Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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Abstract No: 1754

Presentation at ESCV 2015: Oral 1

Characterization of the genome diversity of influenza virus associated with severe form of influenza in children

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Background: Viruses with RNA genomes, including influenza, have very high mutation rates that lead to important genetic diversity. While epidemiological and molecular studies have demonstrated that different influenza virus genotypes co-circulate and assessed antigenic modifications with time, little is known about their consequences on clinical outcomes. Our study aimed to linked within-host whole-genome deep sequencing data to different clinical outcomes.

Methods: Thirty-five respiratory samples from patients hospitalized in emergency pediatric or Intensive Care Units during 2010–2015 were used to sequence influenza virus whole genome sequences using Illumina NextSeq® platform. Clinical and biological metadata were collected reviewing the clinical files and patients were classified into severe influenza ($n=24$) and mild influenza ($n=17$). Four quality controls, constituted of quantified plasmids, were used to support the quality of the protocol of sequencing.

Results: Among these 35 analyzed samples, four samples were excluded because of low depth of coverage. Influenza virus diversity was first analyzed using Shannon diversity index calculated on the raw nucleotides frequency at each position with coverage >1000×. This analysis demonstrated few significant positions different between severe and mild groups for upper respiratory samples ($p<0.01$). Samples coming from lower respiratory tract had higher diversity than the ones in upper respiratory tract. Analysis of low frequency variants filtering sequencing errors are ongoing and should reveal clearer trend in terms of differential hotspots of diversity between patients group.

Conclusions: Very few differences were found in influenza whole genome diversity between patients with mild and severe influenza. However, statistical power was limited due to the different influenza subtypes and heterogeneity of sample types. Differences in genome diversity between lower and upper respiratory tract samples would be interesting to follow up and could provide some understandings on severe respiratory influenza pathogenesis.

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Abstract No: 1608

Presentation at ESCV 2015: Oral 2

Hypertonic saline nasal irrigation and gargling for the common cold: Results of a pilot randomised controlled trial

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Background: Viral upper respiratory tract infections (URTI) are very common and have a significant impact on individuals and the economy. Indirect clinical and lab evidence suggests that hypertonic saline nasal irrigation and gargling (HSNIG) may improve clinical and virological outcomes. We designed a pilot randomised controlled trial (RCT) to assess the feasibility of a larger RCT to estimate the effectiveness of HSNIG.

Methods: Adults (>16 years) within 48 h of URTI were randomised into intervention and control arms minimised by sex/smoking status. We proposed to enrol up to 80 to have at least 30 completers per arm. Intervention arm were shown a video, taught to prepare hypertonic saline (HS) with Cornish sea salt, and the highest comfortable concentration of HS ascertained (1.5–3.0%). Control arm participants received usual care. Those with symptoms >48 hours; chronic illness, allergic rhinitis, immunosuppression; pregnant; on antibiotics; or unable to perform HSNIG

were excluded. Recruitment rate was the primary outcome; sample return/diary completion, compliance, acceptability, quality-of-life, symptom duration and viral shedding were secondary outcomes. A self-taken nasal swab (Copan) was collected at baseline and first thing on days 1-4 to measure change in viral shedding. Validated symptom diaries were maintained up to 14 days or until they were well for two days or needed medical attention.

Results: Between November 2014–March 2015, we recruited 68 participants (average 3.4 participants/week); two were subsequently not included for analysis (on antibiotics; withdrew immediately after randomisation) (Intervention:Control = 32:34). Baseline characteristics were similar between arms. A virus was identified in 72.7% (48/66) of participants (rhinovirus 58.3%; coronaviruses 31.3%). There was no difference between arms in returning diaries/swabs. 81% opted for 3% HS. 89% thought HSNIG was very-moderately comfortable to perform. The intervention arm cleared URTI 1.9 days earlier than the control arm [mean (SD): 6.8 (2.2) vs. 8.7 (3.3) days, $p = 0.012$] with a lower average symptom score (13.2 vs. 16.9, $p = 0.089$). 93% felt HSNIG made a difference. More individuals in the control arm reported over-the-counter medication (86% vs. 50%, $p = 0.004$), and symptoms in individuals at home after them (70% vs 33%, $p = 0.004$). Where feedback was available 61%/25%/14% were likely/undecided/unlikely to use HSNIG in the future.

