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

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MATERIALS & METHODS

A new subclade B3 strain, which was ~4.5% divergent in nucleotides from the B1 causing outbreak in 2014, was identified from June through October 2016 by rRT-PCR (EV-D68 detection, 2014-2016). 11,715 NP specimens were analyzed. The overall positivity was 49.4% in 2014 and none in 2015 (Detection of RhV/EV by FilmArray RP assay, 2014-2016). Positive for RhV/EV were analyzed with an EV-D68-specific rRT-PCR (Applied Maths, Belgium). Phylogenetic analysis was performed using the BioNumerics v7.6 (Applied Maths, Belgium).

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 159/1442 (36.0%) NP specimens from June through October 2016 by rRT-PCR (Table 2). EV-D68 genomes and phylogenetic analysis of 2016 strains. Complete EV-D68 genomes from 22 patient specimens in 2016 were obtained. A new subclade B3 strain, which was ~4.5% divergent in nucleotides from the B1 causing outbreak in 2014, was identified (Table 3, Fig. 3 & Fig. 4).