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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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ABSTRACT

Here we report the draft genome sequence and annotation of *A. veronii* strain Ae52 isolated from the kidney of a morbund, 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-BDGY01000080.

Specifications	
Organism/cell line/tissue	*Aeromonas veronii*
Strain	Ae52
Sex	N/A
Sequencer or array type	Ion PGM
Data format	Analyzed
Experimental factors	Genomic DNA extracted from pure bacterial culture isolated from the kidney of a septicaemic gold fish
Experimental features	Draft genome sequence of *A. veronii* Ae52, assembly and annotation
Consent	N/A
Sample source location	Nittambuwa, Gampaha District, Sri Lanka (7°09′0″N 80°06′00″E)

1. Direct link to deposited data.

http://www.ncbi.nlm.nih.gov/bioproject/PRJDB5119

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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,

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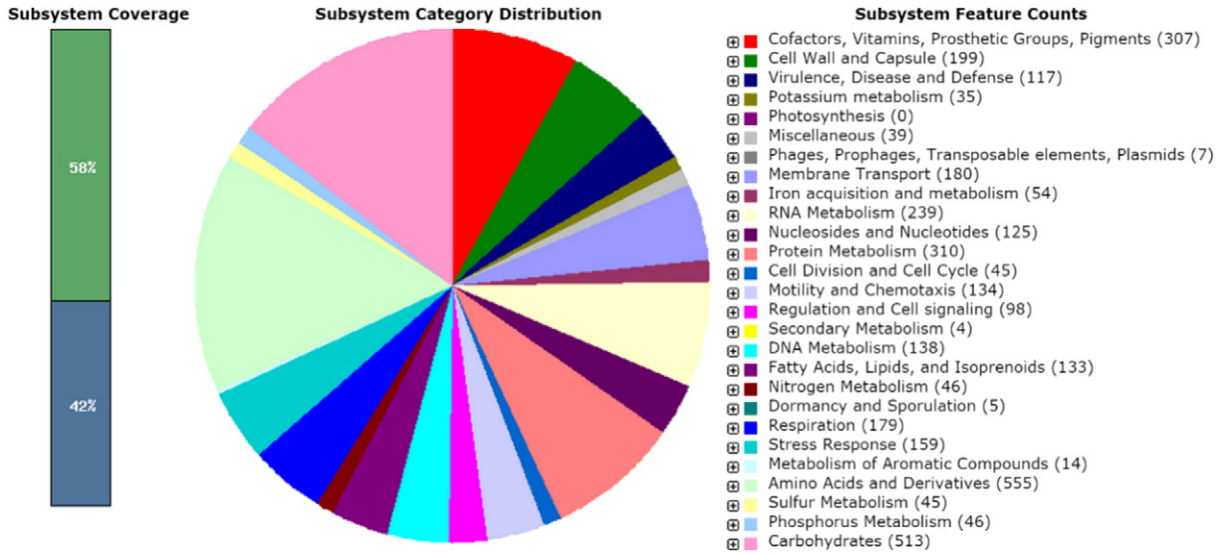

Fig. 1. Subsystem distribution of *A. veronii* Ae52 (based on RAST annotation server).

chloramphenicols, tetracyclines, fluoroquinolones, macrolides and nitrofurans. Genomic DNA was extracted from an overnight culture of *A. veronii* Ae52 on Tryptic Soy Agr (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 Microbial 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 (N_{50} = 158.595 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, cytotoxic 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.

Table 1
Antibiotic resistance profile of *A. veronii* Ae52.

Antimicrobial class	Resistance gene	Predicted phenotype	Accession number	% identity
Aminoglycoside	*strB*	Aminoglycoside resistance	M96392	100
	aph(3′)-Ia	Aminoglycoside resistance	V00359	100
	aadA2	Aminoglycoside resistance	JQ364967	100
	strA	Aminoglycoside resistance	M96392	100
Macrolide, lincosamide and streptogramin B	*mph(A)*	Macrolide resistance	D16251	100
Sulphonamide	*sul1*	Sulphonamide resistance	CP002151	100
Tetracycline	*tet(A)*	Tetracycline resistance	AJ517790	100
	tet(E)	Tetracycline resistance	CP000645	100
Trimethoprim	*dfrA12*	Trimethoprim resistance	AB571791	100
Beta-lactam	*blaOXA-12*	Beta-lactam resistance	U10251	96
	blaCEPH-A3	Beta-lactam resistance	AY112998	95.82
Phenicol	*catA2*	Phenicol resistance	×53796	89.56
	catB1	Phenicol resistance	M58472	84.73

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