Data in Brief

Genome sequencing and annotation of *Aeromonas veronii* strain Ae52, a multidrug-resistant isolate from septicaemic gold fish (*Carassius auratus*) in Sri Lanka

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**A B S T R A C T**

Here we report the draft genome sequence and annotation of *A. veronii* strain Ae52 isolated from the kidney of a moribund, septicaemic gold fish (*Carassius auratus*) in Sri Lanka. This clinical isolate showed resistance to multiple antimicrobials; amoxicillin, neomycin, trimethoprim-sulphonamide, chloramphenicol, tetracycline, enrofloxacin, erythromycin and nitrofurantoin. The size of the draft genome is 4.56 Mbp with 58.66% of G + C content consisting 4328 coding sequences. It harbors a repertoire of putative antibiotic resistant determinants that explains the genetic basis of its resistance to various classes of antibiotics. The genome sequence has been deposited in DDBJ/EMBL/GenBank under the accession numbers BDGY01000001-BDGY0100080.

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1. Direct link to deposited data.

[http://www.ncbi.nlm.nih.gov/bioproject/PRJDB5119](http://www.ncbi.nlm.nih.gov/bioproject/PRJDB5119)

2. Experimental design, materials and methods

*Aeromonas veronii* is a Gram-negative, facultative anaerobic, rod shaped bacterium ubiquitous in aquatic environments [1,2]. It has been isolated from a wide range of vertebrate and invertebrate hosts, with both beneficial and pathogenic outcomes [2,3-4]. *A. veronii* has emerged as an important opportunistic pathogen in humans and has been implicated in a number of intestinal and extra-intestinal infections in both immunocompromised and immunocompetent individuals [5-6]. It has an established role as a fish pathogen and has been associated with motile *Aeromonas* septicaemia and ulcer syndrome in cultured fresh water food fish [7-8] and tropical ornamental fish [9-10], leading to severe economic losses. In recent years, *A. veronii* has gained an increased scientific attention due to its virulence potential in a wide range of hosts both as primary and opportunistic pathogen and its ability to develop multidrug resistant (MDR) phenotypes.

In this study, we present the draft genome of *A. veronii* Ae52 isolated from the kidney of a moribund goldfish showing signs of septicaemia collected from an ornamental fish breeding farm in Nittambuwa in the Gampaha district of Sri Lanka in 2008. This isolate was found to be resistant to several antimicrobials that are commonly used in ornamental fish culture including beta-lactams, aminoglycosides, sulphonamides, etc.

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chloramphenicol, tetracyclines, fluoroquinolones, macrolides and nitrofurans. Genomic DNA was extracted from an overnight culture of *A. veronii* Ae52 on Tryptic Soy Agar (Difco) using the DNeasy Blood and Tissue kit (Qiagen). Sequence analysis of 16S rDNA, gyrB and rpoD genes was performed for confirmatory identification of the isolate prior to genome sequencing [10]. A genomic DNA library was constructed and sequenced on the Ion Torrent PGM (Life Technologies) platform using the Ion 318 chip and 400-bp chemistry as per the manufacturer’s instructions. A total 314,439,134 bp of data corresponding to 1,212,544 reads (average length of 259 bp) was generated and assembled into contigs using SPAdes genome assembler version 3.9.0 [11]. Using the complete genome of *A. veronii* B565 (accession no. CP002607) [12] as a reference genome, the assembly was further improved using the CLC Micrornal Genome Finishing Module add-on to the CLC Genomics Workbench ver. 8 (CLC Bio, Denmark). The final assembly consisted of 80 contigs longer than 500 bp (N₅₀ = 158,959 bp; maximum length, 377,503 bp). The assembly quality was assessed using QUAST version 3.0 [13]. The total size of the draft genome (4,564,863 nucleotides [nt]) and the G + C content (58.7%) are both in good agreement with the respective figures for the published *A. veronii* genomes (4.5 to 4.9 Mb and 58.25 to 58.72%, respectively) [8,12].

