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Complete Genome Sequence of a Phycodnavirus, *Heterosigma akashiwo* Virus Strain 53

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We report the complete genome sequence of *Heterosigma akashiwo* virus strain 53. The virus is a member of the *Phycodnaviridae*, one of the families regarded as giant double-stranded DNA viruses. The 274,793-bp genome contained 246 protein-coding and 3 tRNA-coding sequences.

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Heterosigma akashiwo is a photosynthetic eukaryotic unicellular alga that belongs to the class Raphidophyceae. It is one of the bloom-causing algae, which is widely observed in Pacific Rim regions, including North and South America, eastern Asia, Oceania, and the Northern Atlantic region (1–12). *H. akashiwo* bloom is known to be terminated by algicidal bacteria (13–21) and viruses (22–24). *Heterosigma akashiwo* virus (HaV) was identified as one such bloom-terminating factor (24, 25). Its genome was characterized to be a linear double-stranded DNA (dsDNA), with an estimated size of ~290 kbp (25). It is a member of the *Phycodnaviridae*, one of the viral families regarded as giant dsDNA viruses that possess genomes larger than several hundred kilobase pairs in size (26).

Here, we report the complete genome sequence of HaV strain 53, originally isolated from the Itsukaichi Fishing Port in Hiroshima Bay, Japan (27). HaV53 was propagated on *H. akashiwo*, and viral particles were collected by adding polyethylene glycol 8000 at a final concentration of 6% to the culture medium containing lysed hosts, followed by centrifugation of the mixture at 21,000 × *g*. The HaV53 DNA was extracted from the purified HaV53 particles by proteinase K digestion, followed by chloroform-isoamyl alcohol treatment and ethanol precipitation. A genomic DNA library was prepared using a Nextera XT DNA sample prep kit (Illumina), and 24 million reads were generated by HiSeq 2500 using the 100-bp paired-end mode. Reads with high-quality scores (>28) were assembled using *Platanus* (28), yielding five high-sequence-coverage contigs (73.2, 58.5, 57.6, 41.2, and 33.2 kb) derived from HaV and numerous low-coverage contigs derived from the host DNA. Gaps between the contigs were filled by sequencing of gap-spanning PCR products using ABI3130xl and Illumina MiSeq sequencers. The accuracy of assembly was confirmed by mapping the paired-end reads to the final assemblage using BWA (29).

The genome of HaV53 was 274,792 bp in size, and the A+T content was 69.6%. It was predicted to contain 247 open reading frames (ORFs) by GeneMarkS (30) and 3 tRNAs by tRNAscan-SE (31). Among the 246 ORFs, 105 had significant hits in the NCBI nonredundant protein database (BlastX, searched with *E* value $<10^{-5}$); 4 had best hits to the sequences previously reported for HaV strain 01 (accession numbers BAE06835.1, BAE06251.1, BAB69884.1, and BAB69883.1) and 23 has best hits to other *Phycodnaviridae* members. The 105 ORFs coded for polypeptides with a variety of functions, including gene regulation, metabolism, signal transduction, and ubiquitin-related protein regulation. As the sequence of HaV53 reported here is the first complete genome sequence of HaV, it would help advance research on *Phycodnaviridae*.

Accession number(s). The annotated genome sequence of HaV53 has been deposited in DDBJ/EMBL/GenBank under the accession number KX008963.

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