



Complete Genome Sequence of *Herpesvirus anguillae* Strain HVA980811 Isolated in Chiayi, Taiwan

Chiu-Ming Wen,^a Ping-Chung Liu,^b Fan-Hua Nan^b

Department of Life Sciences, National University of Kaohsiung, Kaohsiung, Taiwan^a; Department of Aquaculture, National Taiwan Ocean University, Keelung, Taiwan^b

ABSTRACT *Herpesvirus anguillae* (HVA), also known as anguillid herpesvirus 1 (AngHV1), is one of the relevant viruses in wild and cultured anguillid eels. Here, the complete genome sequence of strain HVA980811, isolated in Chiayi, Taiwan, is reported. The genotype of the eel herpesviruses in Taiwan is supposed to be identical to the Japanese AngHV1.

Herpesvirus anguillae (HVA), also known as anguillid herpesvirus 1 (AngHV1) and eel herpesvirus, was isolated first in Japan in 1985 from cultured moribund European eels (*Anguilla anguilla*) and Japanese eels (*Anguilla japonica*) (1). Complete genome sequence suggests that AngHV1 and the cyprinid herpesviruses are included within the family *Alloherpesviridae* (2). In Taiwan, eel herpesvirus Formosa (EHVF) and European eel herpesvirus (EEHV) were isolated from cultured diseased Japanese eels in the central regions and European eels in the northern regions, respectively (3, 4). Serological examination and partial sequence alignments proposed that both viruses are homologous to AngHV1 (4–6). Additionally, detection and isolation of AngHV1 have been reported from asymptomatic and diseased wild and cultured anguillid eels in Europe (7–14).

An eel herpesvirus strain, HVA980811, has a sequence (GenBank accession no. HQ992952) identical to the AngHV1 open reading frame 12 (ORF12) and was isolated from hemorrhaged Japanese eel farmed in Chiayi, south Taiwan, in 2009 (15). For genome sequencing, HVA980811 was propagated in EK-1 cells, and the virions were purified according to methods described previously (5). The viral genomic DNA was extracted by phenol extraction and delivered to Welgene Biotech (Taipei, Taiwan). The DNA was further extracted using a WelPrep DNA kit by Welgene and sonicated using a Misonix, Inc. 3000 sonicator for sizes ranging from 400 to 500 bp, and DNA sizing was performed with a bioanalyzer DNA 1000 chip (Agilent Technologies). One microgram of sonicated DNA was end repaired, A-tailed, and adaptor ligated, according to the Illumina TruSeq DNA preparation protocol, and ConDeTri was implemented for trimming (16). Cleaned and filtered nuclear reads were assembled *de novo* using ABySS (17). All obtained sequences were aligned and manually reassembled.

The HVA980811 genome comprises 249,071 bp, including a 10,714-bp terminal direct repeat. The nucleotide sequence is 99% identical to the genome sequence of AngHV1 (GenBank accession no. FJ940765.3) and contains 139 predicted protein-coding open reading frames (ORFs), as does AngHV1. Protein-protein BLAST showed that all the amino acid sequences are 100% identical to the AngHV1 counterparts, except ORF1. The result suggests that the genotype of the eel herpesviruses in Taiwan, including HVA980811, EHVF, and EEHV, is identical to that of the Japanese AngHV1.

Accession number(s). The complete genome sequence of anguillid herpesvirus 1 strain HVA980811 has been deposited in GenBank under the accession no. [KX027736](https://www.ncbi.nlm.nih.gov/nuccore/KX027736).

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Address correspondence to Chiu-Ming Wen, wenchiumin@nuk.edu.tw, or Fan-Hua Nan, fhnan@mail.ntou.edu.tw.

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