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GENOME ANNOUNCEMENT

Genome Sequence of a Novel Human Pathogen, *Aeromonas aquariorum*

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***Aeromonas aquariorum*, a recently described species, is associated with a variety of human diseases. We present here the first genome sequence of *A. aquariorum* strain AAk1, which was isolated as the sole pathogen from the blood of a patient with septicemia and necrotizing fasciitis.**

Members of the genus *Aeromonas*, oxidase-producing Gram-negative rods, are found ubiquitously in aquatic environments worldwide and have been implicated in a variety of human diseases (3). Three species, *Aeromonas hydrophila*, *A. caviae*, and *A. veronii* bv. sobria (previously called *A. sobria*), have the most clinical significance and account for 85% of the clinical isolates recovered (3). However, recent developments in the field of *Aeromonas* taxonomy based on genetic identification have led to a reclassification of aeromonads and to the description of new species. Several clinical *Aeromonas* strains from Taiwan, including strain AAK1, were identified as *A. aquariorum* (2), a recently described species found initially in aquarium water and ornamental fish (5). Clinical strains of *A. aquariorum* possess many virulence genes and are associated with diarrhea, bacteremia, wound infections, and other extraintestinal infections (2). To elucidate the virulence profile contributing to its ability to cause human diseases, we analyzed the sequence of the *A. aquariorum* genome. The study strain, AAK1, was isolated from the blood of a cirrhotic patient as the sole pathogen causing septicemia and necrotizing fasciitis.

Whole-genome sequencing of AAK1 with the exclusion of the plasmid sequence, was performed with 454 pyrosequencing technology. Genomic shotgun and 8-kb mate-paired libraries were constructed and sequenced separately in accordance with the instructions supplied with the 454 GS junior instrument (Roche Diagnostics, Indianapolis, IN). A total of 67,989,514 bp in 156,381 reads from the shotgun library and 34,505,196 bp in 100,929 reads from the 8-kb mate-paired library were assembled into 36 contigs using 454 Newbler (version 2.5; 454 Life Sciences, Branford, CT). Using the connecting pair-end reads, these contigs were clustered into one scaffold. The plasmid of AAK1 was isolated and completely sequenced according to the method described previously (7). The sequencing result was assembled using Vector NTI Advance 11.1 software, leading to the assembly of a circular 4,161-bp plasmid.

The final assembly of the genome sequence of AAK1 contains a circular chromosome of 4,763,532 bp and a circular plasmid of 4,161 bp. The deduced size of the *A. aquariorum* AAK1 genome is 4.81 Mb (the scaffold size is 4,809,649 bp), which is slightly larger than that of *A. hydrophila* ATCC 7966^T (4.47 Mb) (GenBank accession number CP000462) (6), *A. veronii* B565 (4.55 Mb) (GenBank accession number CP002607) (4), or *A. caviae* Ae398 (4.43 Mb) (GenBank accession numbers CACP01000001 to CACP01000149) (1). Nucmer pairwise genome alignments (6) show that the AAK1 genome displays the highest overall synteny with *A. hydrophila* ATCC 7966 (76.5% aligned), followed by *A. caviae* Ae398 (61.3% aligned) and *A. veronii* B565 (57.3% aligned).

Sequence annotation using CLC Genomics Workbench 4.0 and OMIGA 2.0 software shows that AAK1 possesses many putative virulence genes, including those encoding a type IV fimbria, a type IV pilus, a fimbrillin, an adhesin, an RTX toxin, the cytotonic enterotoxin ALT, a hemolysin, phospholipase A1, siderophore synthesis, a ferric uptake regulator (Fur), an invasin, an enolase, an autoinducer synthase, a quorum-sensing regulon activator (AhyR), a collagenase, and a mucin-desulfating sulfatase. The analysis of the whole-genome sequence of this pathogen causing septicemia and necrotizing fasciitis facilitates further research on microbial virulence and host-pathogen interaction.

Nucleotide sequence accession numbers. The assembly reported here was deposited at DDBJ/EMBL/GenBank under accession no. BAFL01000001 to BAFL01000036 and AP012343. The version described in this paper is the first version.

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