

Draft Genome Sequences of *Elizabethkingia meningoseptica*

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***Elizabethkingia meningoseptica* is ubiquitous in nature, exhibits a multiple-antibiotic resistance phenotype, and causes rare opportunistic infections. We now report two draft genome sequences of *E. meningoseptica* type strains that were sequenced independently in two laboratories.**

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The genus *Elizabethkingia* was derived in 2005 following a series of systematic investigations that led to the reclassification of members previously found within the genera *Flavobacterium* and *Chryseobacterium* (1–4). Currently, *Elizabethkingia* is represented by the three species *Elizabethkingia miricola* (5), *Elizabethkingia meningoseptica* (6, 7), and *Elizabethkingia anophelis* (8).

E. meningoseptica expresses a multiple-antibiotic resistance phenotype and causes infections primarily within immunocompromised individuals (9–11). The type strain of *E. meningoseptica* was isolated in 1958 in a case of neonatal meningitis (6, 7). We now report the draft genome sequences of two *E. meningoseptica* type strains, NBRC 12535^T and ATCC 13253^T. Both of these culture collection strains are representatives of the original *E. meningoseptica* strain isolated by Elizabeth King and colleagues (6).

The draft genome sequences of NBRC 12535^T and ATCC 13253^T were prepared at the National Institute of Technology and Evaluation, Tokyo, Japan, using Illumina HiSeq 1000 technology and at Oklahoma State University using the Roche 454 GS Junior platform, respectively. Genomic DNA to be sequenced was isolated from overnight cultures (30°C) of NBRC 12535^T grown on nutrient agar containing 75% artificial seawater and ATCC 13253^T grown in nutrient broth. Sequencing of NBRC 12535^T generated 3,974,452 reads (103× coverage; average read length, 99.4 bp) that were assembled with the Newbler assembler (v2.6). ATCC 13253^T sequencing produced 223,447 reads (29.7× coverage; average read length, 504.9 bp) that were assembled with the Roche GS *de novo* assembler (v2.7). Both draft genome sequences were uploaded to the Rapid Annotations using Subsystems Technology (RAST) server for annotation (12).

The NBRC 12535^T draft genome sequence is 3,840,286 bp in length (36.2% G+C content) and includes 3,519 protein-coding regions distributed in 34 contigs (>500 bp). The ATCC 13253^T draft genome sequence is 3,797,222 bp (35.2% G+C content) in length and includes 3,486 protein-coding regions distributed in 115 contigs (>200 bp). One hundred eleven contigs (representing 3,795,245 bp) of the ATCC 13253^T sequence demonstrated 99 to 100% nucleotide identity with the 34 contigs of the NBRC 12535^T sequence, which indicates that these draft genome sequences are essentially the same.

The nucleotide alignment of several highly conserved genes from the *E. meningoseptica* draft genome sequences and *E. anophelis* R26^T (gene and nucleotide identities are as follows: *gln*, 86%; *gyrB*, 87%; *recA*, 88%; *atpD*, 92%; and *dnaK*, 92%) strongly supports previous findings that *E. anophelis* is at least a separate species (8). The 16S rRNA sequences of these two species are 98% identical, which is not very definitive for speciation (13). *E. meningoseptica* is resistant to β -lactam antibiotics due to the production of metallo- β -lactamases (MBLs) and extended-spectrum β -lactamases (ESBLs) (14–16). Two MBL variants (*bla*_{GOB-17} and *blaB3*) and one ESBL gene (*bla*_{CME-1}) were found in both *E. meningoseptica* draft genome sequences and were aligned with similar *E. anophelis* genes. A comparison of the β -lactamase orthologs from these two species revealed only 74% to 85% amino acid identity. This finding confirms that *Elizabethkingia* species, which are ubiquitous in nature (17), may act as potential reservoirs of novel β -lactamase genes.

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession no. [BARD000000000](https://www.ncbi.nlm.nih.gov/nuccore/BARD000000000) for NBRC 12535^T and [ASAN000000000](https://www.ncbi.nlm.nih.gov/nuccore/ASAN000000000) for ATCC 13253^T.

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