Complete Genome Sequence of a Giant Sea Perch Iridovirus in Kaohsiung, Taiwan

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We report here the complete genome sequence of a megalocytivirus strain, GSIV-K1, isolated from a farmed giant sea perch (*Lates calcarifer*) in Kaohsiung, Taiwan. GSIV-K1 causes mortality in farmed marine fish, including giant sea perch and groupers. The genome sequence is nearly identical to the genome of the orange-spotted grouper iridovirus.

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*M*egalocytivirus, a genus of fish viruses within the family *Irido-viridae*, causes emerging infectious iridovirus diseases that can result in moderate-to-heavy losses in various species of both cultured and wild freshwater and marine fish (1). *Megalocytivirus* contains 3 major subgroups, the infectious spleen and kidney necrosis virus (ISKNV), Red Sea bream iridovirus (RSIV), and turbot reddish body iridovirus (TRBIV) (2). RSIV is included on the list of notifiable terrestrial and aquatic animal diseases compiled by the World Organisation for Animal Health (http://www.oie.int/en/animal-health-in-the-world/oie-listed-diseases-2015/).

In June 2006, a virus designated GSIV-K1 was isolated from a diseased giant sea perch (*Lates calcarifer*) farmed in Kaohsiung, Taiwan (3). The nucleotide sequences of the major capsid protein suggest that GSIV-K1 belongs to the RSIV group (2, 3). GSIV-K1 has a sequence that is identical to that of the orange-spotted grouper iridovirus (OSGIV) genes of ORF35L and ORF39L (4). To obtain the complete genome sequence of GSIV-K1, the virus was cultured on SPB cells (5), and the DNA from purified viral particles was extracted using a WelPrep DNA kit (Welgene Biotech), according to the manufacturer's instructions. For library construction, 10 μg of total DNA was sonicated using a Misonix 3000 sonicator for sizes ranging from 400 to 500 bp. DNA sizing was performed with a bioanalyzer DNA 1000 chip (Agilent Technologies). Sonicated DNA (1 μg) was end repaired, A-tailed, and adaptor ligated, according to the Illumina TruSeq DNA preparation protocol. ConDeTri was implemented for trimming and removal of the reads according to the quality score (6). The total number of high-quality paired-end sequence reads after trimming were 17.66 million. Cleaned and filtered nuclear reads were assembled *de novo* using ABySS (7). Gene predictions were performed using GeneMarkS (8) and annotation based on BlastX results. The resulting predictions were searched against the NCBI nonredundant database using Blastp (http://blast.ncbi.nlm.nih.gov/Blast.cgi).

The circular genome of GSIV-K1 comprises 112,565 bp and has 135 putative open reading frames. A phylogenetic analysis of the genome sequence demonstrated that GSIV-K1 is nearly identical to OSGIV, followed by rock bream iridovirus, RSIV, large yellow croaker iridovirus, ISKNV, and TRBIV.

Nucleotide sequence accession number. The complete genome sequence of GSIV-K1 has been deposited in GenBank under the accession no. KT804738.

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