepacia is a Gram-negative bacterium that typically resides in soil (1, 2). It is an opportunistic pathogen that causes aggressive respiratory infections in individuals with cystic fibrosis and chronic granulomatous disease (1, 3, 4). Study of phage Magia may help advance phage clinical applications for the treatment of *Burkholderia* infections.

Phage Magia was isolated from Nebraska Sandhills soil samples collected from Holt County, Nebraska, in 2018 and was propagated on *B. cenocepacia* strain MS1 grown aerobically in tryptic soy broth/agar at 37°C. Phage isolation and propagation were performed using the soft-agar overlay method (5). DNA was purified following a previously described protocol using the Promega Wizard DNA kit (6), prepared for sequencing with 550-bp inserts using a TruSeq Nano kit (Illumina), and sequenced as paired-end 250-bp reads by Illumina MiSeq sequencing with 500-cycle v2 chemistry. Sequencing raw reads (1,182,570 reads in total) obtained from the library index were checked for quality using FastQC (www.bioinformatics.babraham.ac.uk/projects/fastqc), and the genome was assembled, using SPAdes v3.5.0 (7), from these reads to a contig corresponding to phage Magia with 21-fold coverage. The end sequences of the assembled genome were verified by PCR using PCR primers (5′-ATCATCACCTCTTCGCACTG-3′ and 5′-GTAACGGAGAACAGTACGAGC-3′) facing off the contig ends and Sanger sequencing of the resulting PCR product. Genes were identified using GLIMMER v3 (8) and MetaGeneAnnotator v1.0 (9), and tRNAs were identified using ARAGORN v2.36 (10). The identified genes were assigned putative functions using BLAST v2.9.0 with the nonredundant and Swiss-Prot databases (11, 12), InterProScan v5.33 (13), and TMHMM v2.0 (14). For comparative purposes, whole-genome DNA sequence similarity was assessed using progressiveMauve v2.4 (15). All analyses were conducted using tools hosted on the Center for Phage Technology (CPT) Galaxy and Apollo interfaces (16–18) with default settings (https://cpt.tamu.edu/galaxy-pub).

B. cenocepacia phage Magia has a 44,942-bp genome with a GC content of 65.1%, approximately equivalent to that of its host (19). Seventy protein-encoding genes were identified in phage Magia, with a coding density of 95.4%; of these, putative functions were assigned for 33 proteins. Phage Magia does not appear to be closely related to any other reported phages. Its closest match is *Burkholderia* phage Bups phi1 (GenBank accession numbers EU307292.1 to EU307295.1), with 24.91% nucleotide identity and 33 similar unique proteins, as determined by progressiveMauve and BLASTp, with an E value cutoff of 0.001. A programmed translational frameshift in the tape measure chaperone gene was identified, and the presence of baseplate and tail sheath proteins suggests that the phage is a myophage. Notably, the Magia genome encodes a Cro-like transcriptional regulator, a

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C2-like immunity repressor, and an integrase, suggesting that it is a temperate phage. The Magia genome is also related to elements in *Burkholderia* genomes (e.g., 97% BLASTn identity to the position 3619498 to 3634698 region of the *Burkholderia cepacia* DDS 7H-2 chromosome [GenBank accession number CP007787]). A potential diversity-generating retroelement (DGR), including reverse transcriptase and Avd proteins, was identified in Magia. These systems can introduce variability into the genome via mutagenic retrohoming (20); potential mutagenesis target sequences and initiation of mutagenic homing (IMH) regions were identified in the relatively short reading frames of genes *47* and *57*. This system may allow the phage to adapt to rapidly changing conditions or to alter its host range (21).

Data availability. The genome sequence of phage Magia was deposited under GenBank accession number MT701587 and BioSample accession number SAMN14609636. The BioProject accession number is PRJNA222858, and the SRA accession number is SRR11558336.

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