Draft Genome Sequence of *Aeromonas* sp. Strain EERV15

Elham Ehsani,ᵃ Israel Barrantes,ᵇ Johanna Vandermaesen,ᶜ Robert Geffers,ᵈ Michael Jarek,ᵈ Nico Boon,ᵃ Dirk Springael,ᶜ Dietmar H. Pieper,ᵇ Ramiro Vilchez-Vargasᵃ*

Center for Microbial Ecology and Technology (CMET), University of Ghent, Ghent, Belgiumᵃ; Microbial Interactions and Processes Research Group, Helmholtz Centre for Infection Research, Braunschweig, Germanyᵇ; Department of Earth and Environmental Sciences, KU Leuven, Belgiumᶜ; Genome Analytics, Helmholtz Centre for Infection Research, Braunschweig, Germanyᵈ

* Present address: Ramiro Vilchez-Vargas, Department of Gastroenterology, Hepatology and Infectious Diseases, Otto-von-Guericke-University, Magdeburg, Germany.

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.

Address correspondence to Ramiro Vilchez-Vargas, ramiro.vilchez@med.ovgu.de.

*A*eromonas 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; N_{50}, 173 kbp) 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], L1B53 [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. *pectinolytica* 34mel [30]; together with *A. rivuli* 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

REFERENCES

1. **Igbinosa IH, Igumbor EU, Aghdasi F, Tom M, Okoh AI**. 2012. Emerging *Aeromonas* species infections and their significance in public health. ScientificWorldJournal **2012**:625023.

2. **Palumbo SA, Maxino F, Williams AC, Buchanan RL, Thayer DW**. 1985. Starch-ampicillin agar for the quantitative detection of *Aeromonas hydrophila*. Appl Environ Microbiol **50**:1027–1030.

3. **Ceylan E, Berktas M, Ağaoğlu Z**. 2009. The occurrence and antibiotic resistance of motile *Aeromonas* in livestock. Trop Anim Health Prod **41**:199–204. http://dx.doi.org/10.1007/s11250-008-9175-9.

4. **Neyts K, Huys G, Uyttendaele M, Swings J, Debevere J**. 2000. Incidence and identification of mesophilic *Aeromonas* spp. from retail foods. Lett Appl Microbiol **31**:359–363. http://dx.doi.org/10.1046/j.1472-765x.2000.00828.x.

5. **Janda JM, Abbott SL**. 2010. The genus *Aeromonas*: taxonomy, pathogenicity, and infection. Clin Microbiol Rev **23**:35–73. http://dx.doi.org/10.1128/CMR.00039-09.

6. **Edberg SC, Browne FA, Allen MJ**. 2007. Issues for microbial regulation: *Aeromonas* as a model. Crit Rev Microbiol **33**:89–100. http://dx.doi.org/10.1080/10408410601172180.

7. **Holmberg SD, Farmer JJ III**. 1984. *Aeromonas hydrophila* and *Plesiomonas shigelloides* as causes of intestinal infections. Rev Infect Dis **6**:633–639. http://dx.doi.org/10.1093/clinids/6.5.633.

8. **Mulholland A, Yong-Gee S**. 2008. A possible new cause of spa bath folliculitis: *Aeromonas hydrophila*. Australas J Dermatol **49**:39–41. http://dx.doi.org/10.1111/j.1440-0960.2007.00418.x.

9. **Lee CC, Chi CH, Lee NY, Lee HC, Chen CL, Chen PL, Chang CM, Wu CJ, Ko NY, Tsai MC, Ko WC**. 2008. Necrotizing fasciitis in patients with liver cirrhosis: predominance of monomicrobial Gram-negative bacillary infections. Diagn Microbiol Infect Dis **62**:219–225. http://dx.doi.org/10.1016/j.diagmicrobio.2008.05.016.

10. **Conn HO**. 1964. Spontaneous peritonitis and bacteremia in Laennec's cirrhosis caused by enteric organisms. A relatively common but rarely recognized syndrome. Ann Intern Med **60**:568–580. http://dx.doi.org/10.7326/0003-4819-60-4-568.

