Complete Genome Sequence of Human Coronavirus Strain 229E Isolated from Plasma Collected from a Haitian Child in 2016

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ABSTRACT Human coronavirus strain 229E (HCoV-229E) and human alphaherpesvirus 1 were isolated from the plasma of a Haitian child in 2016 with suspected arbovirus diseases. To our knowledge, this is the first description of HCoV-229E in human plasma, which is the focus of this article.

Human coronavirus strain 229E (HCoV-229E), one of the causative agents of the common cold, is increasingly associated with more severe respiratory infections in children, elders, and individuals with underlying medical conditions (1–4). The virus also has neuroinvasive and neurotropic properties (5). The presence of HCoV-229E within clinical samples (e.g., nasal or throat swabs, nasopharyngeal aspirate, bronchoalveolar lavage, or saliva) is typically confirmed by molecular (e.g., reverse transcription-PCR [RT-PCR] targeting of virus-specific genes) or serological (immunofluorescence assay targeting viral antigen) methods (3, 6–8). Primary isolation of HCoV-229E in cell culture is technically challenging, and few have succeeded at isolating the virus from respiratory specimens (3, 6, 9, 10). The isolation of HCoV-229E from human plasma, to our knowledge, has never been reported.

During a suspected arbovirus outbreak in March 2016, HCoV-229E and human alphaherpesvirus 1 were isolated from the plasma of a Haitian child in 2016 with suspected arbovirus diseases. To our knowledge, this is the first description of HCoV-229E in human plasma, which is the focus of this article.
of HCoV-229E vRNA from Vero E6 cells was accomplished by Sanger sequencing following previously described methods (15) to attain the consensus sequence. In parallel, next-generation sequencing (NGS) with a cDNA library prepared using the NEBNext Ultra RNA library prep kit, and sequencing performed using a version 3 chemistry 600-cycle kit on a MiSeq platform (Illumina), produced the same consensus sequence.

Whole-genome sequence analyses of the Haitian HCoV-229E isolate, designated strain 229E/Haiti-1/2016, revealed close genetic relatedness (>99% nucleotide identity) to several American HCoV-229E strains reported in 2015 (the GenBank accession numbers of the three HCoV-229E sequences with the highest nucleotide similarities as of 22 July 2017 are KY983587, KY684760, and KY967357). Compared to the American strains, the Haitian HCoV-229E genome has unique nucleotide polymorphisms that result in changes within the deduced amino acid sequences of the replicase polyprotein 1ab, spike, accessory, membrane, envelope, and nucleocapsid proteins.

Accession number(s). The complete genome sequence of HCoV-229E strain 229E/Haiti-1/2016 has been deposited in the GenBank database under accession number MF542265.

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REFERENCES