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polymerase chain reaction (RT-PCR) assay. One step RT-PCR was done to detect Rhinovirus C among positive cases.

**Results:** This study included 31 asthmatic children in exacerbations. They were 15 males (48.4%) and 16 females (51.6%). Their ages ranged from 7 months to 12 years with a mean and SD of (4.47 ± 3.15) years. Eight (25.8%) of the total population showed positive Rhinovirus RT-PCR test and 4 (50%) of the HRV positive patients were of the Rhinovirus C genotype (12.9% of the total population). HRV positive patients showed higher positive family history of bronchial asthma (p = 0.002), higher mean values of respiratory rate (p = 0.001) and temperature (p = 0.001), but lower mean value of oxygen saturation (p = 0.011). There were statistically significant differences regarding the exacerbation severity (p = 0.024) and outcome (p = 0.048).

Conclusion: HRVs are major triggers of asthma exacerbations among Egyptian children. The newly described HRV-C genotype accounts for a significant proportion of HRV-associated asthma exacerbations. Further studies on a larger scale are needed for HRV-C and other possibly undiscovered HRV genotypes.

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20.005

**A cross-sectional serosurvey of influenza A and B virus-specific IgG antibodies in Emirati children**

A. Alsuwaidia, L. Al-Mekainib, S. Kamalb, H. Narchic, A.-K. Souidd

a United Arab Emirates University, Al Ain/AE
b Abu Dhabi Health Services Company (SEHA), Abu Dhabi/AE
c United Arab Emirates University, Al Ain, UAE, Pediatrics, Al Ain, UAE/AE

d **Purpose:** Young children are at increased risk of severe influenza disease and are likely to benefit from annual vaccination. Nevertheless, vaccine administration remains infrequent. The study objectives were to measure serologic immunity against these viruses and to plan for influenza vaccination strategy for the region.

**Methods & Materials:** This cross-sectional study involved unselected cohort of children who attended the Well-Child-Care Program of Ambulatory Healthcare Services (Al-Ain, UAE) between July 2014 and September 2015. Serologic immunity (RIDASCREEN® IgG, R-Biopharm AG) for influenza A and B viruses was measured in 236 Emirati children (44 females). Medical records were reviewed for influenza immunization history.

**Results:** The mean ± SD age (y) was 4.4 ± 1.9 (median = 4.1, range = 1.9-12.5). Only one child (7.8 y) had documentation of receiving the influenza vaccine once five years prior to the study sample collection; her serology was negative for influenza A virus and positive for influenza B virus. Overall, the percentage of children who were seropositive for influenza A IgG was 13.6%, equivocal 6.3%, and negative 80.1%. The corresponding values for influenza B IgG were 27.8%, equivocal 8.3%, and negative 63.9%, respectively. The percentage of children who were seropositive for either influenza A or B IgG was 35.7% and for both was only 3.6%.

**Conclusion:** The data demonstrate the majority of children are serologically naïve and, thus, are more susceptible to severe influenza disease. Therefore, annual influenza vaccine is advisable especially for young children. Vaccine policies should target the most common strain in the region.

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20.006

**Genetic characterization of isolated Influenza C viruses in the Philippines, 2006-2012**

V.L.F. Arguelles

Research Institute for Tropical Medicine, Virology, Muntinlupa, ALABANG/PH

**Purpose:** Influenza C virus (ICV) causes mild acute respiratory infection although some studies have reported severe illness causing hospitalization due to pneumonia. Only one study has been reported on ICV infection in the Philippines (Odagiri T et al., 2015). In this study, we had focused on the detection of ICV from 2006 to 2012 in the Philippines and its genetic lineage identification.

**Methods & Materials:** Nasopharyngeal and/or oropharyngeal swabs were collected through national Influenza-Like Illness (ILI) surveillance from 2006 to 2012. Samples were inoculated into MDCK cells and screened for influenza A and B. Samples confirmed negative for influenza A and B were tested by RT-PCR for ICV. Partial sequencing of hemagglutinin esterase (HE) and nonstructural protein (NS) genes was conducted.

