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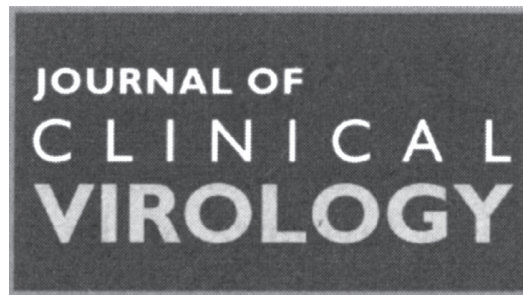
Abstracts of the 19th Annual Meeting of the European Society for Clinical Virology
14th–17th September 2016, Lisbon

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Abstracts of the 19th Annual Meeting of the European Society for Clinical Virology, 14th–17th September 2016, Lisbon

Abstract no: 75

Presentation at ESCV 2016: Oral 1

Medico-economic impact of the rapid diagnosis of influenza in paediatric emergency department by using a new sensitive chromatographic immunoassay



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Background: The practicability of rapid immunochromatographic antigen detection tests (RIADT) for the diagnosis of influenza allows their use by non-trained healthcare professionals, even beside the bed of the patient. Newly designed assays such as the Becton Dickinson (BD) Veritor™ System for Rapid Detection of Flu A + B have shown improved analytical performances. However, the medico-economic impact of their direct implementation in clinical wards has been poorly evaluated.

Objectives: (1) To measure the impact of the rapid diagnosis of influenza by using the Veritor™ System directly in the paediatric emergency room, on the care of patients and notably on the reduction of supplementary investigations and antibiotics during the 2015–2016 winter season, and (2) to verify the analytical performances of this new test.

Study design: A nasopharyngeal aspirate was performed to all the patients aged between 0 and 18 years consulting at the paediatric emergency department of the University Hospital of Saint-Etienne during the 2016 influenza season. The presence of influenza A and B viruses was tested with the Veritor™ System in the emergency room 24/7. The clinical specimen was also sent to the laboratory in order to perform routine tests in the opening hours, including the detection of viral antigens by immunofluorescence (bioMérieux) or of viral RNA by using a laboratory-developed RT-qPCR assay on the BD MAX platform. In case of discrepant result between the different assays, the final diagnosis was assessed by the RT-qPCR assay. Before performing the Veritor™ System, the clinician was asked to fill in a questionnaire listing the tests that he/she would have prescribed in the absence of the rapid testing; the same questionnaire was completed after the result of the Veritor™ test was available.

Results: A total of 514 patients (sex ratio M/F: 1.11; median of age 2.7 years) were included between January 7 and March 19 2016. Comparative results between the RIADT and the routine assays were available for 477 specimens, including 45 and 185 positive ones for influenza A and influenza B, respectively. For influenza virus A, the sensitivity, specificity, negative predictive value and positive predictive value were 94.9, 98.2, 96.4 and 97.4%, respectively; for influenza virus B, they were 97.4, 96.4, 98.2 and 94.9% respectively. The use of the RIADT at the emergency room saved the prescription of: 51.7% of C-reactive protein (CRP) dosage in capillary blood, 47.9% of blood sampling, 49.2% of CRP measurement, 57.4% of procalcitonin dosage, 68.8% of blood culture, 41.6% of urine test strip, 79.2% of cytobacteriological examination of urine, 69.0% of chest X-rays, 77.8% of lumbar puncture, 43.8% of hospitalization and 70.1% of antibiotics.

Conclusions: The excellent analytical performances of the Veritor™ System allow its use as point-of-care test to perform an accurate and rapid diagnosis of influenza at the paediatric emergency room. In addition to deliver a rapid etiological diagnosis, this strategy was found to save the prescription of a considerable amount of unnecessary tests and antibiotics.

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Presentation at ESCV 2016: Oral 2

Molecular characterization of human rhinovirus in Portugal: 2014–2015 season



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Background: Human rhinoviruses (HRV) frequently cause mild upper respiratory tract infections and more severe disease manifestations such as bronchiolitis and pneumonia. Plays an important role in asthma and chronic lung disease exacerbations. Genetic characterization of HRVs detected by molecular methods has revealed much greater diversity, enabling the identification of three species (HRV-A, HRV-B and HRV-C) and a great number of types. The aim of this study is to characterize HRV detected in respiratory specimens from influenza-like illness cases (ILI), received in

the scope of the Portuguese Influenza Surveillance Program, during 2014–2015 season in Portugal.

Methods: During the 2014–2015 season, 411 nasopharyngeal swabs negative for influenza were tested for HRV in a multiplex PCR [1]. 18% (75/411) of the samples were positive for HRV, and from this 83% (62) were sequenced by a nested RT-PCR [2]. Nucleotide sequences of the VP4/VP2 region were used for genotyping and phylogenetic tree construction in Mega 6.0. Demographic and clinical data (according to EU ILI case definition) were recorded in a questionnaire.

