

In-field detection and characterization of B/Victoria lineage deletion variant viruses causing early influenza activity and an outbreak in Louisiana, 2019

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Abstract

In 2019, the Louisiana Department of Health reported an early influenza B/Victoria (B/VIC) virus outbreak. As it was an atypically large outbreak, we deployed to Louisiana to investigate it using genomics and a triplex real-time RT-PCR assay to detect three antigenically distinct B/VIC lineage variant viruses. The investigation indicated that B/VIC V1A.3 subclade, containing a three amino acid deletion in the hemagglutinin and known to be antigenically distinct to the B/Colorado/06/2017 vaccine virus, was the most prevalent circulating virus within the specimens tested. This work underscores the value of portable diagnostics and sequencing platforms for rapid, onsite pathogen characterization.

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