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GENOME ANNOUNCEMENT

Genome Sequence and Comparative Genomics Analysis of a *Vibrio cholerae* O1 Strain Isolated from a Cholera Patient in Malaysia

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The genome sequence analysis of a clinical *Vibrio cholerae* VC35 strain from an outbreak case in Malaysia indicates multiple genes involved in host adaptation and a novel Na^+-driven multidrug efflux pump-coding gene in the genome of *Vibrio cholerae* with the highest similarity to VMA_001754 of *Vibrio mimicus* VMA223.

Cholera, caused by *Vibrio cholerae*, is endemic in many parts of the world, particularly in countries where the water supply and sanitation are inadequate (2). *V. cholerae* O1 biotype El Tor occurs intermittently and causes the majority of outbreaks in Malaysia (10). Inappropriate food handling and personal hygiene practices of food handlers are possible causes (6). *V. cholerae* VC35 was isolated from the stool sample from a cholera case in Kedah, Malaysia. The strain was identified as O1 El Tor and was characterized by pulsed-field gel electrophoresis (PFGE) (7), multiple-locus variable-number tandem repeat analysis (MLVA) (8), multilocus sequence typing (MLST) (9), multi-virulence locus sequence typing (MVLST) (9), and various PCR-based fingerprinting methods (11). The genome sequence of this strain will provide a better understanding of the endemicity of cholera in Malaysia.

Ilumina HiSeq2000 (100-bp paired-end read) was used to accomplish the genome sequencing of *V. cholerae* VC35. The generated reads were trimmed and assembled *de novo* using CLC Genomics Workbench 5.1 (CLC Bio, Denmark). Open reading frames (ORFs), tRNAs, and rRNAs were predicted using RAST (1), tRNAscan-SE (4), and RNAmmer (3), respectively. A total of 104 contigs were generated with an accumulated length of 3,914,529 bp (94-fold coverage) and an average GC content of 47.60%. The contig N_{50} is 201,472 bp in length, and the longest assembled contig is 296,219 bp. A total of 3,526 ORFs, 51 tRNAs, and 3 rRNAs were predicted from the draft genome.

The genome sequence analysis revealed the presence of genes involved in the synthesis of hemolysin, siderophore, and chemotaxis protein, which may explain the survival of strain VC35 in its host. The presence of the *cadA* gene coding for lysine decarboxylase at contig 007 is suggestive of strain VC35's tolerance of gastric juice during passage through the host stomach (5). Interestingly, strain VC35 contains a gene coding for a Na^+-driven multidrug efflux pump at contig 012 that, to the best of our knowledge, has not been reported in the genomes of *V. cholerae*. This gene displays 100% similarity to an ORF designated VMA_001754 from *Vibrio mimicus* VM223. Its presence in addition to the common Na^+-driven multidrug efflux pump-coding genes of *V. cholerae* origin in strain VC35 may further enhance the survival of strain VC35 in the host environment upon exposure to various chemicals. These features in the draft genome of *Vibrio cholerae* strain VC35 will provide additional insights into the host adaptation mechanisms and can potentially be utilized for biomarker design to assess the prevalence of the emerging *Vibrio cholerae* clone in Malaysia.

Nucleotide sequence accession number. This Whole Genome Shotgun project has been deposited in GenBank under accession no. AMBR00000000. The version described in this article is the first version, under Bioproject designation no. PRJNA173392.

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REFERENCES

1. **Aziz RK, et al.** 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics **9**:75. doi:10.1186/1471-2164-9-75.
2. **Igbinosa EO, Okoh AI.** 2008. Emerging *Vibrio* species: an unending threat to public health in developing countries. Res. Microbiol. **159**:495–506.
3. **Lagesen K, et al.** 2007. RNammer: consistent annotation of rRNA genes in genomic sequences. Nucleic Acids Res. **35**:3100–3108.
4. **Lowe TM, Eddy SR.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25**: 955–964.
5. **Merrell DS, Camilli A.** 1999. The *cadA* gene of *Vibrio cholerae* is induced during infection and plays a role in acid tolerance. Mol. Microbiol. **34**: 836–849.
6. **Ministry of Health Malaysia.** 2004. Ministry of Health annual report, p 87–88. Ministry of Health Malaysia, Putrajaya, Malaysia.
7. **Teh CSJ, et al.** 2012. Outbreak-associated *Vibrio cholerae* genotypes with identical pulsotypes, Malaysia, 2009. Emerg. Infect. Dis. **18**:1177–1179.
8. **Teh CSJ, Chua KH, Thong KL.** 2010. Multiple-locus variable-number tandem repeat analysis of *Vibrio cholerae* in comparison with pulsed field gel electrophoresis and virulotyping. J. Biomed. Biotechnol. **2010**:817190. doi:10.1155/2010/817190.
9. **Teh CSJ, Chua KH, Thong KL.** 2011. Genetic variation analysis of *Vibrio cholerae* using multilocus sequencing typing and multi-virulence locus sequencing typing. Infect. Genet. Evol. **11**:1121–1128.
10. **Vadivelu J, Iyer L, Kshatriya BM, Puthucheary SD.** 2000. Molecular evidence of clonality amongst *Vibrio cholerae* O1 biotype El Tor during an outbreak in Malaysia. Epidemiol. Infect. **124**:25–30.
11. **Vimala B, Thong KL, Chong VC.** 2010. Isolation, detection and genomic differentiation of *Vibrio cholerae* and *Vibrio parahaemolyticus* in Bachok, Kelantan. Malays. J. Sci. **29**:1–10.

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