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Complete Genome Sequence of *Epizootic hemorrhagic disease virus* Serotype 6, Isolated from Florida White-Tailed Deer (*Odocoileus virginianus*)

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ABSTRACT Here, we report the complete genome sequence of *Epizootic hemorrhagic disease virus* (EHDV) serotype 6 (EHDV-6), isolated from a Florida white-tailed deer (*Odocoileus virginianus*) in 2016. To our knowledge, this is the first full genome sequence determined for an EHDV-6 isolate from Florida.

*E*pizootic hemorrhagic disease virus (EHDV) is a causative agent of hemorrhagic disease of farmed and wild cervids, including white-tailed deer (1, 2). This epitheliotropic double-stranded RNA virus is a member of the genus *Orbivirus* within the family *Reoviridae* (3). Biting midges of the genus *Culicoides* are confirmed vectors of EHDV (4). Clinical cases of EHDV infection vary from peracute death to a chronic disease course that includes respiratory distress, edema of the head and neck, oral erosions, and sloughing of the hooves (1). Ten EHDV serotypes (EHDV-1 through EHDV-8, 318, and Ibaraki virus) have been described (5), and of these, 7 (EHDV-1, EHDV-2, and EHDV-4 through EHDV-8) are globally distributed (6). Complete genome sequences of EHDV-1 and EHDV-2, isolated from Florida white-tailed deer, were recently reported (7). Although EHDV-6 has been reported in some parts of the United States (8, 9), the complete genome sequence of this serotype from white-tailed deer in Florida had not previously been determined.

A spleen sample was taken from a farmed white-tailed deer (animal no. OV208) suspected of having epizootic hemorrhagic disease (EHD) during a 2016 health assessment conducted by researchers from the University of Florida Cervidae Health Research Initiative. The presence of EHDV virus RNA (vRNA) in a homogenized spleen specimen was confirmed by reverse transcription-PCR (RT-PCR) (10) and followed by observation of virus-induced cytopathic effect (CPE) in Vero E6 cells (*Cercopithecus aethiops* [African green monkey] kidney, ATCC CRL-1586) 20 days postinoculation. The vRNA was then extracted from virions in spent medium using a QIAamp viral RNA minikit (Qiagen). A cDNA library was constructed using a NEBNext Ultra RNA library prep kit and sequenced on an Illumina MiSeq instrument. *De novo* assembly of the paired-end reads was performed in SPAdes v3.10.0 with the default parameters (11). All 10 EHDV segments were recovered from the Florida white-tailed deer isolate OV208. BLASTN analysis of the outer-coat protein (VP2) from isolate OV208 revealed the highest nucleotide identity (99%; 2890/2907) to an EHDV-6 isolate from the spleen of

a white-tailed deer in Ohio in 2012 (12). The OV208 VP2 sequence was aligned in MAFFT 5.8 (13) to 79 orthologous EHDV-1, EHDV-2, and EHDV-6 nucleotide sequences retrieved from the GenBank database. A maximum likelihood (ML) analysis was performed in IQ-TREE (version 1.4.4) using 1,000 nonparametric bootstraps to test the robustness of the clades (14). Similar to the BLASTN results, the ML analysis supported placement of isolate OV208 as a member of the EHDV-6 clade most closely related to an EHDV-6 isolate from a white-tailed deer in Ohio (12).

The current study is the first to report the complete genome sequence of an EHDV-6 isolate from Florida white-tailed deer. A recent investigation (7) and the present study have sought to characterize the EHDV serotypes circulating in Florida white-tailed deer as the first step in the development of an efficacious vaccine to curb the impact of EHD on farmed deer populations.

Accession number(s). The genome sequence for EHDV-6, isolated from a Florida white-tailed deer (animal no. OV208), has been deposited in GenBank under the accession no. MG886400 to MG886409.

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