AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Genome Sequence of KP-Rio/2015, a Novel *Klebsiella pneumoniae* (*Podoviridae*) Phage

Guilherme L. S. Meira,[a] Fabricio S. Campos,[b] Julia P. Albuquerque,[c] Maulori C. Cabral,[a] Sergio E. L. Fracalanzza,[a] Renata M. Campos,[a] Alane B. Vermelho,[a] Davis F. Ferreira[a]

Institute of Microbiology, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil[a]; Veterinary Medicine and Agronomy, University of Brasilia, Brasilia, Brazil[b]; Biomedical Institute, Fluminense Federal University, Rio de Janeiro, Brazil[c]

***Klebsiella pneumoniae* is a pathogen frequently associated with antibiotic-resistant nosocomial infections. Here, we describe the genome of KP-Rio/2015, a novel phage of *K. pneumoniae* belonging to the family *Podoviridae*.**

Received 5 October 2016 **Accepted** 27 October 2016 **Published** 22 December 2016

Citation Meira GLS, Campos FS, Albuquerque JP, Cabral MC, Fracalanzza SEL, Campos RM, Vermelho AB, Ferreira DF. 2016. Genome sequence of KP-Rio/2015, a novel *Klebsiella pneumoniae* (*Podoviridae*) phage. Genome Announc 4(6):e01298-16. doi:10.1128/genomeA.01298-16.

Address correspondence to Davis F. Ferreira, davisf@micro.ufrj.br.

Klebsiella pneumoniae is ubiquitous in nature and predominately associated with antibiotic-resistant nosocomial infections (1). Carbapenemase-producing *K. pneumoniae* is a highly drug-resistant bacterium in the family *Enterobacteriaceae*. It can easily be spread in hospital settings, provoking deadly systemic infections (1, 2). Bacteriophage-based therapy has been regaining the scientific community's attention, and this has led to increased research to identify prospect phages from different sources in order to find candidates that will kill multidrug-resistant bacteria (3). Recent *K. pneumoniae* phage discoveries include KP34, SU503, and SU552A (4, 5).

In this work, we describe the complete genome of KP-Rio/2015, a novel *K. pneumoniae* phage belonging to the family *Podoviridae*. The *K. pneumoniae* bacterium was isolated from a human urine sample, and the phage was isolated from urine antibiogram. The phage was concentrated using polyethylene glycol. Phage DNA was extracted by phenol-chloroform, sequenced in an Illumina HiSeq 2000 sequencing platform by GenOne Biotechnologies (Rio de Janeiro, Brazil). A total of 1,282,326 reads of ~150 bp were assembled with Geneious version 8.1.8. The reads were *de novo* assembled, with a mean coverage of 4,416×. A contig of 43,557 nucleotides comprised the full KP-Rio/2015 genome. With a G+C genomic content of 54.1%, we identified 47 open reading frame candidates, 11 regulatory regions, and five repeat regions in the KP-Rio/2015 genome. Predicted proteins encoded by this virus were DNA/RNA polymerases, a helicase, head and tail phage proteins, and hypothetical proteins; most of them exhibit sequence similarity (83.3 to 94.7%) to other subfamily *Autographivirinae* proteins. The genome sequence of KP-Rio/2015 had nucleotide identities with the following *K. pneumoniae* phages: SU552A (81.0%), SU503 (72.2%), F19 (72.1%), KP34 (74.2%), and NTUH-K2044-K1-1 (73.5%). The identity percentages were calculated by alignment of full-genome sequences. High identity with SU552A suggests that KP-Rio/2015 may have the potential to kill multidrug-resistant *K. pneumoniae*. Further experiments are necessary to confirm such an ability.

Accession number(s). The GenBank accession number is KX856662.

ACKNOWLEDGMENTS

This work was supported by CNPq and FAPERJ. We thank Eric Keen from the University of Miami for phage methodologies support.

FUNDING INFORMATION

This work, including the efforts of Alane B. Vermelho, was funded by MCTI | Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq). This work, including the efforts of Guilherme L.S. Meira and Alane B. Vermelho, was funded by Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ).

REFERENCES

1. **Podschun R, Ullmann U.** 1998. *Klebsiella* spp. as nosocomial pathogens: epidemiology, taxonomy, typing methods, and pathogenicity factors. Clin Microbiol Rev **11**:589–603.
2. **Snitkin ES, Zelazny AM, Thomas PJ, Stock F, NISC Comparative Sequencing Program Group, Henderson DK, Palmore TN, Segre JA.** 2012. Tracking a hospital outbreak of carbapenem-resistant *Klebsiella pneumoniae* with whole-genome sequencing. Sci Transl Med **4**:148ra116. http://dx.doi.org/10.1126/scitranslmed.3004129.
3. **Verbeken G, Pirnay JP, Lavigne R, Ceulemans C, De Vos D, Huys I.** 2016. Viruses that can cure, when antibiotics fail. J Microb Biochem Technol **8**:21–24. http://dx.doi.org/10.4172/1948-5948.1000257.
4. **Drulis-Kawa Z, Mackiewicz P, Kęsik-Szeloch A, Maciaszczyk-Dziubinska E, Weber-Dąbrowska B, Dorotkiewicz-Jach A, Augustyniak D, Majkowska-Skrobek G, Bocer T, Empel J, Kropinski AM.** 2011. Isolation and characterization of KP34—a novel φKMV-like bacteriophage for *Klebsiella pneumoniae*. Appl Microbiol Biotechnol **90**:1333–1345. http://dx.doi.org/10.1007/s00253-011-3149-y.
5. **Eriksson H, Maciejewska B, Latka A, Majkowska-Skrobek G, Hellstrand M, Melefors Ö, Wang JT, Kropinski AM, Drulis-Kawa Z, Nilsson AS.** 2015. A suggested new bacteriophage genus, "Kp34likevirus", within the *Autographivirinae* subfamily of *Podoviridae*. Viruses **7**:1804–1822. http://dx.doi.org/10.3390/v7041804.