Results: HRV were detected throughout the study period, between week 40/2014 (October) and week 9/2015 (March) with a peak in January 2015. Phylogenetic analysis showed that 45% (28/62) strains belonged to species HRV-A, 15% (9/62) to species B and 40% (25/62) to species C. Overall were identified 35 different types. All species co-circulated in Portugal with the exception of the Algarve and Açores, being HRV-A predominant in north region and HRV-C predominant in Alentejo. HRV positives cases had a median age of 42.5. HRV-C were the most frequently detected in all age groups, apart from young adults aged 15 to 44. In this age group HRV-A were identified in 73% (16/22). HRV-B was detected sporadically in all age groups, except in children (5–14 years old). HRV was found in similar proportions in both genders (52% in female; 48% in male). Data on influenza vaccination was reported in 51 HRV positive cases, but only 9 (18%) had been previously vaccinated. Information on chronic diseases was reported in 54 cases, of these 15 (28%) had a chronic disease (mainly cardiovascular or diabetes). HRV was detected in 4 pregnant women, 14% (4/28). Cough, myalgias, weakness and fever were the most frequent symptoms reported by HRV confirmed cases.

Conclusions: During 2014–2015 was observed a co-circulation of the three species of HRV (A, B and C) with a predominance of HRV-A followed by the recently identified species C. A wide genetic diversity of 35 types was identified, with a higher diversity among HRV-A. HRV was most frequently diagnosed in adults. Our study included few children under 5, preventing conclusions about this group. Diabetes and cardiovascular disease were found as a possible risk for HRV infection, highlighting the relevance of respiratory disease prevention measures that should be undertaken. This was the first study to attempt the genetic diversity of rhinovirus circulating in Portugal during a winter season in ILI cases. Further studies in the general population and in high-risk groups for severe respiratory disease will aid knowledge in HRV epidemiology and exacerbation of respiratory infections.

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<http://dx.doi.org/10.1016/j.jcv.2016.08.003>

Abstract no: 224

Presentation at ESCV 2016: Oral 3

Illuminating influenza epidemiology in Scotland using next generation sequencing

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Influenza is one of the most important respiratory pathogens and is a major cause of mortality and morbidity worldwide every

year. Influenza A is a n RNA virus consisting of eight segments, the segmented nature of the genome allows for reassortment to occur, occasionally producing antigenically novel viruses capable of causing influenza pandemics. The ECDC Scottish influenza laboratory currently characterise influenza A isolates by sequencing the HA1 region of the haemagglutinin gene, which allows isolates to be classified into viral clades.

One hundred and fifty clinical isolates positive for influenza A(H3N2) from the 2014/15 influenza season were sequenced by both Sanger sequencing of HA1, in addition to whole genome sequencing using next generation sequencing (NGS) technology on the Illumina MiSeq platform. Influenza nucleic acid was amplified using a single-reaction method, which simultaneously amplifies all eight segments of the influenza genome. This amplified product was then utilised for NGS.

Full segment coverage was achieved for the smaller segments (NS and MP) of all 150 isolates, however coverage generally decreased as the size of the segment increased. In total, 100% genome coverage was achieved in 71 samples, with 100 samples having >90% genome coverage. Sequencing of the haemagglutinin gene was adequate for clade calling for all 150 isolates and phylogenies of the haemagglutinin gene constructed using NGS data had better resolution than those produced using Sanger sequencing of HA1 alone. In addition, using whole genome data we were able to analyse isolates for evidence of viral reassortment and identified a number of intra-clade reassortments in our dataset, involving both the surface glycoproteins and internal genes. The majority of these occurred sporadically, however one reassortant virus persisted in the population.

Current routine influenza surveillance relying on sequencing of the HA1 region allows for classification of influenza A viruses into viral clades. Whole genome sequence data produced using a single-reaction method and NGS allows for economical generation of viral clade classification in addition to sequence data from the other seven segments. In our small dataset we identified a number of viral reassortments, suggesting that such events may occur more often than previously estimated.

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Abstract no: 195

Presentation at ESCV 2016: Oral 4

Long-term impairment attributable to congenital cytomegalovirus infection



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Introduction: Congenital cytomegalovirus infection (cCMV) is the most prevalent congenital infection worldwide and it may lead to symptoms at birth as well as long term sequelae. Limited data on long term sequelae are available, particularly in infants who are asymptomatic at birth and in many studies on long-term consequences a control group is lacking.

Aim and methods: A nation-wide retrospective cohort study was designed to assess the long term consequences of cCMV up to