Conclusions: This pilot has demonstrated our ability to recruit and retain participants, and the acceptability of HSNIG. The significant reduction in duration, symptom severity, over-the-counter medication use and illness within households support the need for a larger RCT of this low cost intervention against the common cold.

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Abstract No: 1602

Presentation at ESCV 2015: Oral 3

Respiratory viruses and sudden death – Cause or innocent bystanders?

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Background: A retrospective study of sudden death cases in the community during 2010–2011 in Wales highlighted deficits in the reporting of respiratory viruses as cause of death despite supporting histological findings. The impact of respiratory viruses other than influenza on sudden death therefore remains underestimated.

Methods: A prospective study was undertaken from Autumn 2014 to determine the baseline level of respiratory pathogens in the respiratory tract of cases of sudden death in the community in all age groups. Pathologists were asked to collect swab samples from both the upper and lower respiratory tract of cases of sudden death at autopsy and submit them for a full respiratory screen by molecular methods and by bacterial culture.

Results: Respiratory viruses are frequently detected in the respiratory tract of cases of sudden death. In infants, the number of viruses detected increases and detection is often isolated to the upper respiratory tract.

Conclusions: The results of the molecular detection, culture and histology will be presented together with how these results were interpreted and reported on the final report to the coroner.

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Heine-Medin Medal

Abstract No: 1638

Viral population dynamics in the lower respiratory tract of ICU-admitted patients with influenza H1N1pdm09 infections during the 2014–2015 season in Northern Italy

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Background: During the 2014–2015 influenza season 75% of circulating influenza A strains in Europe were A/H3N2 and 25% were A/H1N1pdm09 (http://flunewseurope.org/). Few amino acid changes have been shown to increase transmissibility, replicative efficiency and tissue tropism range. For instance, amino acid changes at a single position (D222G/N) in the hemagglutinin (HA) gene were associated with increased lower respiratory tract (LRT) replication and worse clinical outcome (Kilander et al., 2010; Baldanti et., 2011; Piralla et al., 2011). The aims of this study were to: (i) describe the circulation of respiratory viruses in patients admitted to intensive care unit (ICU) and (ii) investigate the dynamics of viral population in the LRT of A/H1N1pdm09-infected patients using next generation sequencing (NGS).

Methods: During the 2014–2015 influenza season, respiratory samples from 88 ICU patients were analyzed. A diagnostic panel covering a broad range of respiratory viruses using quantitative real-time assays was performed (Piralla et al., 2014). The typing of Influenza A positive samples and sequencing of HA gene were performed as previously described (Piralla et al., 2011). NGS assay was performed in LRT samples and if available in samples of URT in order to monitor the dynamics of viral population. The analysis also focusing in the antigenic sites and amino acid involving in the receptor binding site of H1N1pdm09 strains (e.g. 222 codon).

Results: The median age of patients analyzed in this study was 62 years (range 4 months-83 years). Of these, 40 (45.5%) were infected by A/H1N1pdm09 strains and 15 (17.0%) by H3N2 strains. In 10 A/H1N1pdm09-infected patients, both samples from URT and LRT were available and viral load was significantly different in the two respiratory compartment ($p < 0.05$; median 3×104 vs 4.2×107 copies/ml respiratory sample). The NGS analysis was performed in these samples and in BAL samples ($n = 4$) from additional 4 A/H1N1pdm09-infected patients. NGS analysis showed the presence of multiple amino acid changes at position 222 suggesting the presence of mixed variants population in the LRT.

Conclusions: In the present study the H1N1pdm09 strains outnumbered H3N2 at ratio near 3:1 in patients admitted to the ICUs. In addition, our results support the hypothesis that the D222G/N changes may result from adaptation of viral receptor specificity to the lower respiratory tract and is associated with increased virulence.

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