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

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The *Burkholderia cenocepacia* 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 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. 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. 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.

Nucleotide sequence accession numbers. The *B. cenocepacia* BC7 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ALIZ00000000. The version described in this paper is the second version, ALIZ01000000. The *B. cenocepacia* K56-2 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ALJA00000000. The version described in this paper is the second version, ALJA01000000.
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REFERENCES