Data Article

Genome data of shrimp acute hepatopancreatic necrosis disease causative *Vibrio parahaemolyticus* strains isolated from South Korea aquaculture farms

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**A B S T R A C T**

The *Vibrio parahaemolyticus* is a gram-negative bacterium, which is responsible for acute hepatopancreatic necrosis disease (AHPND) in shrimp and has various virulent factors. So, to intensify the knowledge on pathogenic mechanism, the heterogeneous *V.parahaemolyticus* strains genome are indeed. Here, genome of seven *V.parahaemolyticus* strains, which are virulent to shrimps were sequenced by PacBio platform and the virulence was confirmed through the presence of

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plasmid (~69 Kb) with binary toxin genes (i.e., pirA and pirB) with PCR method.

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| Specifications Table |
|----------------------|
| **Subject** | Parasitology |
| **Specific subject area** | Microbiology, Genomics |
| **Type of data** | Genome sequence, predicted genes and virulent plasmid of seven *Vibrio parahaemolyticus* strains. |
| **How data were acquired** | Complete DNA from each strain was sequenced with PacBio sequel system. |
| **Data format** | Assembled contigs and plasmids in fasta and the predicted genes co-ordinates are in gff3 file formats. |
| **Parameters for data collection** | Genomic DNA from pure culture. |
| **Description of data collection** | *Vibrio parahaemolyticus* strains were collected from hepatopancreas of infected shrimps (*Litopenaeus vannamei*) and water samples of the respective aquaculture ponds. The samples were inoculated on the thiosulfate citrate bile salt sucrose plates and incubated at 25°C for 24h. |
| **Data source location** | The shrimps (*Litopenaeus vannamei*) and water samples were collected from the aquaculture farms located in Incheon, Pyeongtaek, Gyeonggi-do, Shinan, and Jeollanam-do of Korea in 2016 of South Korea, at 2016, which were experienced massive death. |
| **Data accessibility** | This Whole Genome Shotgun project has been deposited at GenBank (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA482034) under the accession QPQB00000000 - QPQH00000000. |

**Value of the Data**

- Draft genome of each strain, could be an additional data set to assess the virulence level upon the genetic variation encoded in plasmid.
- These pandemic strains genome can be an additional dataset to characterize the diversity of *Vibrio parahaemolyticus* virulence potential parameters, which aid to estimate/prevent the mortality rate in shrimp farms.
- These genomes could be valuable resource to conduct the metagenome/comparative genomic analysis among *Vibrio parahaemolyticus* strains.

**1. Data**

In this article, the Table 1, explains the summary of seven *Vibrio parahaemolyticus* shrimp pathogen strains (SC4, SK, SM3, SM4, WC15, WS, WY3) genome, which are sequenced by pacific biosciences (PacBio) and the summary of sequenced bases, which are assembled into chromosomes and plasmids. Further, the summary of structural annotations such as rRNA, tRNA and genes were also given in Table 1. In Table 2, along with the sequenced strains genome and the details of other twenty genomes, which were collected from the GenBank to assess the functional group of our sequenced genomes. These twenty genomes are grouped into four major groups, i.e., AHPND (Shrimp+/Human–), Pathogenic (Shrimp+/ Human+), Non-pandemic (Shrimp+/Human–), and Non-pathogenic (Shrimp-/Human–). Fig. 1, is the conformation of PCR gel image for the binary toxin genes (PirA and PirB) of AHPND, which explains the shrimp pathogenicity property of sequenced strains. Fig. 2, illustrate the comparative heap-map representation of other major virulent genes of *Vibrio parahaemolyticus* strains from the sequenced genomes along with the genomes selected from GenBank. Fig. 3, expains the phylogenetic
Fig. 1. PCR based virulence conformation of sequenced *Vibrio parahaemolyticus* strains with the universal markers (PirA and PirB).
Fig. 2. Profile of virulent associated genes from the *Vibrio parahaemolyticus* sequenced genomes along with other group of genomes. AHPND (Shrimp+/Human−), AHPND (Korea; In this article) (Shrimp+/Human−), Pathogenic (Shrimp+/ Human+), Non-pandemic (Shrimp+/Human−), Non-pathogenic (Shrimp−/ Human−). +/−: pathogenic nature
tree from the 46 single copy genes, which are selected from ortholog analysis conducted with OrthoMCL method. The assembled contigs and plasmids were deposited in GenBank (https://www.ncbi.nlm.nih.gov/) under the accession QPQ00000000 - QPQH0000000. Further, facilitate the easy access to the strains which used in this article, the cultures were deposited in Korean collection for type cultures (KCTC) (https://kctc.kribb.re.kr) under the accession number KCTC13702BP-KCTC13708BP (Table 1). All the figure source files were given in the supplementary folder, which named as figures source files. The README file has all the basic information of the files, which used for the figure two and three.

