Draft Genome Sequence of Aeromonas sp. Strain EERV15

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We report here the draft genome sequence of Aeromonas sp. strain EERV15 isolated from sand filter. The organism most closely related to Aeromonas sp. EERV15 is Aeromonas veronii B565, with an average 83% amino acid sequence similarity of putatively encoded protein open reading frames.

Aeromonas spp. are present in a wide range of habitats (1). These bacteria are associated with an aquatic environment and can be isolated from different environmental sources, such as food, invertebrates, fish, birds, ticks, insects, domesticated pets, and natural soils (2–4). Aeromonas spp. are classified as mesophilic or psychrophilic. The mesophilic group, comprising Aeromonas hydrophila, is associated with human infections, whereas the psychrophilic group, comprising Aeromonas salmonicida as the only species was associated so far with diseases in fish (5). Aeromonas clinical infections are divided into four categories (5), which are gastrointestinal tract syndromes (6, 7), wound and soft tissue infections (8, 9), blood-borne dyscrasias (10, 11), and miscellaneous infections (5, 12, 13). Most clinical infections are caused by A. hydrophila, A. caviae, and A. veronii biovar sobria (14). Here, we announce the draft genome sequence of Aeromonas sp. strain EERV15 (taxon ID: 1833892), previously named Aeromonas sp. strain K62 (J. Vandermaesen, B. Lievens, D. Springael, submitted for publication).

The genome was sequenced using the Illumina MiSeq platform, which generated paired-end read sequences of 250 bp. These were assembled using Edena (15, 16), producing 207 contigs, with a total genome size of 4,464,577 bp (58% G+C content; N50, 173 kb) and a coverage average of 200×. Automatic annotation was performed using the RAST server version 4.0 (17), generating 4,017 potentially protein-coding genes (open reading frames [ORFs]).

In order to find the closest related strain to EERV15 at the genome level, a comparison between the draft genome of Aeromonas sp. strain EERV15 and 33 genomes or draft genomes (six Aeromonas isolates, HZM (18); ZOR0001 [accession no. PRJNA205571], ZOR0002 [accession no. PRJNA205572], LIB53 [accession no. PRJNA270791], 159 [19], and MDS8 [20]; 10 Aeromonas veronii strains, AMC34 [accession no. PRJNA71515], AMC35 [accession no. PRJNA71519], Hm21 [21], AER39 [accession no. PRJNA71513], AER397 [accession no. PRJNA71517], B565 [22], CECT4257 [accession no. PRJEB7044], CECT4486 [accession no. PRJEB7050], CIP 107763 [accession no. PRJEB7047], and A. veronii biovar sobria [accession no. PRJEB7051]; 10 Aeromonas hydrophila strains, J-1 [accession no. PRJNA227242], YL17 [accession no. PRJNA234473], NJ-35 [accession no. PRJNA226230], pc 104A [23], Ae34 [24], ML09-119 [25], 4AK4 [26], ATC7966 [27], AL09-71 [28], and AL06-06 [29]; two Aeromonas salmonicida strains, CBA100 [accession no. PRJNA257751] and A. salmonicida subsp. piscicida [30]; together with A. rivalii DSM 22539 [accession no. PRJEB7035], A. enteropelogenes CECT4487 [accession no. PRJEB7028], A. dhakensis CECT7289 [accession no. PRJEB7020], A. diversa CECT4254 [accession no. PRJEB7026], and A. media WS [31]) was performed. The results showed that the closest related strain to EERV15 is Aeromonas veronii strain B565, with an 83% average similarity of ORFs. The two strains share 3,371 ORFs with >80% similarity, and 390 ORFs observed in the genome of the strain EERV15 were absent from the genome of strain B565.

Strain EERV15 harbors two copies of the high-persistence gene hipA and one copy of the hipB gene (32, 33), similar to those found in A. media WS, whereas in four A. hydrophila strains (pc 104A, ML09-119, NJ-35, and AL09-71), only hipA was detected. The hipA gene was found to be an important persistence factor in Escherichia coli inducing dormancy, while the hipB gene neutralizes the effect of the hipA gene. The hipA gene cannot be expressed in the absence of hipB because of its deleterious effects on cell growth (34, 35). Thus, strain EERV15 potentially possesses the ability to be persistent against antibiotics inducing dormancy.

Accession number(s). This draft genome sequencing project has been deposited at EMBL-EBI European Nucleotide Archive (ENA) under the accession numbers FKKY02000001 to FKKY02000207.

ACKNOWLEDGMENTS

This work was founded by a research grant from the Geconcerteerde Onderzoeksacties (GOA) of Ghent University (BOF15/GOA/006) and the
We thank Cristina Pintucci for her critical comments.

REFERENCES


