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 optimal specimen types and collection swabs for NAAT vs. PCR. Units initially lacked appropriate sampling supplies for NAAT. Providers complained of needing to confirm negative NAAT for patients 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)
Galiazar Alicia, PharmD, PhD1; Lourdes Vicent, MD, MD2; Iago Sousa-Casanovas, MD3; Mariela Valero, MD, PhD2; Miriam Juárez, MD2; Pilar Catalán, PharmD3; Carolina Devesa-Cordero1; Vanessa Bruria, MD3; Manuel Martinez-Selles, MD, PhD3; Emilio Bouza, MD, PhD2; Patricia Muñoz-García-Paredes, MD PhD2; Hospital General Universitario Gregorio Marañón. Clinical Microbiology and Infectious Diseases Department. Madrid, Spain; 2Hospital General Universitario Gregorio Marañón. Cardiology Department, Madrid, Spain

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Results. Influenza was detected in 14/198 (7.1%) patients (11 FluA, 3 FluB) and initial 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® Flu/RSV assay. Clinical data were registered.

Conclusion. Seven percent of patients admitted to the C-ICU had influenza, only half of the influenza cases diagnosed were suspected at admission and only half of the patients with indication for flu vaccination, received the vaccine. A clinical score to recognize influenza in these patients is needed.

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1785. Dengue Outbreaks and Predominant Circulating Virus Serotypes and Genotypes Over More Than Two Decades in a Hyperendemic Region
Lalit Dar, MD; Aashish Choudhary, MD; Megha Brijwal, MD; Monalisa Sabu, MD; Janya Sachdev, MD; All India Institute of Medical Sciences, New Delhi, India

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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 data can help to identify patterns of 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.

1786. An Automated Method to Assess Oligonucleotide Primer and Probe Complementarity to Genomic Targets in Infectious Disease qPCR Assays
Rohita Sinha, PhD; Mark Wissel, PhD; Katelyn Bartlett, MS; James Granthan, BS; Steve Kleboeker, DVM, PhD; Viracor Eurofins, Lee's Summit, Missouri

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Background. Success of real-time TaqMan PCR (qPCR) in detecting pathogen targets and quantifying pathogen load is dependent upon frequent assay monitoring. This is due to the high degree of complementarity needed between primers/prob es and genomic targets for assay accuracy and ii) natural pathogen variation and evolution. Failure to monitor and refine may result in false negativity or under quantification. Here we present a bioinformatics tool to identity potential problems resulting from newly discovered genomic mutations in primer/probe regions.

Methods. The tool performs an unbiased and automated search of the NCBI database, collects relevant genomic sequences based on user-defined Taxon-ID and executes a Python program to discard synthetic sequences. A profile of primer/probe sequence complementarity to targets is then generated. This profile can be used for any microbe, here we present results for our laboratory's SARS-COV-2 and genotyping targets for assay accuracy and ii) natural pathogen variation and evolution. Failure to monitor and refine may result in false negativity or under quantification. Here we present a bioinformatics tool to identify potential problems resulting from newly discovered genomic mutations in primer/probe regions.

Results. The tool retrieved 8,732 sequences from NCBI and compared these to the CMV qPCR primers and probes. The tool found 2,501 alignments between the primers/probes and the downloaded genomic data (~15 minutes to finish (6 CPUs)). A total of 64% (1,624/2,501) of BLASTn alignments were exact matches between all primers/probes and viral genomic sequences. 17.5% (439/2,501) of alignments had no match at either 5' or 3' terminus, and 1% (25/2,501) of alignments had two mismatches with the primers/probes. Similar results were found using a primarily manual approach (which took approx. 5 hours computing time and 20 hours of labor).

Conclusion. This new bioinformatics approach performed indistinguishably vs. a manual approach and did so in minutes rather than days. Both methods led to the conclusion that, by virtue of our design involving overlapping primers and probes,