11. **Janda JM, Guthertz LS, Kokka RP, Shimada T**. 1994. *Aeromonas* species in septicemia: laboratory characteristics and clinical observations. Clin Infect Dis **19**:77–83. http://dx.doi.org/10.1093/clinids/19.1.77.

12. **Khan MI, Walters G, Metcalfe T**. 2007. Bilateral endogenous endophthalmitis caused by *Aeromonas hydrophila*. Eye (Lond) **21**:1244–1245.

13. **Pinna A, Sechi LA, Zanetti S, Usai D, Carta F**. 2004. *Aeromonas caviae* keratitis associated with contact lens wear. Ophthalmology **111**:348–351. http://dx.doi.org/10.1016/j.ophtha.2003.05.012.

14. **Chuang HC, Ho YH, Lay CJ, Wang LS, Tsai YS, Tsai CC**. 2011. Different clinical characteristics among *Aeromonas hydrophila*, *Aeromonas veronii* biovar sobria and *Aeromonas caviae* monomicrobial bacteremia. J Korean Med Sci **26**:1415–1420. http://dx.doi.org/10.3346/jkms.2011.26.11.1415.

15. **Hernandez D, François P, Farinelli L, Osterås M, Schrenzel J**. 2008. *De novo* bacterial genome sequencing: millions of very short reads assembled on a desktop computer. Genome Res **18**:802–809. http://dx.doi.org/10.1101/gr.072033.107.

16. **Hernandez D, Tewhey R, Veyrieras JB, Farinelli L, Østerås M, François P, Schrenzel J**. 2014. *De novo* finished 2.8 Mbp *Staphylococcus aureus* genome assembly from 100 bp short and long range paired-end reads. Bioinformatics **30**:40–49. http://dx.doi.org/10.1093/bioinformatics/btt590.

17. **Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O**. 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics **9**:75. http://dx.doi.org/10.1186/1471-2164-9-75.

18. **Chua P, Har ZM, Austin CM, Yule CM, Dykes GA, Lee SM**. 2015. Genome sequencing and annotation of *Aeromonas* sp. HZM. Genom Data **5**:38–39. http://dx.doi.org/10.1016/j.gdata.2015.05.008.

19. **Chan XY, Chua KH, Puthucheary SD, Yin WF, Chan KG**. 2012. Draft genome sequence of an *Aeromonas* sp. strain 159 clinical isolate that shows quorum-sensing activity. J Bacteriol **194**:6350. http://dx.doi.org/10.1128/JB.01642-12.

20. **Raychaudhuri S, Saha A, Ghoshal T, Thakur AR**. 2013. Draft genome sequence of ammonia-producing *Aeromonas* sp. MDS8 strain MCC2167 from sludge of a dairy effluent treatment plant. Genome Announc **1**(5):e00710-13. http://dx.doi.org/10.1128/genomeA.00710-13.

21. **Bomar L, Stephens WZ, Nelson MC, Velle K, Guillemin K, Graf J**. 2013. Draft genome sequence of *Aeromonas veronii* Hm21, a symbiotic isolate from the medicinal leech digestive tract. Genome Announc **1**(5):e00800-13. http://dx.doi.org/10.1128/genomeA.00800-13.

22. **Li Y, Liu Y, Zhou Z, Huang H, Ren Y, Zhang Y, Li G, Zhou Z, Wang L**. 2011. Complete genome sequence of *Aeromonas veronii* strain B565. J Bacteriol **193**:3389–3390. http://dx.doi.org/10.1128/JB.00347-11.

23. **Pridgeon JW, Zhang D, Zhang L**. 2014. Complete genome sequence of a moderately virulent *Aeromonas hydrophila* strain, pc104A, isolated from soil of a catfish pond in West Alabama. Genome Announc **2**(3):e00554-14. http://dx.doi.org/10.1128/genomeA.00554-14.

