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Genome Sequence of *Vibrio rotiferianus* Strain DAT722[▽]

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Vibrio rotiferianus **is a marine pathogen capable of causing disease in various aquatic organisms. We announce the genome sequence of *V. rotiferianus* DAT722, which has a large chromosomal integron containing 116 gene cassettes and is a model organism for studying the role of this system in vibrio evolution.**

Vibrio rotiferianus was assigned a species designation in 2003 on the basis of <70% DNA hybridization similarity value to its most closely related species, *V. campbellii* and *V. harveyi*, although they share 99% identity in 16S rRNA gene sequences (6). The microorganism was named after its isolation source, rotifer cultures, which serve as important nutrients for fish and crustaceans in aquaculture industries (6). *V. rotiferianus* DAT722, a mild pathogen of mud crab larvae (2), was isolated from a mud crab larva aquaculture tank in the Northern Territory of Australia (3).

The genome of DAT722 was sequenced using Roche 454 GS FLX Titanium technology at The Ramaciotti Centre for Gene Function Analysis, University of New South Wales in Sydney, Australia. Raw sequence reads (628,892) were assembled using the Newbler software program (release 2.3) into 79 long (>500 nt) contigs with an average of 40× coverage. This consisted of 53 contigs >10 kb and including 18 contigs of over 100 kb. Based on this assembly, the genome of DAT722 is approximately 5.3 Mb, with an average G+C content of 44.75%. The contigs were tiled against the genome of *V. harveyi* ATCC BAA-1116 (project identifier 19857) using the Mauve software program (version 2.3.1) (4, 8) to predict their chromosomal organization. From this, scaffolds assigned accession numbers AFAJ01000001.1 to AFAJ01000047.1 are predicted to lie on chromosome 1, and AFAJ01000048.1 to AFAJ01000065.1 are predicted to lie on chromosome 2. However, 14 contigs (accession no. AFAJ01000066.1 to AFAJ01000079.1) that displayed little or no similarity to the BAA-1116 genome could not be allocated a putative chromosomal location, probably because the majority of genes contained within these untiled scaffolds encode hypothetical proteins as suggested by outputs from the RAST annotation server (1). The chromosomal integron described previously (3) is located on chromosome 1 (contig AFAJ01000036.1) and is a major differentiating factor between DAT722 and the *V. harveyi* genome, which does not have an integron but possesses a plasmid (pVIBHAR) that is absent in DAT722.

In contrast to the *V. harveyi* ATCC BAA-1116 genome, the DAT722 genome has a number of genes capable of elevating its pathogenic capacity (2). Of these, the accessory cholera toxin genes *ace* and *zot* are most significant. Both these genes are present on the contig assigned accession number AFAJ01000031.1 in chromosome 1. The *ace* gene product shows 65% identity and the *zot* product shows 71% identity, at the amino acid level, to the respective proteins in *Vibrio alginolyticus* 12G01 (ZP_01261017.1). In *Vibrio cholerae*, the *zot* gene product leads to increased permeability of the intestinal mucosa (5) whereas the *ace* product causes fluid accumulation (9). DAT722 also has an accessory colonization factor gene, *acfA*, on chromosome 2, the product of which has 77% identity to the *Vibrio parahaemolyticus* RIMD 2210633 (NP_800205) and 76% identity to the *V. parahaemolyticus* AQ3810 (ZP_01989146) *acfA* gene products. Interestingly, the *acfA* gene in *V. cholerae* is under the control of a transcriptional activator encoded by *toxR* (7), which is also present in the DAT722 genome. The role played by all these candidate pathogenic genes in *V. rotiferianus* DAT722 is as yet unknown.

Nucleotide sequence accession numbers. The whole-genome shotgun sequence of DAT722 has been deposited in GenBank under accession numbers AFAJ01000001 to AFAJ01000079.

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