Draft Genome Sequence of the Oyster Larval Probiotic Bacterium Vibrio sp. Strain OY15

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We report the draft genome sequence of Vibrio sp. strain OY15, a Gram-negative marine bacterium isolated from an oyster (Crassostrea virginica) digestive tract and shown to possess probiotic activity. The availability of this genome sequence will facilitate the study of the mechanisms of probiotic activity as well as virulence capacity.

C ontrolling microbial pathogens in aquaculture using probiotic bacteria is becoming increasingly preferred over the use of chemical treatments, such as disinfectants or antibiotics (1). The marine Vibrio sp. OY15 is a naturally occurring bacterium isolated from the digestive gland of an adult oyster (Crassostrea virginica) and has been shown to significantly improve survival of oyster larvae to metamorphosis when challenged with a pathogenic Vibrio strain (2). Here we announce the genome sequence of strain OY15 in order to facilitate identification of processes involved in probiotic activity and to ascertain virulence potential.

A single colony of strain OY15 was grown in marine broth 2216 (Difco) at 28°C and DNA was extracted using the Wizard genomic DNA purification kit (Promega). Sequencing was done using an Illumina MiSeq benchtop sequencer. The read library contained 9,221,838 paired-end reads with 284 average read length and average coverage of 430X. De novo assembly of the paired reads was done using CLC Genomics Workbench (CLC Bio/Qiagen) yielding 45 contigs with an average length of 115,533 bp and 5,198,998 total bp. The N50 is 544,789 bp with a G+C composition of 44.6%. Gene prediction and annotation using RAST (Rapid Annotation using Subsystem Technology) (3), generated 4,814 open reading frames. The closest neighbors identified by SEED viewer 2.0 (4) were Vibrio sp. EX25 (score = 534) and V. alginolyticus 40B (score = 489).

The genome carries genes for regulators luxU, luxO, and hapR and a homoserine lactone efflux pump—suggesting that quorum sensing is likely important for colonization (5)—as well as sctABC systems involved in Vibrio swarming (6). A ferric siderophore transporter, vibrioferin/ferrichrome siderophores, and the Fur and IrgB regulators may also play roles in colonization of the digestive tract (7). A cluster of 17 genes for mannose-sensitive hemagglutinin (MSHA) biogenesis proteins were identified, which may also play roles in adhesion and colonization (8). Candidates for probiotic activity include several Rhs family genes, which mediate intercellular competition (9) and may stimulate host immunity (10), and three alginate lyase precursors, which disrupt biofilms (11). Gene clusters associated with exopolysaccharide production—rbm and vps—are present, which may play a role in antibiofilm activity (12). Bacteriocin (colicin V) and bacteriocin tolerance genes were also found.

While phage-related genes encoding putative RTX and zona occludens toxins were identified in the OY15 genome, genes encoding Vibrio GTX phage (13) appear to be absent. Virulence-related secretory HlyD, several hemolysins, the tosRS and vicSB virulence regulators, and genes encoding types I, III, and VI secretion system components were found. On the other hand, tdh and trh genes associated with virulent V. para humiliationis (14, 15) were not identified, which is consistent with the finding that OY15 tested negative in a mammalian-cell bioassay for cytotoxity (J. Jones, U.S. FDA, personal communication). Genomic and phenotypic studies of OY15 will improve our understanding of probiosis and pathogenesis mechanisms of Vibrio spp.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number JPL0000000. The version described in this paper is the first version, JPL01000000.

ACKNOWLEDGMENTS
We thank Diane Kapareiko for providing strain OY15 and technical support, Sabeeha Nazar and Ryan McDonald for assistance with genome sequencing, and Jeanette Davis for help with the genome assembly and submission.

Support was provided by Dr. Gary Wikfors, NOAA Fisheries Northeast Fisheries Science Center Milford Laboratory, and grant NA11SEC4810002 from the NOAA-EPP Living Marine Resources Cooperative Research Center.

REFERENCES