**Results:** Influenza C virus was detected in 33 of 325 samples negative for Influenza A or B viruses (IAV, IBV) from the total of 58,668 samples collected from 2006 to 2012. Thirty one out of Thirty three (31/33, 94%) of cases were from children under five years old and were detected during the influenza season. Phylogenetic analysis of the HE gene using the Neighbor-joining method showed that all 33 strains formed distinct clusters within C/Sao Paulo/378/82 strain lineage.

**Conclusion:** Influenza C virus was found to be a cause of ILI in young children. Continued surveillance for ICV will help to better understand the epidemiology, including seasonality, severity and risk factors for the disease in the tropical zone.

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20.007

**High-throughput bead based suspension array for the detection of acute respiratory viral pathogens among children aged <5 years in Pakistan**

F. Aziza, J. Samad, I. Rizvi, A. Sami, S. Qureshi, I. Nisar, N. Brown, F. Jehan

a Aga Khan University, Karachi/PK
b Salisbury NHS trust, Salisbury/UK

d **Purpose:** Viruses play an important role in causing respiratory infections in children worldwide. The burden of viruses in respiratory infections among children in Pakistan is unknown, largely due to absence of good quality diagnostic facilities. Rapid detection and identification of these pathogens, having potential to cause pandemics is important to restrict the burden of viral pathogens among children. Advanced molecular biology techniques offer great advantage as they are more sensitive and have faster identification of respiratory pathogens. Magpix system is a high throughput multiplexed microsphere-based suspension array platform capable of analyzing up to 50 unique assays in a single microplate well. The purpose of this study was to identify the burden of common respiratory viruses among children less than 5 years of age with acute respiratory infections using Magpix platform.

**Methods & Materials:** Total 935 nasopharyngeal swabs of children with acute respiratory infections were collected in viral transport medium and spiked with Bacteriophage MS2 extrinsic control to check the efficacy of nucleic acid amplification. Nucleic
Acid extraction was performed with a MagNaPure LC instrument by using the total-nucleic-acid kit. Amplified products were identified using a bead-based suspension array for the detection of a wide range of viruses and subtypes. Data were analysed and reported as median fluorescent intensity using xMAP.

Results: Upon testing 935 nasopharyngeal swabs 451 (48%) were positive for enterovirus, 58 (6.2%) for parainfluenza type III and RSV, 48 (5.1%) metapneumovirus, 39 (4%) parainfluenza type IV, 35 (3.7%) bocavirus, 31 (3.3%) adenovirus, 30 (3.2%) coronavirus OC43, 20 (2.1%) parainfluenza type I, 18 (1.9%) influenza B, 16 (1.7%) H1N1 2009, 14 (1.5%) influenza A subtype H3, 9 (0.9%) corona HUK1, 8 (0.8%) parainfluenza type II, 7 (0.7%) corona NL63 and influenza A matrix, 5 (0.5%) corona 229E and 1 (0.1%) was positive for influenza A subtype H1.

Conclusions: Accurate and timely diagnosis of respiratory viruses in children using high throughput techniques has potential benefits, including improved treatment, decreasing the costs and reducing the empirical use of antibiotics thus preventing the emergence of anti-microbial resistance.

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20.009

Short period incidence sTudy of severe acute respiratory infection (SPRINT-SARI) initial data from a global observational study to better describe SARI epidemiology in critically ill patients

G.L. Carson a,*, L. Castle b, M. George c, P. Horby d, K.-S. Longuere e, L. Merson f, S. Murthy g, G. O‘neill h, R. Pardinaez-Solis e, S. Webb e

a University of Oxford (ISARIC), Nuffield Department of Medicine, Oxford, OXFORDSHIRE/UK
b University of Oxford, Nuffield Department of Medicine, Oxford/UK
c Monash University, Department of Epidemiology and Preventive Medicine, Melbourne/AU
d University of Oxford, Tropical Medicine-ERGO, Oxford/UK
e University of Oxford, ISARIC, Oxford/UK
f Oxford University, Infectious Diseases Data Observatory, Oxford/UK

