P0821 Enterovirus D68 biennial circulation in New York, USA, 2014-2018

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Background: Enterovirus D68 (EV-D68) infection has been associated with severe respiratory illness and acute flaccid myelitis (AFM). Following a nationwide outbreak in the US in 2014, only limited EV-D68 detection was reported in 2016 and no data are available thereafter. The objectives of this study were to determine whether EV-D68 continued circulating in the Lower Hudson Valley, New York, and to compare the viral strains recognized since 2014 at regional, national and global levels.

Materials/methods: Nasopharyngeal (NP) specimens collected from 2013 through August 2018 from patients in the Lower Hudson Valley, New York were examined for Rhinovirus/Enterovirus (RhV/EV) by the FilmArray Respiratory Panel. Selected RhV/EV-positive and negative NP specimens were analyzed using two EV-D68-specific rRT-PCR assays, Sanger sequencing and a RNA-Seq-based metagenomic next-generation sequencing. Genomic sequences of all EV-D68 strains since 1962 were also retrieved from the GenBank and analyzed for strain genotypes (clades) using genome-based algorithms.

Results: A total of 2,264 NP specimens from 2013 through 2018 were examined for EV-D68. EV-D68 was detected in NP samples collected in 2014 (29.4%, 94/320), 2016 (26.6%, 160/602), 2017 (0.9%, 5/562) and 2018 (14.4%, 80/556), respectively, but not in those collected in 2013 (n=25) or 2015 (n=199). Comparative genomic analysis confirmed that distinct EV-D68 strains were circulating and caused outbreaks in New York in 2014 (subclades B1 and B2) and 2016 (subclade B3) with a relatively high viral load in patient specimens. Only low levels of clade D strains were detected in 2017. The majority of EV-D68 strains (92.3%, 24/26) circulating in 2018 belonged to subclade B3. Bioinformatics analysis of 2,746 sequences worldwide (1962-2018) revealed temporal and spatial diversity in EV-D68 population but a shared global evolutionary trend.

Conclusions: We reported a biennial regional outbreak and circulation of EV-D68 in the lower Hudson Valley, New York, USA from 2014 to 2018. The establishment of distinct viral strains and variable levels of circulation provides essential information for surveillance, diagnosis and control of EV-D68 infection in the US and worldwide.