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Genome Sequence of the Emerging Pathogen *Aeromonas caviae*▽

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***Aeromonas caviae* is a Gram-negative, motile and rod-shaped facultative anaerobe that is increasingly being recognized as a cause of diarrhea in children. Here we present the first genome sequence of an *A. caviae* strain that was isolated as the sole pathogen from a child with profuse diarrhea.**

Aeromonads are Gram-negative organisms belonging to the *Gammaproteobacteria*. Nineteen species of *Aeromonas* can be distinguished by biochemical and molecular techniques (5); most do not have a strong association with disease. However, *Aeromonas salmonicida* is a well-established fish pathogen, and *Aeromonas caviae*, *Aeromonas hydrophila*, and *Aeromonas veronii* account for 85% of isolates derived from human infections (5). While *Aeromonas* sp. can be isolated from ca. 2% of healthy individuals, association with stools from patients with diarrhea has been reported to be as high as 10.8% (4, 5). Here we report the genome sequence of *A. caviae* Ae398. This strain was isolated from a 17-month-old male at the Hospital Universitário Pedro Ernesto, Rio de Janeiro, Brazil. The patient presented with gastroenteritis and diarrhea, without mucus or blood, approximately three times a day for 3 weeks. *A. caviae* Ae398 was isolated as the sole pathogen from a stool specimen collected 3 weeks after onset of symptoms and was identified by conventional biochemical tests (3). The isolate presented extracelullar enzymatic activities, resistance to several antibiotics, and adherence to epithelial cell monolayers (2, 3, 7, 9, 10).

Whole-genome shotgun sequencing of *A. caviae* Ae398 was performed by a combination of 454 GS-FLX (162,066 shotgun reads of average length 358 bp) and Illumina sequencing (25,272,910 51-bp paired-end reads), leading to a final assembly of 149 contigs >200 bp. The assembly represented 4,339,218 bp, with a mean contig size of 29,793 bp, an N50 value of 76,364 bp (where N50 is the contig length such that at least 50% of the bases of the assembly are contained within contigs of this size or greater), and an average G+C content of 61.4%. Nucmer pairwise genome alignments (6) show the *A. caviae* Ae398 genome displays the highest overall synteny with *A. hydrophila* ATCC 7966 (70.4% aligned) and *A. salmonicida* A449 (61.7% aligned) and average nucleotide identities of 88.8% and 86.8% across aligned regions, respectively.

The deduced size of the *A. caviae* Ae398 genome (4.43 Mb) is similar to those of *A. hydrophila* ATCC 7966 (4.47 Mb) and *A. salmonicida* A449 (4.70 Mb). *A. caviae* Ae398 harbors at least one conjugative plasmid of >30 kb, although it remains in several contigs in the assembly. Five different insertion (IS) element types are present in *A. caviae* Ae398, whereas *A. salmonicida* possesses 88 copies of 10 different IS elements and *A. hydrophila* completely lacks IS elements (8, 11). An ~33-kb putative prophage bounded by 55-bp repeats is found at the tRNA-Leu attachment site in *A. caviae* Ae398; the 3′ region shares high identity with *phi*O18P (1), whereas the 5′ region is most similar to structural genes from non-*Aeromonas* phage genomes.

A. caviae contains many putative virulence genes, including those encoding a type 2 secretion system (11), an RTX toxin, and polar flagella. The genome sequence of *A. caviae* Ae398 is an important milestone in understanding the diversity and pathogenesis of *A. caviae*, opening new avenues for investigating the pathogenic processes of this organism and allowing robust diagnostics to be developed.

Nucleotide sequence accession numbers. The assembly was deposited at the WGS division of DDBJ/EMBL/GenBank under accession no. CACP01000001 to CACP01000149.

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