3-2-2017

Upsurge of Enterovirus D68 Infection in the Lower Hudson Valley, New York, 2016

Taliya Farooq
New York Medical College, taliya_farooq@nymc.edu

Esther C. Yoon
New York Medical College, esther_yoon@nymc.edu

Jian Zhuge
New York Medical College

Changhong Yin
New York Medical College, changhong_yin@nymc.edu

Wei-Hua Huang
New York Medical College, weihua_huang@nymc.edu

See next page for additional authors

Follow this and additional works at: https://touroscholar.touro.edu/nymc_fac_posters

Part of the Virus Diseases Commons

Recommended Citation

This Poster is brought to you for free and open access by the Faculty at Touro Scholar. It has been accepted for inclusion in NYMC Faculty Posters by an authorized administrator of Touro Scholar. For more information, please contact jogrady@nymc.edu.
MATERILAS & METHODS

In 2014, a nationwide outbreak of severe respiratory illness associated with Enterovirus D68 was reported in the US. There were no EV-D68 cases during the 2015 enterovirus season per CDC’s National Enterovirus Surveillance System (NESS).

Upsurge of EV-D68 infection were reported in Europe in 2016 [1-2], but there were only sporadically cases in the US per CDC [3]. The aims of this study are to determine if EV-D68 was circulating in patients in the Lower Hudson Valley, New York in 2016, and if so, whether there were any significant variations in the virus genome or the severity of clinical diseases.

RESULTS

Detection of RhV/EV by FilmArray RP assay, 2014-2016. A total of 11,715 NP specimens were analyzed. The overall positivity was 49.4% by RP, with ~25% positive for RhV/EV (Fig. 1 & Table 1).

EV-D68 detection, 2014-2016. EV-D68 was confirmed in 94 cases in 2014 and none in 2015 (Fig. 2).

EV-D68 was detected in 1/108 (0.9%) RhV/EV-positive NP specimens from January through May 2016, and 159/442 (36.0%) NP specimens from June through October 2016 by rRT-PCR (Fig. 2).

EV-D68 rRT-PCR and Next-Generation Sequencing. NP specimens positive for RhV/EV were analyzed with an EV-D68-specific rRT-PCR assay [4] and next-generation sequencing (NGS) on the Illumina MiSeq [5].

Phylogenetic analysis was performed using the BioNumerics v7.6. (Applied Maths, Belgium).

CONCLUSIONS


Multiple mutations in the viral genomes of B3 strains and variations in the spectrum and severity of clinical diseases were observed.

Enhance surveillance and more accurate lab diagnostic testing for detection of EV-D68 in clinical specimens are warranted.

REFERENCES


* Contributed equally to this work.