AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Near-Complete Genome Sequences of 12 Peruvian Strains of Infectious Hypodermal and Hematopoietic Necrosis Virus Infecting the Shrimp *Penaeus vannamei*

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ABSTRACT Infectious hypodermal and hematopoietic necrosis virus (IHHNV) is a shrimp virus listed by the World Organisation for Animal Health (OIE). In this study, we report the genomic sequences of 12 IHHNV strains obtained from shrimp samples from aquaculture cultures from the Tumbes region of Peru.

Penaeus vannamei is the shrimp with the highest commercial value, and therefore it is the most widely cultivated species around the world, including Peru (1, 2).

Infectious hypodermal and hematopoietic necrosis virus (IHHNV; genus, *Penstyldensovirus*; subfamily, *Densovirinae*; family, *Parvoviridae*) is one of the smallest penaeid shrimp viruses (3). This virus was first reported in the 1980s in Hawaii (4, 5). Phylogenetic analysis revealed the introduction of this virus to the American continent in the 1970s (6). Interestingly, IHHNV causes high mortality in *Penstyldensovirus stylirostris*; however, in *P. vannamei* and *P. monodon*, mortality has not been reported. In these species, IHHNV causes slow growth and deformities in the exoskeleton (called Runt deformity syndrome) (7).

IHHNV is a 22-nm parvovirus with a nonenveloped icosahedral capsid; it has a genome of ≈3.9 kb of single-stranded DNA encoding 3 open reading frames (ORFs). IHHNV infection is considered benign and of low risk, but recent studies in *P. monodon* show that high viral loads can produce a significant economic impact (8, 9).

Sequences from Peruvian IHHNV strains have not been described. In this work, we report 12 partial genomic sequences of IHHNV strains detected in the Aquaculture Health Laboratory of the National Fisheries Health Agency (SANIPES), from shrimp from different productive zones and natural environments of the Tumbes region in Peru.

The sampling area included culture systems (9 samples) and natural areas (3 samples) from the north, center, and south of the coast of the Tumbes Department. DNA was isolated from 25 mg of homogenized pleopod tissue from *P. vannamei* using the DNeasy blood and tissue kit (Qiagen, Germany). The DNA was quantified with the Qubit 4 fluorometer (Invitrogen, USA). The samples were screened by endpoint PCR using the primers 309F/R, following the recommendations described in the Manual of Diagnostic Tests for Aquatic Animals from the World Organisation for Animal Health (OIE) (Fig. 1) (10).

Subsequently, to cover the IHHNV genome, 8 endpoint PCRs were performed per sample with specific primers to cover 3.9 kb using 50 to 100 ng of DNA (Fig. 1), following the protocols of Silva et al. (2014), with modifications to the amplification time (11). The PCRs were performed with high-fidelity *Taq* platinum (Thermo Scientific, USA). Sequencing was carried out using dideoxy-chain termination sequencing with the fluorescent nucleotides method. The sequences were assembled using Geneious Prime 2020.0.5 software (Biomatters, Inc.), generating a consensus sequence of ≈3.7 kb. The base calling was done with a quality score of 99.9% accuracy ($Q > 30$). The sequencing covered 96% of the genome (compared to the reference Hawaii IHHNV strain; GenBank

Citation Salcedo-Mejía LA, Durán-Ramirez Y, Velazco-Peña RZ, Pinto JA, Rebaza-Caballero A. 2021. Near-complete genome sequences of 12 Peruvian strains of infectious hypodermal and hematopoietic necrosis virus infecting the shrimp *Penaeus vannamei*. Microbiol Resour Announc 10:e00169-21. https://doi.org/10.1128/MRA.00169-21.

Editor Jelle Matthijnssens, KU Leuven

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We dedicate this article to the memory of biologist Juan José Bonifacio (1985 to 2020), who actively participated in the execution of this project.

Received 14 February 2021
Accepted 19 April 2021
Published 20 May 2021

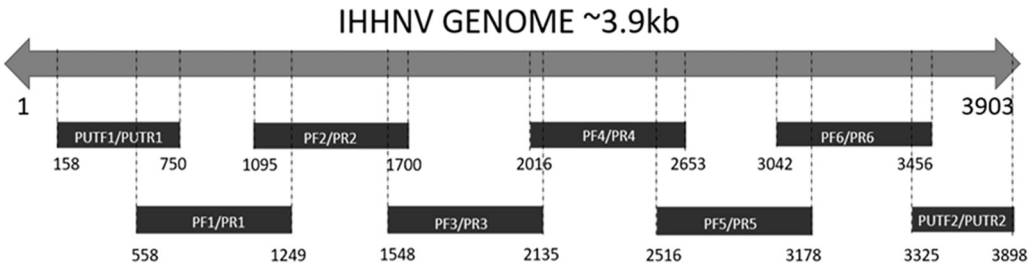

FIG 1 Location of the oligonucleotides in the IHHNV genome.

accession number AF218266.2), containing 3 complete ORFs. In total, 186 nucleotides corresponding to the 5′ and 3′ untranslated regions (UTRs) were not covered in the analysis.

This draft assembly described the sequences of IHHNV strains isolated in Peru. Further investigation should be conducted to evaluate the pathogenicity of the strains present on the coast of Tumbes, Peru.

Data availability. The assembled genomic sequences were deposited in GenBank under accession numbers MW357689, MW357690, MW357691, MW357692, MW357693, MW357694, MW357695, MW357696, MW357697, MW357698, MW357699, and MW357700.

ACKNOWLEDGMENTS

This project was financed by the National Program for Innovation in Fisheries and Aquaculture (PNIPA) of the Ministry of Production of Peru through contract number 002-2018-PNIPA-SUBPROJECT.

We declare no conflicts of interest with this research.

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