2. Experimental Design, Materials, and Methods

2.1. Samples

White shrimps (Litopenaeus vannamei) collected from the aquaculture farms located in Incheon, Pyeongtaek, Gyeonggi-do, Shinan, and Jeollanam-do of Korea at 2016, which experienced massive death. The water collected from ponds and hepatopancreas excised from shrimps were inoculated on the thiosulfate citrate bile salt sucrose plates (TCBS supplemented with 1.5% NaCl) and incubated at 25°C for 24 h. The colonies of isolated bacteria were cultured on tryptic soy agar plates (TSA supplemented with 1.5% NaCl). The AHPND property was determined by the PCR method using genomic DNA [1].
2.2. Genomic DNA isolation, sequencing, and assembly

The complete experimental procedures were conducted based on the instructions given in the respective products/kits. The below sequential steps from DNA isolation to sequencing procedures were conducted by DNALink, the authorized sequence service provider (http://www.dnalink.com/korean/index.html). Genomic DNA of these strains were extracted using the Genomic DNA Purification Kit (Qiagen, Hilden, Germany). DNA was examined by 1% agarose gel electrophoresis and quantified by a NanoDrop 2000 spectrophotometer (Thermo Scientific, MA, USA). A 10-KB library was prepared and sequenced using the PacBio (Pacific Biosciences) platform. One SMRT cell for each strain was used for sequencing, and those sequences are assembled separately by using the hierarchical genome assembly process (HGAP 2.0) [2]. Each assembly was constructed using more than 1 Gb of PacBio reads, and assembled contigs are polished with Quiver to reach final consensus accuracy.

2.3. Genome annotation

Gene prediction was carried out using Glimmer method [3], and small RNAs (i.e., tRNA and tRNA) were predicted using RNAmmer [4] and tRNAscan-SE v1.21 [5] methods respectively. Finally, the functional gene annotation was carried out based on homology searches against NR database and gene ontology (GO) database using Blast2GO method [6].
2.4. Polymeric chain reaction for pirA and pirB

Genomic DNA was extracted from cultured bacteria using high pure PCR template preparation kit according to manufacturer instructions (Roche Life Science). PCR reaction mixture is prepared with PuRe Taq ready-to-go PCR beads (GE Healthcare). To detect AHPND, PCR was performed with DNA templates using duplex primer sets of PirA and PirB genes (i.e., VpPirA-284F: TGACTATTCTCACGATTGGACTG, VpPirA-284R: CACGACTAGCGCCATTGTTA, VpPirB-392F: TGATGAAGTGATGGGTGCTC, VpPirB-392R: TGTAGCGCGGTGACTCA) under the following PCR conditions: initial denaturation at 94°C for 3min, followed by 35 cycles of 94°C for 30 sec, 60°C for 30 sec, and 72°C for 30 sec, and a final extension at 72°C for 7 min [1]. The PirA- and PirB-cloned plasmids and Distilled water were used as the positive control and negative control, respectively. The PCR products were electrophoresed on QIAXcel (Qiagen)
2.5. Phylogenetic tree

The sequenced and selected genomes from GenBank are subjected to ortholog analysis by using OrthoMCL method [7]. The single copy genes (which have only one copy of gene in each genome) were selected from OrthoMCL cluster file. These concatenated single copy proteins are aligned using the MAFFT v7.2 [8] with default parameters. The multiple alignment initially corrected with Gblocks v0.91 [9] and subjected to phylogenetic tree reconstruction using IQ-TREE v1.5.0 [10]. The tree imported to FigTree v1.4.3. (http://tree.bio.ed.ac.uk/software/figtree/) to obtain the phylogenetic tree.

2.6. Data deposition

This Whole Genome Shotgun project has been deposited at GenBank under the accession QPQB00000000 - QPQH00000000. The microbial cultures were deposited in Korean collection for type cultures (KCTC) under the accession number KCTC13702BP-KCTC13708BP.

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Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi: 10.1016/j.dib.2020.105697.

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