

Complete Genome Sequence of a Moderately Virulent *Aeromonas hydrophila* Strain, pc104A, Isolated from Soil of a Catfish Pond in West Alabama

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***Aeromonas hydrophila* pc104A is a moderately virulent strain isolated from the soil of a catfish pond in west Alabama in 2010. Its full genome is 5,023,829 bp. The availability of this genome will allow comparative genomics to identify the virulence genes that are important for pathogenesis or immunogens for the purpose of vaccine development.**

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The Gram-negative bacterium *Aeromonas hydrophila* is the causative agent of motile aeromonad septicemia (MAS) (1), also known as epizootic ulcerative syndrome (2). Typical symptoms of MAS in fish include red sores, necrosis, ulceration, and hemorrhagic septicemia (3). In west Alabama, MAS disease outbreaks have led to an estimated annual loss of >3 million pounds of food-sized channel catfish since 2009 (4–8). The complete genome of highly virulent isolates of *A. hydrophila* ML09-119 and *A. hydrophila* AL09-71 from the western Alabama MAS disease outbreak were recently published (8, 9). Lateral gene transfer has been implicated as the molecular basis of the emergence of an *A. hydrophila* epidemic outbreak (10). Strain *A. hydrophila* pc104A was isolated from the soil of catfish pond in west Alabama in 2010. Virulence studies revealed that *A. hydrophila* pc104A was at least 1,000-fold-less virulent than *A. hydrophila* AL09-71 based on estimated 50% lethal dose (LD₅₀) values. It was unknown whether the less virulent *A. hydrophila* pc104A and the highly virulent isolates, such as *A. hydrophila* AL09-71 or *A. hydrophila* ML09-119, were different at the genomic DNA level. Therefore, the complete genome sequence of *A. hydrophila* pc104A was determined in this study.

The genome of *A. hydrophila* pc104A was sequenced using the Illumina 1500 HiSeq platform. BioNumerics (Applied Maths) was used to assemble a total of 23,280,526 sequence reads, with an average length of 100.18 bp (estimated 464× coverage). Using the west Alabama epidemic isolate *A. hydrophila* ML09-119 genome (accession no. CP005966) as a reference, the assembled genome of *A. hydrophila* pc104A is 5,023,829 bp, with a G+C content of 60.8%. RNAmmer (11) predicted 11, 10, and 10 copies of 5S RNA, 16S RNA, and 23S RNA, respectively, in the genome of *A. hydrophila* AL09-71, which is similar to those in the genomes of *A. hydrophila* ML09-119 (8) or *A. hydrophila* AL09-71 (9). The RAST server (12) predicted 4,492 genes belonging to 534 subsystems, including 466 involved in carbohydrate metabolism, 437 in amino acids and derivatives, 295 in cofactors, vitamins, prosthetic groups, or pigments, 263 in protein metabolism, 224 in RNA me-

tabolism, 189 in cell wall and capsule synthesis, 183 in membrane transport, 172 in respiration, 159 in stress response, 136 in fatty acid and lipids synthesis, 127 in nucleosides and nucleotides, 127 in motility and chemotaxis, 124 in DNA metabolism, 100 in regulation and cell signaling, 89 in virulence, disease, and defense, and 19 in the subsystem of phages, prophages, transposable elements, and plasmids.

Nucleotide sequence accession number. The complete genome sequence of *A. hydrophila* pc104A was deposited at GenBank under the accession no. CP007576.

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