Draft Genome Sequences of Burkholderia cenocepacia ET12 Lineage Strains K56-2 and BC7

John Varga, Emory University
Liliana Losada, The J. Craig Venter Institute
Adrian Zelazny, National Institutes of Health
Maria Kim, The J. Craig Venter Institute
Jamison McCorrison, The J. Craig Venter Institute
Lauren Brinkac, The J. Craig Venter Institute
Elizabeth Sampaio, National Institutes of Health
David Greenberg, National Institutes of Health
Indresh Singh, The J. Craig Venter Institute
Cheryl Heiner, Pacific Biosciences

Only first 10 authors above; see publication for full author list.

Journal Title: Genome Announcements
Volume: Volume 1, Number 5
Publisher: American Society for Microbiology: Genome Announcements | 2013-09, Pages e00841-13
Type of Work: Article | Final Publisher PDF
Publisher DOI: 10.1128/genomeA.00841-13
Permanent URL: http://pid.emory.edu/ark:/25593/fm191

Final published version: http://genomea.asm.org/content/1/5/e00841-13

Copyright information:
© 2013 Varga et al.
This is an Open Access work distributed under the terms of the Creative Commons Attribution 3.0 Unported License (http://creativecommons.org/licenses/by/3.0/).

Accessed April 10, 2020 1:12 PM EDT
Draft Genome Sequences of *Burkholderia cenocepacia* ET12 Lineage Strains K56-2 and BC7

John J. Varga, a,b,c Liliana Losada, c Adrian M. Zelazny, d,e Maria Kim, f Jamison McCorrison, f Lauren Brinkac, f Elizabeth P. Sampaio, d David E. Greenberg, g,h Indresh Singh, c Cheryl Heiner, g William C. Nierman, a,h Steven M. Holland, a Joanna B. Goldberg a,b

Department of Microbiology, Immunology, and Cancer Biology, University of Virginia Health System, Charlottesville, Virginia, USA; Department of Pediatrics and the Center for Cystic Fibrosis Research, Emory University School of Medicine, Children's Healthcare of Atlanta, Inc., Atlanta, Georgia, USA; The J. Craig Venter Institute, Rockville, Maryland, USA; Microbiology Service, Department of Laboratory Medicine, Clinical Center, National Institutes of Health, Bethesda, Maryland, USA; Laboratory of Clinical Infectious Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, USA; University of Texas Southwestern Medical School, Dallas, Texas, USA; Pacific Biosciences, Menlo Park, California, USA; The George Washington University, Washington, DC, USA

J.J.V. and L.L. contributed equally.

The *Burkholderia cepacia* complex (BCC) is a group of closely related bacteria that are responsible for respiratory infections in immunocompromised humans, most notably those with cystic fibrosis (CF). We report the genome sequences for *Burkholderia cenocepacia* ET12 lineage CF isolates K56-2 and BC7.

The BCC consists of 17 genetically related but phenotypically distinct betaproteobacterial species. BCC species can be found in a variety of niches and are capable of infecting numerous hosts. The most well-known member of the BCC is *Burkholderia cenocepacia*, a pathogen of onions and immunocompromised humans (1). We report the genome sequences of *B. cenocepacia* strains BC7 (2) and K56-2 (3), members of the highly transmissible genomovar III ET12 lineage (4, 5). While a genome sequence exists for the ET12 lineage strain J2315 (6, 8), sequence data confirm the presence of the plasmid was previously detected in K56-2, BC7, and J2315 (8). Sequence data confirm the presence of the plasmid in BC7 and K56-2, with practically no differences between the three strains except for the presence of an additional copy of an insertion element in the J2315 plasmid, pBCJ2315 (6). The genomes were annotated using the annotation pipeline of the J. Craig Venter Institute (JCVI) (http://www.jcvi.org) and submitted to GenBank. Sequence data indicate that K56-2 and BC7 have similar gene contents to that of J2315 and used to recruit and locally assemble reads into the gaps to merge the adjacent contigs. The resulting assembly is 296 contigs in 7 scaffolds.

As in J2315, each genome has 3 chromosomes and 1 plasmid (6). The chromosomes in BC7 and K56-2 have very similar sizes to those reported in J2315 (3.83 Mb, 3.19 Mb, and 0.88 Mb), except for chromosome 1 in K56-2, which has an estimated size of 3.67 Mb, due to the absence of the large duplication in J2315. The presence of the plasmid was previously detected in K56-2, BC7, and J2315 (8). Sequence data confirm the presence of the plasmid in BC7 and K56-2, with practically no differences between the three strains except for the presence of an additional copy of an insertion element in the J2315 plasmid, pBCJ2315 (6). The genomes were annotated using the annotation pipeline of the J. Craig Venter Institute (JCVI) (http://www.jcvi.org) and submitted to GenBank. Sequence data indicate that K56-2 and BC7 have similar gene contents to that of J2315, with 7,714 and 7,930 open reading frames (ORFs), respectively.

**Nucleotide sequence accession numbers.** The *B. cenocepacia* BC7 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ALIZ0000000. The version described in this paper is the second version, ALIZ0100000.

The *B. cenocepacia* K56-2 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ALJA0000000. The version described in this paper is the second version, ALJA0100000.

---

The *Burkholderia cepacia* complex (BCC) consists of 17 genetically related but phenotypically distinct betaproteobacterial species. BCC species can be found in a variety of niches and are capable of infecting numerous hosts. The most well-known member of the BCC is *Burkholderia cenocepacia*, a pathogen of onions and immunocompromised humans (1). We report the genome sequences of *B. cenocepacia* strains BC7 (2) and K56-2 (3), members of the highly transmissible genomovar III ET12 lineage (4, 5). While a genome sequence exists for the ET12 lineage strain J2315 (6, 8), sequence data confirm the presence of the plasmid was previously detected in K56-2, BC7, and J2315 (8). Sequence data confirm the presence of the plasmid in BC7 and K56-2, with practically no differences between the three strains except for the presence of an additional copy of an insertion element in the J2315 plasmid, pBCJ2315 (6). The genomes were annotated using the annotation pipeline of the J. Craig Venter Institute (JCVI) (http://www.jcvi.org) and submitted to GenBank. Sequence data indicate that K56-2 and BC7 have similar gene contents to that of J2315, with 7,714 and 7,930 open reading frames (ORFs), respectively.

**Nucleotide sequence accession numbers.** The *B. cenocepacia* BC7 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ALIZ0000000. The version described in this paper is the second version, ALIZ0100000.

The *B. cenocepacia* K56-2 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ALJA0000000. The version described in this paper is the second version, ALJA0100000.
ACKNOWLEDGMENTS

This project has been funded in part with federal funds from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services, under contract no. HHSN272200900007C and N01-AI30071. PacBio kindly contributed sequence reads for B. cenocepacia K56-2. J.J.V. was supported in part by the National Institutes of Health grant no. 5T32AI055432 awarded to the University of Virginia.

REFERENCES


