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Research note

Complete Genome Sequence of *Vibrio parahaemolyticus* Strain IJWP7-11 Isolated from Coastal Water in Korea

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ABSTRACT - *Vibrio parahaemolyticus* is a major seafood-borne pathogen responsible for acute gastroenteritis in humans. This study presents the complete genome information of the strain IJWP7-11 isolated from coastal water in Gyeongsang Province, which includes chromosome 1 (3,366,158 bp and 45.25% GC content) and chromosome 2 (1,778,791 bp and 45.53% GC content). Additional analysis revealed that the strain harbored 151 virulence genes, and four antimicrobial resistance genes including *tet*(35), *norM*, $bla_{\text{CARB-18}}$, and *catC*. Multi-locus sequence typing assigned the strain to sequence type ST1696.

Key words: *V. parahaemolyticus*, Coastal water, Whole genome sequencing, One Health

Vibrio parahaemolyticus is a Gram-negative halophilic bacterium widely distributed in coastal marine environments and seafood, including fish and shellfish. Consumption of raw or undercooked seafood is the primary route of human infection, causing gastroenteritis, wound infections, and septicemia. The global dissemination of this pathogen has been accelerated by ocean warming[1,2]. The thermolabile hemolysin gene (*tlh*), present in all *V. parahaemolyticus* strains, is widely used as a species-specific genetic marker[2,3]. The pathogenicity of *V. parahaemolyticus* is largely attributed to specific hemolysins and two different clusters of type III secretion systems (T3SSs). Thermostable direct hemolysin (TDH) and TDH-related hemolysin (TRH), encoded by *tdh* and *trh*, respectively, are major virulence markers and are predominantly detected in clinical isolates. T3SSs are classified into T3SS1 and T3SS2. T3SS1 is present in all *V. parahaemolyticus* strains and contributes to cytotoxicity and lethality, whereas T3SS2 is associated with enterotoxicity and environmental persistence[3]. Despite the increasing prevalence of *V. parahaemolyticus* in Korea, complete genome information for environmental isolates remains limited. Therefore, genomic characterization of environmental isolates is important for understanding their virulence potential and antimicrobial resistance (AMR) profiles. In this study, we report the complete genome sequence and genomic features of *V. parahaemolyticus* strain IJWP7-11 isolated from coastal water in Korea.

V. parahaemolyticus strain IJWP7-11 was isolated from coastal water in Gyeongsang Province, Korea, according to a previously described protocol[4]. Whole-genome sequencing (WGS) was performed using the Illumina NovaSeq 6000 platform and Oxford Nanopore sequencing technology. For Illumina sequencing, genomic DNA was extracted using the iDetect® gDNA prep kit for Microbes (ConnectaGen Inc., Seoul, Korea). Sequencing libraries were prepared using the TruSeq nano DNA prep kit (Illumina, San Diego, CA, USA) and sequenced using 2×150 bp paired-end reads. Raw reads were quality-checked using FastQC (v.0.11.8). For Oxford Nanopore sequencing, libraries were prepared using a ligation sequencing kit (Oxford Nanopore Technologies, Oxford, UK), and base-calling was performed using Guppy (v.4.2.2). Hybrid de novo genome assembly was conducted using Unicycler (v.0.5.0). Genomic features were identified using the Bacterial and Viral Bioinformatics Resource Center (BV-BRC, v.3.53.31), and genome annotation was performed using Prokka (v.1.14.6)[5,6].

AMR genes were detected using AMRFinder Plus (v.4.2.7), and virulence-associated genes were predicted using VF analyzer in Virulence Factor Database (VFDB) (https://www.mgc.ac.cn/VFs/). Because the *trh* gene was not included in the VFDB dataset used in this study, its presence was additionally assessed by in silico PCR using UGENE (v.52.1) based on previously reported primers[7-9]. Sequence type was determined using MLST software (v.2.23.0) based

