Draft Genome Sequences of *Citrobacter freundii* Strains CF04 and A41 Isolated from Moribund, Septicemic Giant Gourami (*Osphronemus goramy*) in Sri Lanka

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*Citrobacter freundii* is a Gram-negative opportunistic pathogen associated with many infectious conditions including septicaemia in humans and animals. Here, we announce the draft genome sequences of two multidrug-resistant *C. freundii* strains (CF04 and A41) isolated from septicemic giant gourami (*Osphronemus goramy*) collected from aquaria in Sri Lanka.

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C. *freundii* is an infrequent but established cause of systemic infections in farmed food fish and aquarium fish (1, 2). During an investigation to identify septicaemia causing bacterial pathogens of fresh water ornamental fish in Sri Lanka, the occurrence of *Citrobacter* spp. was only second to *Aeromonas* spp. (3). *C. freundii* has received increasing attention as an opportunistic pathogen that causes diarrhea, urinary tract infections, and septicaemia in humans (4). However, to our knowledge the information on genome sequences of *C. freundii* isolated from diseased fish was not available. Further, *C. freundii* has shown a strong ability to developing resistance to antibiotics used in human therapy and aquaculture (5, 6). It is therefore imperative to advance our understanding of pathogenic, multidrug-resistant *C. freundii* strains associated with fish in order to identify antimicrobial resistance and virulence determinants.

Two *C. freundii* strains, CF04 and A41, were isolated from the kidneys of two moribund giant gourami (*Osphronemus goramy*) fish showing signs of generalized septicaemia collected from aquaria in Kandy, Sri Lanka.

Genomic DNA was extracted with the DNeasy Blood and Tissue kit (Qiagen). Genomic DNA libraries were constructed using the Ion Xpress Plus fragment library kit and sequenced on an Ion Torrent PGM (Life Technologies) platform using the ion 318 chip and the 400-bp kit following standard protocols. A total of 1,328,195 reads equivalent to 340,760,015 bp of data and the 400-bp kit following standard protocols. A total of 5,301,254 bp and 51.5% G+C content. The total size of the draft genomes and G+C contents are in agreement with published *C. freundii* genomes (4.9 to 5.0 Mb and 51.6% G+C) (9–11).

Functional annotation using RAST (12) revealed 5,777 and 5,253 coding sequences (CDS) in the draft genomes of CF04 and A41, respectively. The presence of genes involved with virulence, disease and defense, quorum sensing, and biofilm formation as well as genes encoding resistance to different antibiotics confirms the clinical significance of these isolates. Moreover, RAST indicated that both organisms carry genes encoding resistance to antibiotics that include fluoroquinolone, macrolides, beta-lactams, rifampin, chloramphenicol, tetracycline, aminocoumarin, aminoglycoside, polymyxin, and vancomycin. PHAST, a phage search tool (13), predicted six intact phages in CF04 and seven intact phages in A41.

Accession number(s). The draft genome sequences of *C. freundii* A41 and CF04 have been deposited in DDBJ/EMBL/GenBank under the accession numbers BDFK01000001 to BDFK01000153 and BDFL01000001 to BDFL01000058, respectively.

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