AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

Genome Sequence of the Antibiotic-Resistant Pathogen *Elizabethkingia miricola* DSM 14571 Isolated from a Russian Space Station

Elizabethkingia miricola DSM 14571 was isolated from condensation water aboard a Russian space station and cultured on cysteine-lactose-electrolyte-deficient medium agar before genome sequencing, which revealed 4,064 predicted genes including virulence and resistance-associated elements.

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Genome of *Elizabethkingia miricola* DSM 14571

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Abstract

Elizabethkingia miricola DSM 14571 is a Gram-negative opportunistic and antibiotic-resistant human pathogen Isolated from a Russian space station. The genome contains 4,064 genes, including virulence factors and secondary metabolic clusters. This research could offer further insight into pathogenicity, environmental resilience, resistance mechanisms, and zoonotic risks.

Announcement

First section (introduction and rationale)

Elizabethkingia miricola DSM 14571 is a Gram-negative, rod-shaped bacterium isolated from condensation on the Russian space station in 2003 (1). Astronauts used sterile swabs to sample the condensation water and cultured the bacteria on cystein-lactose-electrolyte-deficient medium agar (2). *E. miricola* is primarily an opportunistic human pathogen associated with immunocompromised individuals, and has been isolated from other organisms, including amphibians (3). Sequencing its genome is necessary for understanding its pathogenicity, mechanisms of antibiotic resistance, and virulence factors, as well as insight into its ecological role and genetic potential (4). These findings will enhance our understanding of antibiotic-resistant pathogens and opportunistic pathogenicity, which will remain global health threats (5)

Overall, the sequencing of this genome is part of a broader study led by the Joint Genome Institute to explore microbial diversity and its functional implications in public health and environmental microbiology.

Second section (methods and related outcomes)

Details on organism growth and DNA isolation to be provided by DSMZ. The draft genome was sequenced at the DOE Joint Genome Institute (JGI) using Illumina technology (6). A standard Illumina shotgun library was prepared and sequenced on the Illumina HiSeq 2000 platform, generating 8,984,416 reads with a total output of 1,347.7 Mb. The raw Illumina sequence data was processed using DUK, a program developed at JGI, to remove known Illumina sequencing and library preparation artifacts (7). The sequencing depth was 270X, with a read length of 2×150 bp. Genome assembly was performed using Velvet (version 1.2.07), with the default settings applied (8). The final genome assembly was deemed 100% complete, with a contamination level of 0.35% (9). Annotation was conducted using the standard JGI Microbial Genome Annotation Pipeline (10).

Final section (results)

Feature	Finding
Genome Length (bp)	4295221
No. of scaffolds	37
Scaffold N50 (bp)	303726
Average fold coverage (x)	598
GC content (%)	35.81
No. of genes	4064
No. of protein-coding genes	4006
No. of rRNA genes	6

No. of tRNA genes	46

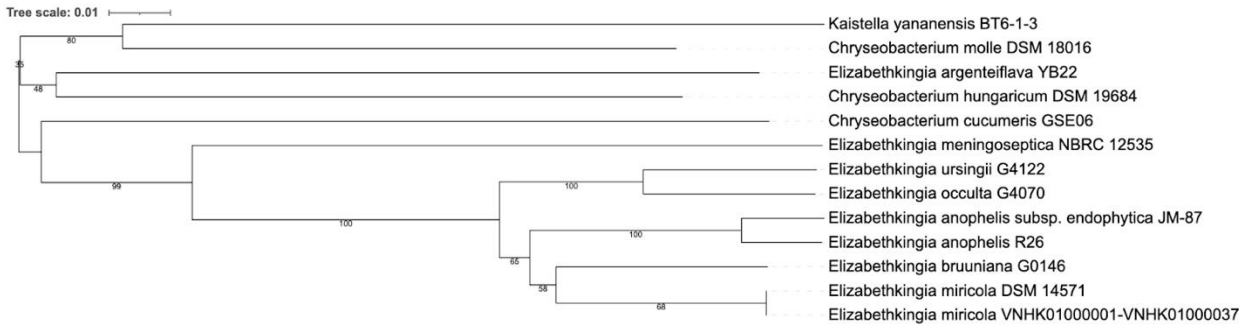

Figure 1. Whole-genome-based phylogenetic classification of *Elizabethkingia miricola* DSM 14571. The genome BLAST distance phylogeny (GBDP) tree was generated with the Type Strain Genome Server (TYGS [8]; accessed 15 March 2025).Tree inferred with FastME 2.1.6.1 [7] from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula *d5*. The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 75.3 %. The tree was rooted at the midpoint [8].

Virulence factors that were found in the area of the genome include: carbamoyl phosphate synthase (Pyrimidine biosynthesis-Nutritional/Metabolic factor), endopeptidase Clp ATP-binding chain C (Stress survival), urease beta subunit UreB (Stress survival), urea amidohydrolase (Adherence), Hsp60 60K heat shock protein HtpB (Adherence), chaperonin GroEL (Adherence), botulinum neurotoxin (Exotoxin), and type 8 capsular polysaccharide synthesis protein Cap8D (Capsule-Immune modulation) (11). Analysis using the Comprehensive Antibiotic Resistance Database (CARD) (12) identified the presence of blaB-26 and GOB-32, both metallo-β-lactamase genes associated with resistance to carbapenems, penicillin-class beta-lactams, and cephalosporins. Types of secondary metabolite clusters that were detected include: Non-alpha poly-amino acids like e-Polylysin, Class I lanthipeptides like nisin (most similar known cluster is pinensins), RRE-element containing cluster, NRPS-independent, IucA/IucC-like siderophores (most similar cluster is fulvivirgamide A2/fulvivirgamide B2/fulvivirgamide B3/fulvivirgamide B4) (13).

Data availability statement

The whole genome shogun sequence has been deposited in GenBank under the accession number VNHK01000000.The raw reads have been deposited in the NCBI SRA under the accession number SRX6767152. Additional data can be explored or downloaded from the JGI Integrated Microbial Genomes with Microbiomes (IMG/M) portal using the taxon ID 2593339301.

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