**Draft Whole-Genome Sequences of 14 *Vibrio parahaemolyticus* Clinical Isolates with an Ambiguous K Serogroup**

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*Vibrio parahaemolyticus* is a bacterial pathogen responsible for mild to severe gastroenteritis, wound infections, and septicemia resulting from the ingestion or handling of raw or undercooked contaminated seafood. Here, we report the draft whole-genome sequences and annotations of 14 Canadian *V. parahaemolyticus* clinical isolates that were serologically identified as K group II using polyvalent antisera but were not specifically K serogrouped using monovalent antisera.

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*Vibrio parahaemolyticus* is a halophilic marine bacterium that is widely distributed in temperate estuaries and is one of several etiological agents of human vibriosis. Since 2000, there has been an increasing prevalence of *V. parahaemolyticus* infections in Canada (1). However, the true incidence of infection is likely underestimated, due to a lack of awareness of the disease and its self-limiting nature. For effective *V. parahaemolyticus* epidemiological surveillance, including source attribution, strain delineation is necessary. Serology, the classic method of *V. parahaemolyticus* surveillance, has been unreliable in tracking the spread of outbreak-associated clonal complexes (CC), since several serovariants can simultaneously be associated with illness (2). In particular, two serotypes (O4:K12 and O12:K12) of CC36 are responsible for outbreaks associated with the consumption of raw oysters harvested on the North American Pacific coast; the two serotypes are descended from a common sequence type 36 (ST36) ancestor (3). So far, the genomic sequence of only one strain belonging to the *V. parahaemolyticus* CC36 (serotype O4:K12) has been published (3).

Between 2000 and 2009, several *V. parahaemolyticus* clinical isolates originating from provincial public health laboratories along the Pacific coast were submitted to the National Microbiology Laboratory (Public Health Agency of Canada), British Columbia Centre for Disease Control (BCCDC), and the Bureau of Microbial Hazards (BMH) (Health Canada). Twenty-six of these isolates were identified as ST36 and O4, indicating inclusion in CC36, but only weakly agglutinated with the polyvalent antiserum K group II and failed to agglutinate with any of the seven associated monovalent antisera (K agglutinins 9, 10, 11, 12, 13, 15, and 17) (4). Each of these 26 isolates was positive for both the *tdh* and *tdi* genes.

**TABLE 1** Sequencing and annotation results of 14 *V. parahaemolyticus* KII clinical isolates

| Strain identification no. | Biosample | Accession no. | Genomic coverage (%) | Genome size (bp) | No. of nonoverlapping contigs | No. of ORFs b | No. of tRNAs | No. of rRNAs |
|---------------------------|-----------|---------------|----------------------|-----------------|-------------------------------|---------------|--------------|--------------|
| 04-1290                   | SAMN03287716 | JXVK000000000 | 111.05               | 5,143,304       | 97                            | 4,767         | 122          | 27           |
| 09-3216                   | SAMN03287714 | JXVI000000000 | 99.81                | 5,100,021       | 78                            | 4,715         | 125          | 37           |
| 10-4293                   | SAMN03287764 | JXYA000000000 | 50.09                | 5,202,165       | 58                            | 4,841         | 123          | 30           |
| 10-4303                   | SAMN03287766 | JXYU000000000 | 55.97                | 5,106,734       | 52                            | 4,708         | 117          | 29           |
| 10-7197                   | SAMN03287767 | JXUX000000000 | 30.68                | 5,091,435       | 56                            | 4,684         | 116          | 26           |
| 10-4298                   | SAMN03287765 | JXUZ000000000 | 44.87                | 5,233,510       | 76                            | 4,829         | 118          | 29           |
| 10-4288                   | SAMN03287763 | JXV0000000000  | 70.12                | 5,109,523       | 61                            | 4,717         | 128          | 28           |
| 10-4274                   | SAMN03287762 | JXVC000000000 | 73.38                | 5,115,101       | 96                            | 4,751         | 120          | 26           |
| 10-4241                   | SAMN03287715 | JXVI000000000 | 43.68                | 5,104,503       | 57                            | 4,719         | 128          | 28           |
| 10-4242                   | SAMN03287757 | JXH0000000000  | 54.82                | 5,126,748       | 74                            | 4,758         | 124          | 29           |
| 10-4245                   | SAMN03287758 | JXVG000000000 | 66.30                | 5,097,053       | 70                            | 4,697         | 121          | 28           |
| 10-4246                   | SAMN03287759 | JXVF000000000 | 79.87                | 5,098,357       | 74                            | 4,704         | 124          | 27           |
| 10-4247                   | SAMN03287760 | JXVE000000000 | 106.56               | 5,124,180       | 84                            | 4,745         | 124          | 29           |
| 10-4248                   | SAMN03287761 | JXVD000000000 | 101.56               | 5,112,922       | 117                           | 4,737         | 122          | 37           |

