



Genome Sequence of OXA-726-Encoding *Aeromonas dhakensis* Igbk (Sequence Type 1171) from an Edible Snail Traded in Nigeria

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ABSTRACT *Aeromonas dhakensis* is the most virulent *Aeromonas* species pathogenic to both animals and humans. The degree of its risk to health seems masked by misidentifications. We present the genome sequence of *A. dhakensis* Igbk (sequence type 1171), associated with snails, harboring the OXA-726 gene in the chromosome.

Aeromonas dhakensis is an important pathogen isolated from the environment (1, 2), animals (3, 4), and humans (5, 6). It was first isolated from children with diarrhea (5). *A. dhakensis* is frequently misidentified as *Aeromonas hydrophila* by phenotypic methods and matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) (7, 8). A strain of *A. hydrophila* (GenBank accession number [MK530176](https://ncbi.nlm.nih.gov/nuccore/MK530176)) that was recently identified from edible snails in a different study in Nigeria using 16S rRNA gene sequencing (9) might also have been misidentified due to the strong similarities of the 16S rRNA gene.

Here, we report the genome sequence of an OXA-726-encoding *A. dhakensis* isolate that was obtained in October 2021 from a raw snail (*Achatina achatina*) traded in the wet market at Igboukwu Town, southeast Nigeria. An intestinal section (50 g) was aseptically collected and homogenized with 450 mL of peptone water (Oxoid, Hampshire, UK); aliquots were enriched for 24 h in nutrient broth (Oxoid) containing 3% NaCl and were subsequently plated on thiosulfate-citrate-bile salts-sucrose agar (Titan, Delhi, India) with incubation at 35°C for 24 h. Presumptive colonies were subcultured on blood agar (bioMérieux, Marcy-l’Etoile, France) for 24 h at 35°C. MALDI-TOF MS (Bruker, Bremen, Germany) with Biotyper software v4.1.100 was used for identification of the isolate. Genomic DNA was extracted using the MagAttract high-molecular-weight (HMW) DNA kit (Qiagen, Hilden, Germany). Genomic libraries were prepared using the Nextera XT kit (Illumina, San Diego, CA, USA) and sequenced (2 × 300-bp reads) on a MiSeq instrument. Raw reads were assembled using SPAdes v3.15.2 (<https://cab.spbu.ru/software/spades>) and quality controlled using FastQC v0.11.7 and Trimmomatic v0.36. Whole-genome-based taxonomic analyses were performed using digital DNA-DNA hybridization (dDDH) (<https://tygs.dsmz.de>) and the Tetra Correlation Search (TCS) (<http://jspecies.ribohost.com/jspeciesws>). MALDI-TOF MS identified our strain as *A. hydrophila*, whereas dDDH and TCS identified it as *A. dhakensis* (93.9% and 0.99988 Z-score identity, respectively, with respect to *A. dhakensis* CIP 107500). A multilocus sequence typing (MLST) scheme was engaged to assign a new sequence type (ST), ST-1171, to *A. dhakensis* strain Igbk. An *ad hoc* core genome MLST scheme with 2,928 targets was created with SeqSphere+ v8.3.1 (Ridom, Münster, Germany) and used for comparison with all *A. dhakensis* strains available from GenBank. This comparison showed 669 allelic differences from a *A. dhakensis* strain isolated in 2019 from a rectal swab sample in Thailand. The NCBI Prokaryotic Genome Annotation Pipeline (PGAP) was used for annotation (10). Genome data for *A. dhakensis* Igbk are presented in Table 1. The strain was further characterized using the

Editor Julie C. Dunning Hotopp, University of Maryland School of Medicine

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The authors declare no conflict of interest.

Received 8 April 2022

Accepted 8 May 2022

Published 31 May 2022

TABLE 1 Genomic features of *Aeromonas dhakensis* Igbk (ST-1171)

Attribute	Finding
Assembly size (bp)	4,829,827
No. of reads	1,255,396
Avg read length (bp)	252
No. of contigs	260
N_{50} (bp)	80,959
GC content (%)	61.6
Genome coverage (×)	57
Total no. of genes	4,585
No. of coding genes	4,380
No. of RNA genes	155
No. of noncoding RNA genes	7
No. of pseudogenes	50
Antimicrobial resistance genes	<i>bla</i> _{OXA-726} , <i>adeF</i> , <i>rsmA</i> , <i>imiH</i> , EF-Tu, <i>ampH</i> , <i>cphA8</i>

Comprehensive Antibiotic Resistance Database (CARD), MobileElementFinder (<https://cge.cbs.dtu.dk/services/MobileElementFinder>), and PathogenFinder (<https://cge.cbs.dtu.dk/services/PathogenFinder>). Default parameters were used for all software except where otherwise noted. Our strain harbored a range of antimicrobial genes (Table 1), notably *bla*_{OXA-726}, which codes for a type of class D β -lactamase purported to be a looming global public health threat (11). Virulence genes and plasmids were not detected. The pathogenic probability was 0.771, matching 31 pathogenic gene families. The presented features of *A. dhakensis* Igbk (ST-1171) will contribute data useful to public health authorities for comparative genomics.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number JALGBK000000000 (BioProject accession number PRJNA819262 and BioSample accession number SAMN26920427). This is the first version of this genome. The raw sequence reads have been deposited in the Sequence Read Archive (SRA) under the accession number SRR18516351.

ACKNOWLEDGMENTS

This work was supported by a research scholarship (Ernst-Mach grant MPC-2021-00071) awarded to A.C.O. that was financed by the Austrian Federal Ministry of Science, Research, and Economy (BMBWF) and administered by the Austrian Agency for Education and Internationalisation (OeAD).

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