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.

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 to a final concentration of 6% to the culture medium containing lysed hosts, followed by centrifugation of the mixture at 8000 g. The HaV53 DNA was extracted from the purified HaV53 particles by proteinase K digestion, followed by chloroform-isooamyl 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 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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