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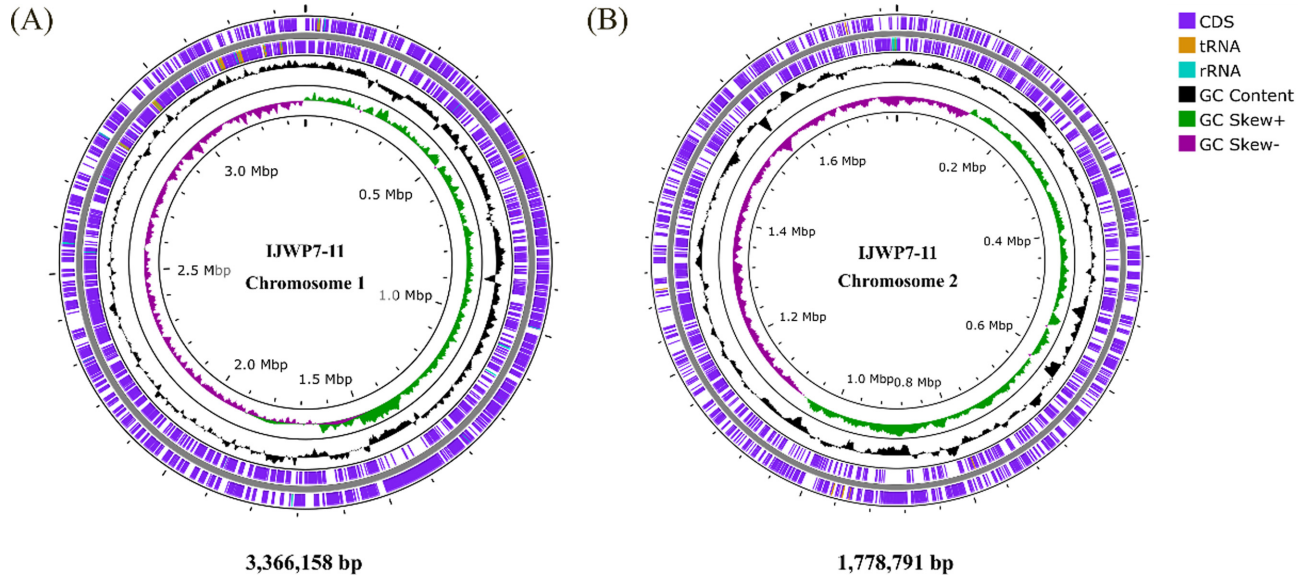

Fig. 1. Complete genome map of *V. parahaemolyticus* IJWP7-11. (A) Chromosome 1, (B) Chromosome 2 are presented via the Proksee (https://proksee.ca). The visualized rings, arranged from outer to inner, represent coding sequence (CDS) forward strands, CDS reverse strands, tRNA, rRNA, GC content and GC skew.

Table 1. Genomic features of *V. parahaemolyticus* strain IJWP7-11

Genomic features	Characteristics	
	Chromosome 1	Chromosome 2
Genome size (bp)	3,366,158	1,778,791
GC content (%)	45.25	45.53
No. of CDSs	3,146	1,633
No. of rRNA	34	3
No. of tRNA	115	14
AMR genes	*tet*(35), *norM*	$bla_{\text{CARB-18}}$, *catC*
No. of virulence genes	131	20
tlh	-	1
trh	-	-
tdh	-	-
T3SS1	38	-
T3SS2	-	-
Sequence type (ST)	ST1696	

on seven housekeeping genes (*dnaE, gyrB, recA, dtdS, pntA, pyrC,* and *tnaA*)[10].

The complete genome of *V. parahaemolyticus* strain IJWP7-11 consists of two circular chromosomes: chromosome 1 (3,366,158 bp; GC content, 45.25%) and chromosome 2 (1,778,791 bp; GC content, 45.53%) (Table 1 and Fig. 1). The genome encodes 4,779 coding sequences (CDSs) and 166 non-coding RNA genes, including 37 rRNA and 129 tRNA genes. Four AMR genes were identified. Chromosome 1 harbored *tet*(35), associated with tetracycline resistance, and *norM*, encoding a multidrug efflux pump, whereas chromosome 2 contained $bla_{\text{CARB-18}}$, encoding a class A β-lactamase, and *catC*, encoding chloramphenicol acetyltransferase[11-14].

The species-specific marker gene *tlh* was identified on chromosome 2. A total of 151 virulence-associated genes were identified, including 131 on chromosome 1 and 20 on chromosome 2. Major virulence determinants, including *tdh*, *trh*, and T3SS2-associated genes, were not detected; however, 38 T3SS1-associated genes were identified on chromosome 1. MLST analysis assigned strain IJWP7-11 to sequence type ST1696, which has previously been reported in environmental isolates from China according to the PubMLST database. These genomic data provide a valuable resource for understanding the virulence potential and AMR characteristics of environmental *V. parahaemolyticus* isolates in Korea.

Data Availability Statement

The genome sequence data have been deposited in the NCBI under BioSample accession number SAMN60635698.

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국문요약

*Vibrio parahaemolyticus*는 사람에서 급성 위장관염을 유발하는 주요 수산식품 매개 병원체이다. 본 연구에서는 경상도 연안수에서 분리된 *V. parahaemolyticus* 균주 IJWP7-11의 complete genome 정보를 분석하였다. 해당 균주의 유전체는 chromosome 1 (3,366,158 bp, GC 함량 45.25%)과 chromosome 2 (1,778,791 bp, GC 함량 45.53%)로 구성되었다. 유전체 분석 결과 총 151개의 병원성 관련 유전자와 *tet*(35), *norM*, $bla_{CARB-18}$, *catC*의 4개의 항생제 내성 유전자가 확인되었다. 또한 multi-locus sequence typing (MLST) 분석을 통해 본 균주가 sequence type ST1696에 속하는 것으로 확인되었다. 본 연구에서 확보한 완전 유전체 정보는 국내 환경 유래 *V. parahaemolyticus*의 병원성 및 항생제 내성 특성 이해를 위한 기초자료로 활용될 수 있을 것으로 기대된다.

Conflict of interests

The authors declare no potential conflict of interest.

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