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Complete Genome Sequence of *Aeromonas veronii* Strain B565▽

Yanxia Li,[1]† Yuchun Liu,[2]† Zhemin Zhou,[1,3] Huoqing Huang,[1] Yan Ren,[1,3,4] Yuting Zhang,[2] Guannan Li,[1] Zhigang Zhou,[2]* and Lei Wang[1,3,4]*

Key Laboratory of Molecular Microbiology and Technology, Ministry of Education, Tianjin 300457, People's Republic of China[1]; Key Laboratory for Feed Biotechnology of the Ministry of Agriculture, Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing 100081, People's Republic of China[2]; TEDA School of Biological Sciences and Biotechnology, Nankai University, Tianjin 300071, People's Republic of China[3]; and Tianjin Biochip Corporation, 23 Hongda Street, TEDA, Tianjin 300457, People's Republic of China[4]

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***Aeromonas veronii* strain B565 was isolated from aquaculture pond sediment in China. We present here the complete genome sequence of B565 and compare it with 2 published genome sequences of pathogenic strains in the *Aeromonas* genus. The result represents an independent stepwise acquisition of virulence factors of pathogenic strains in this genus.**

Aeromonas veronii is a Gram-negative, rod-shaped bacterium, commonly isolated from clinical, environmental, and food samples (1). It can cause wound infections, diarrhea, or septicaemia in immunocompromised patients (4, 6, 10). *A. veronii* is also the causative agent of bacterial hemorrhagic septicemia in fish and is becoming a major economic problem in the fish-farming industry (2). *A. veronii* strain B565, isolated from aquaculture pond sediment in Tianjin, China, was found to have the ability to produce chitinase to control fungal or Myxozoa-related diseases in a separate study.

Whole-genome sequencing of *A. veronii* B565 was performed with a combined strategy involving Roche/454 (8) and Solexa paired-end sequencing technology (3). Genomic libraries containing 5.8-kb inserts were constructed, and 225,134 paired-end reads were generated using the GS FLX system, giving 18.8-fold coverage of the genome. A total of 94.65% of the reads were assembled into 3 large scaffolds, including 62 nonredundant contigs, using a 454 Newbler assembler (454 Life Science, Branford, CT). A total of 4,340,032 reads (2-kb insert) were generated to reach a depth of 95-fold coverage with an Illumina Solexa GA IIx and mapped to the scaffolds using a Burrows-Wheeler alignment (BWA) tool (7). The interscaffold and intrascaffold gaps were filled by local assembly of Roche and Solexa reads around or sequencing PCR products using an ABI 3730 capillary sequencer. The analysis of the genome was performed as described previously (5, 13).

The complete genome sequence of B565 contains a circular 4,551,783-bp chromosome, with a GC content of 58.72%. There are 4,057 protein-coding genes, 10 rRNA operons, and 102 tRNA genes in its genome. B565 encodes some putative virulence factors, such as hemolysins, RTX protein, adhesion factor, flagella, and mannose-sensitive hemagglutinin (MSHA) (12), all of which were shared with at least one of the sequenced genomes for *Aeromonas hydrophila* ATCC 7966 (11) and *A. salmonicida* A449 (9). There are 5 genes encoding chitinase in B565, and all could be found in ATCC 7966 and A449, indicating an important role for these conserved chitinases in *Aeromonas*.

There are fewer virulence genes in B565 than in ATCC 7966 and A449, suggesting a less virulent or nonvirulent character. There are 346 genes shared by ATCC 7966 and A449 but absent in B565. Some of these genes encode putative virulence factors such as hemolysins and the type III secretion protein. There are 329 and 666 unique genes in ATCC 7966 and A449, respectively, some of which are virulence genes and often form large clusters, such as the *rtx* cluster in ATCC 7966 and the flagellar gene cluster in A449, or are related to mobile elements such as phages and transposons, illuminating their lateral transfer history.

The comparison represents a two-stepwise process during the acquisition of virulence in these pathogenic *Aeromonas* species: some weapons were acquired a long time ago and inherited from their common ancestors, while others can be obtained quickly by lateral transfer.

Nucleotide sequence accession number. The sequence and annotation of the *A. veronii* B565 are available in GenBank under accession number CP002607.

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* Corresponding author. Mailing address for Zhigang Zhou: Key Laboratory for Feed Biotechnology of the Ministry of Agriculture, Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing 100081, People's Republic of China. Phone: 86-10-82106073. Fax: 86-10-82106054. E-mail: zhou_zg@msn.com. Mailing address for Lei Wang: Key Laboratory of Molecular Microbiology and Technology, Ministry of Education, Tianjin 300457, People's Republic of China. Phone: 86-22-66229592. Fax: 86-22-66229596. E-mail: wanglei@nankai.edu.cn.

† The first two authors contributed equally to this paper.

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