Draft genome was annotated using Rapid Annotations using Subsystems Technology (RAST) [14] server. RAST identified 4328 protein-coding sequences of which 58% was annotated belonging to 522 subsystems and the rest of 42% was not present in RAST subsystems (Fig. 1). RAST also identified a total of 75 RNA regions. 66 tRNAs were predicted by ARAGORN v1.2.37 [15]. *A. veronii* Ae52 contains genes encoding for type I, II, IV and type VIII protein secretion systems, biofilm formation, type IV pili, aerolysin, cytotoxicy enterotoxin (act) and integrase I. PHAST [16] detected four incomplete prophages carrying integrases, transposases and proteases. Antibiotic resistance genes annotation using the Resistance Gene Identifier software of the comprehensive antibiotic resistance database (CARD) [17] and ResFinder-2.1 server [18] identified an array of resistance genes (Table 1) that explains the genetic background of the multidrug resistance of this isolate.

Further analysis of this genome and other sequenced *A. veronii* genomes will shed light on the physiology, virulence and antimicrobial resistant mechanisms of this emerging pathogen of fish and humans.

### 3. Nucleotide sequence accession number

The draft genome sequences have been deposited in DDBJ/EMBL/GenBank under the accession numbers BDGY01000001–BDGY01000080.

### Conflict of interest

The authors declare that there is no conflict of interests on the work published in this paper.

| Antimicrobial class   | Resistance gene | Predicted phenotype   | Accession number | % identity |
|-----------------------|-----------------|-----------------------|------------------|------------|
| Aminoglycoside        | strB            | Aminoglycoside resistance | M96392          | 100        |
|                       | aph(3’)A          | Aminoglycoside resistance | V00359          | 100        |
|                       | aadA2           | Aminoglycoside resistance | JQ364967       | 100        |
| Macrolide, lincosamide and streptogramin B | strA | Aminoglycoside resistance | M96392          | 100        |
| Sulphonamide          | mph(A)          | Macrolide resistance | D16251          | 100        |
| Tetracycline          | tet(A)          | Tetracycline resistance | AJ517790       | 100        |
|                       | tet(e)          | Tetracycline resistance | CP000645       | 100        |
| Trimethoprim          | dfrA12          | Trimethoprim resistance | AB571791       | 100        |
| Beta-lactam           | blodOXA-12      | Beta-lactam resistance | U100251        | 96         |
|                       | blodEPF-A3      | Beta-lactam resistance | AY112998       | 95.82      |
| Phenicol              | catA2           | Phenicol resistance | +53796         | 89.56      |
|                       | catB1           | Phenicol resistance | M58472         | 84.73      |
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References

[1] F.W. Hickman-Brenner, K.L. MacDonald, A.G. Steigerwalt, G.R. Fanning, D.J. Brenner, J.J. Farmer. Aeromonas veronii, a new ornithine decarboxylase-positive species that may cause diarrhea. J. Clin. Microbiol. 25 (5) (1987) 900–906.

[2] J.M. Janda, S.L. Abbott, The genus Aeromonas: taxonomy, pathogenicity, and infection. Clin. Microbiol. Rev. 23 (2010) 35–73.

[3] A.C. Silver, D. Williams, J. Faucher, A.J. Horneman, J.P. Gogarten, J. Graf. Complex evolutionary history of the Aeromonas veronii group revealed by host interaction and DNA sequence data. PLoS One 6 (2) (2011), e16751, http://dx.doi.org/10.1371/journal.pone.0016751.

[4] M. Rahman, P. Colque-Navarro, I. Kuhn, G. Huys, J. Swings, R. Mollby, Identification and characterization of pathogenic Aeromonas veronii biovar sobria associated with epizootic ulcerative syndrome in Misgurnus anguillicaudatus. J. Fish Dis. 39 (2016) 777–81, http://dx.doi.org/10.1111/jfd.12413.

[5] Y. Kang, X. Pan, Y. Xu, S.A. Siddiqui, C. Wang, X. Shan, A. Qian, Complete genome sequence of the fish pathogen Aeromonas veronii TH0426 with potential application in biosynthesis of pullulanase and chitinase. J. Biotechnol. 227 (2016) 81–82, http://dx.doi.org/10.1016/j.jbiotec.2016.04.005.