b ORFs, open reading frames.
trh virulence markers (4). Since K group II isolates are a prevalent cause of Canadian illness, genome sequencing was undertaken as an approach to further investigate the genetics underlying ambiguous serological classification.

Briefly, sequencing was performed as described by Petronella et al. (5) and Pightling and Pagotto (6). Sequencing libraries were prepared from DNA extracted using the Maxwell 16 SEV cell DNA purification kit (Promega, Madison, WI). The short-read sequence data were generated by preparing a paired-end library with the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA) and sequencing the library on a MiSeq benchtop sequencer (Illumina) for 500 cycles. The reads were assembled de novo into high-quality draft genomes with SPAdes version 3.1.1 (7), utilizing the MismatchCorrector tool, and error correction was performed with BayesHammer (8). This resulted in nonoverlapping contiguous sequences for each genome (Table 1), each of which had a total G+C content of 45%. The gene predictions and annotations were performed by the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) (9).

Nucleotide sequence accession numbers. These nucleotide sequences have been deposited at DDBJ/EMBL/GenBank as Bio-Project PRJNA272927 under the accession numbers provided in Table 1.

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REFERENCES

1. Public Health Agency of Canada. 2014. National Enteric Surveillance Program (NSEP). Public Health Agency of Canada, Winnipeg, Manitoba, Canada. https://www.nml-lnm.gc.ca/NESP-PNSME/index-eng.htm.
2. Paranjpye R, Hamel OS, Stojanowski A, Liermann M. 2012. Genetic diversity of clinical and environmental Vibrio parahaemolyticus strains from the Pacific Northwest. Appl Environ Microbiol 78:8631–8638. http://dx.doi.org/10.1128/AEM.01531-12.
3. Gonzalez-Escalona N, Strain EA, De Jesús AJ, Jones JL, DePaola A. 2011. Genome sequence of the clinical O4:K12 serotype Vibrio parahaemolyticus strain 10329. J Bacteriol 193:3405–3406. http://dx.doi.org/10.1128/JB.05044-11.
4. Banerjee SK, Kearney AK, Nadon CA, Peterson C-L, Tyler K, Bakouche L, Clark CG, Hoang L, Gilmore MW, Farber JM. 2014. Phenotypic and genotypic characterization of Canadian clinical isolates of Vibrio parahaemolyticus collected from 2000 to 2009. J Clin Microbiol 52:1081–1088. http://dx.doi.org/10.1128/JCM.05044-14.
5. Petronella N, Kenwell R, Pagotto F, Pightling AW. 2014. Draft genome sequences of two Clostridium botulinum group II (nonproteolytic) type B strains (DB-2 and (KAPB-3). Genome Announc 2(6):e01111-14. http://dx.doi.org/10.1128/genomeA.01111-14.
6. Pightling AW, Pagotto F. 2014. Draft genome sequence of Cronobacter sakazakii clonal complex 45 strain HP5174, isolated from a powdered infant formula facility in Ireland. Genome Announc 2(4):e00778-14. http://dx.doi.org/10.1128/genomeA.00778-14.
7. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol http://dx.doi.org/10.1089/cmb.2012.0021.
8. Nikolenko SI, Korobeynikov AI, Alekseyev MA. 2013. BayesHammer: Bayesian clustering for error correction in single-cell sequencing. BMC Genomics 14(Suppl 1):S7. http://dx.doi.org/10.1186/1471-2164-14-S1-S7.
9. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyripides N, Madupu R, Markowitz V, Tatusova T, Thompson N, White O. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta)genomic annotation. Omics 12:137–141. http://dx.doi.org/10.1089/omi.2008.0017.