24. **Jagoda SS, Tan E, Arulkanthan A, Kinoshita S, Watabe S, Asakawa S**. 2014. Draft genome sequence of *Aeromonas hydrophila* strain Ae34, isolated from a septicemic and moribund koi carp (*Cyprinus carpio koi*), a freshwater aquarium fish. Genome Announc **2**(3):e00572-14. http://dx.doi.org/10.1128/genomeA.00572-14.

25. **Tekedar HC, Waldbieser GC, Karsi A, Liles MR, Griffin MJ, Vamenta S, Sonstegard T, Hossain M, Schroeder SG, Khoo L, Lawrence ML**. 2013. Complete genome sequence of a channel catfish epidemic isolate, *Aeromonas hydrophila* strain ML09-119. Genome Announc **1**(5):e00755-13. http://dx.doi.org/10.1128/genomeA.00755-13.

26. **Gao X, Jian J, Li WJ, Yang YC, Shen XW, Sun ZR, Wu Q, Chen GQ**. 2013. Genomic study of polyhydroxyalkanoates producing *Aeromonas hydrophila* 4AK4. Appl Microbiol Biotechnol **97**:9099–9109. http://dx.doi.org/10.1007/s00253-013-5189-y.

27. **Seshadri R, Joseph SW, Chopra AK, Sha J, Shaw J, Graf J, Haft D, Wu M, Ren Q, Rosovitz MJ, Madupu R, Tallon L, Kim M, Jin S, Vuong H, Stine OC, Ali A, Horneman AJ, Heidelberg JF**. 2006. Genome sequence of *Aeromonas hydrophila* ATCC 7966ᵀ: jack of all trades. J Bacteriol **188**:8272–8282. http://dx.doi.org/10.1128/JB.00621-06.

28. **Pridgeon JW, Zhang D, Zhang L**. 2014. Complete genome sequence of the highly virulent *Aeromonas hydrophila* AL09-71 isolated from diseased channel catfish in West Alabama. Genome Announc **2**(3):e00450-14. http://dx.doi.org/10.1128/genomeA.00450-14.

29. **Tekedar HC, Karsi A, Akgul A, Kalindamar S, Waldbieser GC, Sonstegard T, Schroeder SG, Lawrence ML**. 2015. Complete genome sequence of fish pathogen *Aeromonas hydrophila* AL06-06. Genome Announc **3**(2):e00368-15. http://dx.doi.org/10.1128/genomeA.00368-15.

30. **Pavan ME, Pavan EE, López NI, Levin L, Pettinari MJ**. 2013. Genome sequence of the melanin-producing extremophile *Aeromonas salmonicida* subsp. *pectinolytica* strain 34melᵀ. Genome Announc **1**(5):e00675-13. http://dx.doi.org/10.1128/genomeA.00675-13.

31. **Chai B, Wang H, Chen X**. 2012. Draft genome sequence of high-melanin-yielding *Aeromonas media* strain WS. J Bacteriol **194**:6693–6694. http://dx.doi.org/10.1128/JB.01807-12.

32. **Balaban NQ, Merrin J, Chait R, Kowalik L, Leibler S**. 2004. Bacterial persistence as a phenotypic switch. Science **305**:1622–1625. http://dx.doi.org/10.1126/science.1099390.

33. **Schumacher MA, Piro KM, Xu W, Hansen S, Lewis K, Brennan RG**. 2009. Molecular mechanisms of HipA-mediated multidrug tolerance and its neutralization by HipB. Science **323**:396–401. http://dx.doi.org/10.1126/science.1163806.

34. **Buts L, Lah J, Dao-Thi MH, Wyns L, Loris R**. 2005. Toxin-antitoxin modules as bacterial metabolic stress managers. Trends Biochem Sci **30**:672–679. http://dx.doi.org/10.1016/j.tibs.2005.10.004.

35. **Gerdes K, Christensen SK, Løbner-Olesen A**. 2005. Prokaryotic toxin-antitoxin stress response loci. Nat Rev Microbiol **3**:371–382. http://dx.doi.org/10.1038/nrmicro1147.