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Draft Announcement

Title: Reference Echovirus 7 and 19 Genomes from Nigeria

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ABSTRACT

We describe the genomes of two Echovirus isolates from Nigeria as reference enterovirus species B genomes for the region. These Echovirus 7 and 19 genomes have 7,411nt and 7,426nt, and were recovered from sewage contaminated water (in 2010) and an acute flaccid paralysis case (in 2014), respectively.

Word count: 47 words

Keywords: Echovirus 7; Echovirus 19; Nigeria; Enterovirus Species B; Complete Genome

Echoviruses belong to Species B within the genus Enterovirus, Family *Picornaviridae*, Order *Picornavirales.* They have been recovered from clinical manifestations that range from respiratory disease to acute flaccid paralysis (1). Majority of the non-polio enteroviruses recovered in the RD and L20B cell line based algorithm recommended by the WHO (2), yield Enterovirus species B (EV-B) members. Here, we describe the genome of two EV-Bs (Echoviruses) from Nigeria as references for the region.

The two isolates [E7 from sewage contaminated water (2010) and E19 from a child with acute flaccid paralysis (2014)] were initially cultured in RD cell line, produced cytopathic effect and were subsequently, passaged twice in RD cell line before further analysis. Thereafter, the RNA genomes were isolated using the Total RNA extraction kit (Jena Bioscience, Jena, Germany). SCRIPT cDNA synthesis kit (Jena Bioscience, Jena, Germany) was then used to convert the RNA genomes to cDNA as recommended by the manufacturer. The genomes were subsequently amplified in overlapping fragments of 2 – 3kb using the Redload PCR kit (Jena Bioscience, Jena, Germany) and a combination of previously described primers (3-8). For each isolate, the overlapping genomic fragments were pooled and shipped to a commercial facility (MR, Texas, USA) where library preparation and NextGen sequencing was done. Library preparation was done using the Nextera DNA sample preparation kit (Illumina) following the

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manufacturer's user guide. Sequencing was done paired end for 300 cycles using the HiSeq system (Illumina). Assembly was done using the Kiki Assembler v0.0.9

The E7 and E19 genomes contain 7,411nt (2,194aa) and 7,426nt (2,196aa), respectively. The E7 genome has nucleotide base count of 2111, 1732, 1809 and 1759 for A, C, G and T, respectively. Hence, it has a G+C content of 47.8%. The E19 genome has nucleotide base count of 2108, 1716, 1831 and 1771 for A, C, G and T, respectively. Hence, the E19 genome also has a G+C content of 47.8%. The E7 genome is most similar to MG451805; another E7 recovered from sewage in the United Kingdom in 2016 but suggested to be of sub-Saharan Africa origin (9). The E19 genome on the other hand is most similar to KY792585; an E19 recovered in 1996 from the stool of a child with persistent diarrhea in India. In spite of their most similar genomes being from two different continents outside Africa, recombination analysis in both SimPlot version 3.5 and RDP4 show that the non-structural regions of both genomes are very similar and must have emerged from a pool of genomes that has been recombining over time. Considering both genomes were recovered in Nigeria in 2010 and 2014, this finding suggest the non-structural regions of both genomes might be indigenous to Nigeria and possibly sub-Saharan Africa.

Here, we describe the genomes of two EV-Bs from Nigeria. These will serve as reference genomes for future EV-B genomic studies in the region.

Accession number

The genomes described have been deposited in GenBank under the accession numbers MH732737 and MH745407.

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