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GENOME ANNOUNCEMENT

Draft Genome Sequence of an *Aeromonas* sp. Strain 159 Clinical Isolate That Shows Quorum-Sensing Activity

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***Aeromonas* is a pathogenic organism that is often found to infect humans. Here we report the draft genome of a clinical isolate in Malaysia, *Aeromonas* sp. strain 159, which shows *N*-acylhomoserine lactone production. In the draft genome of strain 159, *luxI* and *luxR* homologue genes were found to be located at contig 47, and these genes are believed to be important for the quorum-sensing system present in this pathogen.**

Aeromonas has long been known to be associated with human disease, especially diarrhea (1, 6). Strains of *Aeromonas* spp. can be isolated from various specimens from a patient's body, including blood, pus, and peritoneal fluid (2). It has been reported previously that *Aeromonas* spp. rely on quorum sensing to regulate the expression of virulence factors (9). *Aeromonas* spp. pose a threat to public health due to the emergence of antibiotic-resistant strains (4). In this study, the clinical *Aeromonas* sp. strain 159 was isolated from the stool sample of a patient admitted to the University of Malaya Medical Center, Kuala Lumpur. We had reported earlier that this strain produced *N*-acylhomoserine lactone (AHL) molecules (2). Therefore, in order to further understand the genetic makeup of the quorum-sensing system, whole-genome sequencing was performed.

Total genomic DNA of *Aeromonas* sp. strain 159 was extracted with the QIAamp DNA minikit (Qiagen, Germany). Purified DNA was subjected to whole-genome shotgun sequencing on an Illumina HiSeq 2000 (Illumina, Inc., CA) platform, generating 4,526,466 paired-end reads. After trimming, 2,627,667 quality reads were *de novo* assembled with CLC Genomic Workbench 5.1 (CLC Bio, Denmark). A total of 126 contigs with a length of at least 500 bp and an N_{50} of approximately 39 kb were generated.

The draft genome of this *Aeromonas* isolate contained 4,470,895 bases, with an average coverage of 37-fold and G+C content of 59.3%. Gene prediction was performed with the prokaryote gene prediction algorithm, Prodigal (version 2.60) (5), while tRNA and rRNA were predicted with tRNAscan SE (v.1.21) (8) and RNAmmer (7). Subsequently, it was annotated with Blast2Go (3) and searched against the NCBI-NR and Uniprot databases. On this draft genome, 3,171 open reading frames (ORFs), 46 tRNAs, and a copy each of 5S rRNA, 16S rRNA, and 23S rRNA were identified.

The complete ORFs of *Aeromonas* strain 159 *luxI* and *luxR* homologues were predicted to be located at contig 47. These two genes are 60 bp apart, with the *luxR* gene located upstream of the contig. The whole-genome sequence allows an in-depth understanding of the genetics of *Aeromonas*, and its link to the quorum-sensing-mediated pathogenicity and virulence determinants of this clinical pathogen that is emerging in Malaysia.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. ALOT00000000. The version described in this paper is the first version, ALOT01000000.

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