In 2016, an outbreak centered in Wisconsin was originally attributed to *Elizabethkingia meningoseptica*. Using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) with an in-house database, optical mapping of genomic DNA, and whole-genome sequences, we were able to identify the agent as *Elizabethkingia anophelis*. Described in 2011 (1), *E. anophelis* belongs to the historically defined *Elizabethkingia* genomospecies 1 (2). The genomospecies of *Elizabethkingia* display no consistent distinguishing phenotypic characteristics (3); therefore, advanced identification techniques are required to differentiate them.

Isolates were grown on heart infusion agar supplemented with 5% rabbit blood at 35°C. DNA was extracted using the Zymo Fungal/Bacteria DNA MicroPrep kit (Zymo Research Corporation, Irvine, CA). Libraries were prepared using the NEBNext Ultra DNA library prep kit for Illumina (New England BioLabs, Ipswich, MA), and 20-kb SMRTbell libraries were generated using the Pacific Biosciences DNA template preparation kit and sequenced on the RSII instrument (Pacific Biosciences, Menlo Park, CA). The genome sequences have been deposited at GenBank under BioProject no. PRJNA315668. The accession and BioSample numbers for the strains associated with this outbreak have been deposited in the Sequence Read Archive (SRA).

**Table 1**. BioSample and accession numbers for each strain shown in Table 1.

| Strain       | BioSample no. | Accession no. | Rearrangement configuration |
|--------------|---------------|---------------|------------------------------|
| CSID_3015183678 | SAMN04567744   | CP014805      | A-Brc-Crc                    |
| CSID_3015183681 | SAMN04567745   | CP015068      | C-B-Arc                      |
| CSID_3015183684 | SAMN04590540   | CP015066      | A-Brc-Crc                    |
| CSID_3000521207 | SAMN04567738   | CP015067      | C-Brc-Arc                    |

The complete circularized genome sequences of selected specimens from the largest known *Elizabethkingia anophelis* outbreak to date are described here. Genomic rearrangements observed among the outbreak strains are discussed.

**Table 1** shows accession numbers for strain CSID_3015183678 and three additional outbreak strains that were selected for this publication. Unmapped reads were collected and de novo assembled; no insertions or episomal elements were found. Two deletions were found in strain CSID_3000521207. An in-frame, 1,515-bp deletion at position 3142444 (positions of the genome features are based on strain CSID_3015183678) joins two adjacent S41 family peptidases into a new hybrid S41 family peptidase. The 76,250-bp deletion at position 3779423 removes 77 protein-coding genes.

Three segments, A, B, and C at position 3929927, appear to undergo ordered rearrangement. B in the middle can be present in either direct or reverse complement (rc) orientation; flanking elements A and C exchange locations and will be in either direct and or reverse complement, depending on location, resulting in four configurations for the region: A-B-Crc, C-B-Arc, A-Brc-Crc, and C-Brc-Arc. Among all of the outbreak strains, isolates have reads consistent with one, two, or more configurations. This indicates that the region can be stable or may undergo rearrangement during cell growth.

The genomes were annotated by the NCBI Prokaryotic Genome Annotation Pipeline. Reads for the strains associated with this outbreak have been deposited in the Sequence Read Archive (SRA).

**Nucleotide sequence accession numbers.** The complete genome sequences have been deposited at GenBank under BioProject no. PRJNA315668. The accession and BioSample numbers for each strain are shown in Table 1.
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