g University of British Columbia, Faculty of Medicine, Vancouver/CA

Purpose: The majority of the burden of SARI-related mortality in developed countries is within intensive care units (ICUs). Increasingly, intensive care is becoming a standard element of the health care system in low and middle-income countries. However, the availability of high-quality data for critically ill patients in the early phases of a SARI outbreak is often poor. The lack of pre-populated ethics approvals, data sharing agreements, and research infrastructure makes this data often slow to help guide clinical practice for severely affected patients. This study aims to establish a rapid clinical research response capability for a future epidemics or pandemics of severe respiratory disease

Methods & Materials: This is a multi-centre, prospective, short period incidence observational study of patients in participating ICUs with SARI. The study period will comprise a 5 to 7-day cohort study enrolling patients, of all ages, meeting a modified SARI case-definition, who are newly admitted to the ICUs at participating sites. Through this, we have developed standardized case-report forms and a data-capture platform to better establish global readiness for evidence generation for critically ill patients with SARI.

Results: As of writing, we have ethics approval in 231 institutions, representing every continent and income group, with further expansion imminent. 115 sites have opened for recruitment and data collection for the first season in the Northern Hemisphere is currently completed with Southern Hemisphere collection to be completed between July and September 2016. The primary challenge in establishing this infrastructure is in obtaining ethical approvals and ensuring data quality is maintained. Preliminary results of the first season of recruitment will be presented.

Conclusion: Through SPRINT-SARI, we are creating a sustainable infrastructure for real-time data collection for better describing critically ill patients with SARI, in all regions of the planet. Creation of this enterprise will allow for effective risk-adjustment for SARI, as well as providing new insight into the changing epidemiology of SARI and management strategies among critically ill patients around the world. This infrastructure will iteratively improve over subsequent years to ensure data quality, accuracy of denominator projections, and applicability to diverse clinical contexts.

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20.010

Cyclical patterns of flu incidence dynamics and their associations with variations in the diseases of the circulatory system in USA for the years 1993-2007

B.D. Dimitrov

University of Southampton, Primary Care and Population Sciences, Southampton/UK

Purpose: Multicomponent (multiannual and seasonal) variations in the dynamics of flu incidence were found earlier in different countries (e.g., cycles of 1, 2-3, 5-6 and 11 years). The first aim of this study was to test the hypothesis for the existence of such cyclical patterns in the monthly flu incidence variations in USA (1993-2007). The second aim was to extend earlier research on possible associations of such variations in the flu incidence with the dynamics of most fatal diseases of the circulatory system (e.g., acute myocardial infarction, stroke) and validate such relationships across the 4 US census regions.

Methods & Materials: Monthly data on the hospitalised cases (incidence) with the diagnosis of flu, acute myocardial infarction (AMI) and stroke for the years 1993-2007 (n=180 months) were kindly provided by Foster and co-authors (Epidemiol Infect 2013; 141(4): 735–44, doi:10.1017/S0950268812002890). The incidence time series contained information as stratified by US census region and age groups (e.g., below and above 65 years). Autocorrelation, periodogram regression (PRA), trigonometric approximation and cross-correlation analyses were applied. Statistical significance was assumed at p<0.05. All analyses were performed by using routine (e.g., SAS, R) and specialised (6D-STAT) software packages.

Results: A total of 123,611 cases of influenza hospitalisation had been reported over the study interval of 180 months. A mean value per region per month ranged from 102 to 248 cases (maximum from 1800 to 4992). Cyclical patterns of flu incidence variations in all 4 census regions of USA were described, including seasonality (period T = 12 months) as well as transyears (e.g., T=17 months) and other low-frequency (longer) cycles (T = 27, T = 38 months). Linear ear lagged cross-correlations (lag-periods δT=0, 3, 12 months, etc.) were established with diseases of the circulatory system (e.g., AMI) in the same regions and time intervals, especially among patients aged 65 and over (e.g., Pearson’s r values from 0.17 to 0.36).