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

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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 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 CF isolates K56-2 and BC7. The BC7 assembly was initially in 7 scaffolds and 785 contigs. Since additional sequencing was not pursued for this genome, a reference-guided gap closure pipeline was employed to resolve hundreds of gaps found throughout the assembly. The gap sequences were predicted from the closed-genome reference (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.
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REFERENCES