[6] S. Krishnan, R. Philip, I.S. Singh, Characterization and virulence potential of phenotypically diverse Aeromonas veronii isolates recovered from moribund freshwater ornamental fishes of Kerala, India. A. Van. Leeuw. J. Microb. 103 (2013) 53–67, http://dx.doi.org/10.1007/s10482-012-9786-z.

[7] S.S. Jagoda, T.G. Wijewardana, A. Arulkanthan, Y. Igarashi, E. Tan, S. Kinoshita, S. Watabe, S. Asakawa, Characterization and antimicrobial susceptibility of motile aeromonads isolated from freshwater ornamental fish showing septicaemia. Dis. Aquat. Organ. 109 (2014) 127–137, http://dx.doi.org/10.1035/jad0273.

[8] A. Bankevich, S. Nurk, D. Antipov, A.A. Gurevich, M. Dvorkin, A.S. Kulikov, V.M. Lesin, S.I. Nikolenko, S. Pham, A.D. Prijibelski, A.V. Pyshkin, A.V. Sirotkin, N. Vyahhi, G. Tesler, M.A. Alekseyev, P.A. Pevzner, SPAdes: a new genome assembly algorithm and its application to single-cell sequencing. J. Comput. Biol. 19 (2012) 455–477, http://dx.doi.org/10.1089/cmb.2012.0021.

[9] Y. Li, Y. Liu, Z. Zhou, H. Huang, Y. Ren, Y. Zhang, G. Li, Z. Zhou, L. Wang, Complete genome sequence of Aeromonas veronii strain B565. J. Bacteriol. 193 (2011) 3389–3390.

[10] A. Gurevich, V. Saveliev, N. Vyahhi, G. Tesler, QUAST: Quality assessment tool for genome assemblies. Bioinformatics 29 (8) (2013) 1072–1075, http://dx.doi.org/10.1093/bioinformatics/btt886.

[11] A.G. McArthur, N. Waglechner, F. Nizam, A. Yan, M.A. Azad, A.J. Baylay, K. Bhullar, M.J. Canova, P.G. De, L. Ejim, L. Kalan, A.M. King, K. Koreva, M. Morar, M.R. Mulvey, J.S. O’Brien, A.C. Pawlowski, L.J. Piddock, P. Spanogiannopoulos, A.D. Sutherland, I. Stevens, O. Vassieva, V. Vonstein, A. Wilke, O. Zagnitko, The RAST server: rapid annotations using subsystems technology. BMC Genomics 9 (2008) 75, http://dx.doi.org/10.1186/1471-2164-9-75.

[12] D. Laslett, B. Canback, ARAGORN, a program for the detection of transfer RNA and transfer-messenger RNA genes in nucleotide sequences. Nucleic Acids Res. 32 (2004) 11–16.

[13] Y. Zhou, Y. Liang, K.H. Lynch, J.J. Dennis, D.S. Wishart, PHAST: a fast phage search tool. Nucleic Acids Res. 39 (2011) [Web Server issue]. (W347–W52).

[14] A.G. McArthur, N. Waglechner, F. Nizam, A. Yan, M.A. Azad, A.J. Baylay, K. Bhullar, M.J. Canova, P.G. De, L. Ejim, L. Kalan, A.M. King, K. Koreva, M. Morar, M.R. Mulvey, J.S. O’Brien, A.C. Pawlowski, L.J. Piddock, P. Spanogiannopoulos, A.D. Sutherland, I. Tang, P.L. Taylor, M. Thaler, W. Wang, M. Yan, Y. Yu, G.D. Wright, The comprehensive antibiotic resistance database. Antimicrob. Agents Chemother. 57 (2013) 3348–3357, http://dx.doi.org/10.1128/AAC.00419-13.

[15] E. Zankari, H. Hasman, S. Cosentino, M. Vestergaard, S. Rasmussen, O. Lund, F.M. Aarestrup, M.V. Larsen, Identification of acquired antimicrobial resistance genes. J. Antimicrob. Chemother. 67 (2012) 2640–2644, http://dx.doi.org/10.1093/jac/dss261.