Methods. A retrospective review of influenza diagnostic 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 optimal sampling supplies, and EHR prompts for appropriate indications. A subset of UU patients tested by both NAAT and PCR within a 48 hour period were identified from the corporate data warehouse as Pre (September 2016 through March 2018) or Post reinforcement (October 2018 through March 2019). Agreement within PCR/NAAT test pairs was determined, with chart reviews of patients with discrepant results. Time of testing from the onset of symptoms was noted, and flu-like symptoms were defined as fever (>38°C) and cough or sore throat.

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 pre- and post-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.

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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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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. Prospective study at a tertiary institution including all patients admitted to a C-ICU during 2017–2018 flu season. A nasopharyngeal swab was collected at admission from all patients who consented (198/201, 98.5%) and tested using Xpert® test procedures when both methods were done is shown in the Figure. Agreement within PCR/NAAT test pairs was determined, with chart reviews of patients with discrepant results. Time of testing from the onset of symptoms was noted, and flu-like symptoms were defined as fever (>38°C) and cough or sore throat.

Results. The predominant serotypes identified were DENV 2 (1996), followed temporally by DENV 1 (1997–2002), DENV 3 (2003–2007), DENV 1 (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 a few years can precipitate an outbreak. Analysis of temporal patterns and 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.

1785. Dengue Outbreaks and Predominant Circulating Virus Serotypes and Genotypes over More Than Two Decades in a Hyper-endemic Region

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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 polymerase 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 albopictus 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 (1997–2002), DENV 3 (2003–2007), DENV 1 (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 a few years can precipitate an outbreak. Analysis of temporal patterns and 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.

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none of the identified mismatches are predicted to lead to false negativity or under quantification in our current CMV qPCR assay.

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1787. The Effects of a Systemwide Diagnostic Stewardship Change on West Nile Virus Disease Ordering Practices
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Background. Neuroinvasive West Nile Virus (WNV) often leads to prolonged neurological deficits and carries a high case fatality rate. The CSF IgM (MAC-ELISA) is preferred over the CSF nucleic acid-based test (NAAT) by the CDC due to its higher sensitivity. However, our hospital system was observed to have an over utilization of NAAT testing compared with MAC-ELISA testing. The primary objective was to compare the number of MAC-ELISA and NAAT WNV tests ordered before and after a diagnostic stewardship intervention. The secondary objectives were to determine whether this change to lead to any cost savings and increased detection of probable cases of WNV-ND.

Methods. In an effort to increase the use of the MAC-ELISA and to decrease unnecessary NAAT testing, the NAAT test was removed in April 2018 from the test menu in the electronic health record of a health system comprising five hospitals in the Maryland and Washington, D.C. area. NAAT testing remained possible via a paper order form. This study was a retrospective review of WNV testing done on CSF samples from July 2016 through December 2018. The seasonal and yearly number of total tests, positive tests, and total costs were determined from the period of July, 2017 to April, 2018 and were compared with May, 2018 to January, 2019. A paired t-test was performed to evaluate for differences in total testing, total positives, and total costs during non-winter months before and after the intervention.

Results. A total of 12.59 MAC-ELISA tests/month (95% CI: 10.29, 14.89) increased to 41 tests/month (95% CI: 34.35, 47.65) which was significantly different (P < 0.001). In contrast, there were 46.23 NAAT tests/month (95% CI: 39.55, 52.91) which decreased to 0 NAAT tests/month after the intervention (P < 0.001). This resulted in an average decrease in WNV test spending from $7200 per month to $471 per month (P < 0.001). Preceding the intervention in test ordering, 0.23% of WNV CSF tests were positive (NAAT+MAC-ELISA) while 2.44% WNV CSF tests were positive after the intervention (<0.001). In contrast, there were 46.23 NAAT tests/month (95% CI: 39.55, 52.91) which decreased to 0 NAAT tests/month after the intervention (P < 0.001). This resulted in an average decrease in WNV test spending from $7200 per month to $471 per month (P < 0.001). Preceding the intervention in test ordering, 0.23% of WNV CSF tests were positive (NAAT+MAC-ELISA) while 2.44% WNV CSF tests were positive after the intervention (P < 0.03).

Conclusion. Elimination of electronic WNV NAAT ordering is an effective way of decreasing inappropriate WNV NAAT testing, decreasing associated costs, and may lead to improved diagnosis of WNV-ND.

1788. The Utility of Next-Generation Sequencing for Detection of Candidate Pathogens in Bronchoalveolar Lavage Fluid from Pediatric Patients with Respiratory Failure
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Background. In the field of infectious diseases, identification of etiologic pathogen is essential for definitive diagnosis and decisions regarding appropriate management. Bronchoalveolar lavage fluid (BALF) is considered a sterile type of specimen that is suitable for detecting pathogens of respiratory infections. Recently, next-generation sequencing (NGS) has been applied in the field of infectious diseases and has enabled us to identify pathogenic microorganisms comprehensively. The aim of this study was to comprehensively identify pathogens using NGS in BALF samples from immunocompetent pediatric patients with respiratory failure.

Methods. Ten patients hospitalized in the pediatric intensive care unit with respiratory failure were included. BALF samples obtained in the acute phase were used to prepare DNA- and RNA-sequencing libraries. The libraries were sequenced on MiSeq, and the sequence data were analyzed using metagenome analysis tools.

Results. A mean of 2,041,216 total reads were sequenced for each library. A significant number of four types of bacterial reads was detected in three BALF samples with DNA-sequencing, whereas pathogenic respiratory viruses were detected in seven of 10 patients with RNA-sequencing. Candidate pathogens were detected in three patients in whom etiologic agents were not identified by conventional methods. A summary of the detected pathogens is listed in Table 1. Sequence coverage and depth of each reference bacterial and viral genome are shown in Figures 1 and 2, respectively. The complete genome of enterovirus D68 was identified in two patients without underlying diseases, and phylogenetic analysis suggested that both strains belong to subclade B3, which is an epidemic strain that has spread worldwide in recent years.

Conclusion. We demonstrated the utility of the NGS-based approach for detection of candidate pathogens in BALF from pediatric patients with severe respiratory failure. Our results suggest that NGS can be applied for comprehensive molecular diagnostics as well as surveillance of pathogens in the field of infectious diseases.

Table 1. Sequence reads using NGS for detection of pathogens from BALF samples

| Pathogen | NGS reads | Conventional methods |
|----------|-----------|---------------------|
| E. coli  | 1000 reads | 0 reads |
| S. aureus| 500 reads  | 0 reads |
| H. influenzae| 200 reads | 0 reads |

Disclosures. All authors: No reported disclosures.

Figure 1. West Nile virus CSF testing (A) and costs (B) from July 2016 to January 2019. A red arrow indicates the time of removal of WNV NAAT from the order test menu.