1784. The Value of a Systematic Screening of Influenza Virus and Vaccination on Emergent Admissions to a Cardiac Intensive Care Unit (C-ICU)

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Session: 170. Viral Diagnostics
Friday, October 4, 2019: 12:15 PM

Background. Influenza is a potential inducer of acute cardiac events. However, the incidence of influenza in patients admitted to a C-ICU, the accuracy of clinical suspicion and the compliance of influenza vaccination of high-risk patients, are not well known. Objectives: To evaluate the incidence of influenza at C-ICU admission during influenza season, the potential underdiagnosis and the vaccination rate. 

Methods. A retrospective review of influenza diagnostics pre- and post-reinforcement of proper test procedures was performed across a university healthcare system, including a 650-bed tertiary care and 100-bed cancer hospital. During August 2018, providers and staff involved in testing were interviewed to describe their practices. Gaps were addressed in September 2018 with flyers outlining procedures, providing optional specimen collection swabs for NAAT vs. PCR. Units initially lacked appropriate sampling supplies for NAAT. Providers complained of needing to confirm negative NAAT for inpatients with questionable symptoms, and supported the reinforcement to target follow-up PCR in those clearly symptomatic or immunocompromised. Concordance with NAAT and PCR post- and pre-reinforcement of proper test procedures when both methods were done is shown in the Figure.

Results. Prior to reinforcement, most hospital staff were unaware of the optimal specimen type and collection swab for NAAT vs. PCR. Units initially lacked appropriate sampling supplies for NAAT. Providers complained of needing to confirm negative NAAT for inpatients with questionable symptoms, and supported the reinforcement to target follow-up PCR in those clearly symptomatic or immunocompromised. Concordance with NAAT and PCR post- and pre-reinforcement of proper test procedures when both methods were done is shown in the Figure.

Conclusion. Diagnosis of influenza is important in hospitalized patients. In addition to selecting a sensitive assay, attention to optimize test performance is critical. Our results suggest there is a need to train and monitor clinicians in identifying who to test and when, what specimen to collect and how, and in interpreting results.

Disclosures: Kimberly Hanson, MD, MHS, BioFire: Consultant, Grant/Research Support; T2 Biosystems: Consultant.

1786. An Automated Method to Assess Oligonucleotide Primer and Probe Complementarity to Genomic Targets in Infectious Disease qPCR Assays

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Session: 170. Viral Diagnostics
Friday, October 4, 2019: 12:15 PM

Background. Dengue is the most widespread arboviral disease globally. Serotyping of dengue viruses and their genotyping is important in tracing the epidemiology of the disease, monitoring trends and anticipating the possibility of outbreaks in a community.

Methods. This study is a retrospective analysis, based on data from a tertiary care center from Delhi, India and their correlation with reported literature on circulation and outbreaks of dengue in this region of North India since 1996, when the first virus isolation confirmed outbreak of dengue was reported by our virology laboratory (an Apex Laboratory of the National Vector Borne Disease Control Program, Government of India). Circulating serotypes of DENV were detected and identified from serum samples of suspected dengue patients with fever of 5 days duration or less, by virus isolation in cell culture and/or by real-time or conventional reverse transcription poly- merase chain reaction (PCR). Representative serum samples of patients with suspected dengue with duration of fever <5 days were inoculated onto the C6/36 clone of Aedes aegypti cells, and the isolates were identified by indirect immunofluorescence using serotype-specific monoclonal antibodies. Sequencing was done for representative strains as required.

Results. The predominant serotypes identified were DENV 2 (1996), followed temporally by DENV 1 (1996–1997), DENV 3 (2003–2007), DENV 4 (2008–2012), DENV 2 (2013–2015), and DENV 3 (2016–2018). In 2003, Delhi became hyper-endemic for dengue, with all dengue serotypes co-circulating. Predominant serotypes continued to circulate for 3–6 years. Outbreaks occurred either in the year a serotype was introduced after a gap of a few years to become the predominant serotype, or in the following year; except in 2015, when there was a genotypic lineage change in a DENV 2 serotype which had been predominant since 2 years prior to the outbreak year.

Conclusion. Re-introduction of a dengue serotype which was out of circulation for some years can be predicted using limited patient data and epidemiologic data. Close monitoring of circulating virus strains, particularly at either end of the transmission season, may help in early prediction of the trend for a given year, providing an opportunity to put in place control measures well in time.

Disclosures. All authors: No reported disclosures.