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Abstract No: 1626

Presentation at ESCV 2015: Oral 16
Routine sequencing of enteroviruses in clinical materials identifies the presence of new Group-C enterovirus types in the Netherlands

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Background: Enteroviruses (EV) that infect humans belong to four EV groups (A–D) while the rhinoviruses can be divided into three genogroups (A–C). While rhinoviruses are seen primarily as respiratory pathogens, EV can cause a wide variety of diseases in affecting different organ systems. The fact that respiratory infections may be caused by EV infections has been clear since the identification of EV-D68 in 1962. During the summer and fall of 2014, the largest EV-D68 outbreak took place in the USA and it was shown that the strains of the EV-D68 outbreak in North America also circulated in Europe. EV types are defined by sequence divergence in the VP-1 capsid coding region. Ongoing mutations and recombination of the viruses is causing the appearance of new EV types. The newest additions to the expanding cloud of EV types were identified either as new variants found in the poliovirus surveillance programs or in respiratory secretions that were sampled as part of studies investigating respiratory viruses.

Methods: During a four-year period, all samples from patients with clinical presentations compatible with EV infections were screened using a laboratory-developed test. All EV isolates were subsequently genotyped by sequencing the VP1 region. To complete the data with samples from secondary hospital care and general practice, EV isolates from two regional laboratories were included in the routine genotyping program.

Results: Enteroviruses were detected in 657 clinical samples, and genotypes could be obtained from 607. EV was detected in 88 CSF samples, 7 vesicular fluids, 13 plasma and serum samples, 85 respiratory samples, and in 338 fecal samples. 76 were unidentified materials from general practice. Genotypes from all four EV groups were found with EV-D68 being the only representative of group D. Group C enteroviruses were found either in respiratory samples and/or fecal samples. In respiratory materials, we found the following group C enteroviruses: CV-A21 (n = 4), EV-C104 (n = 1), EV-C105 (n = 1), EV-C109 (n = 5), and EV-C117 (n = 1). Phylogenetic analysis shows that the four CV-A21 isolates are similar to the isolates found in North America in 2006. The EV-C109 isolates show 8–10% divergence from the other strains identified to date.

Conclusion: Enteroviruses are increasingly identified as causes or respiratory disease. Routine sequencing followed by sequencing provides essential information about which enteroviruses are circulating and how new genotypes evolve.

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Respiratory viruses in children attending Kindergarten

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Background: Many studies have investigated the prevalence of respiratory viruses in hospitalized children, but little is known about this prevalence outside hospitals.

Methods: We examined 1–6 years old children attending 2 kindergartens four times from 2012 to 2014 and included a total of 379 cases. Near 80% of all children participated in the study. The children were clinically examined by a pediatrician for signs of respiratory tract infection (RTI). A nasopharyngeal swap was used to collect a nasopharyngeal secret (NPS) at each examination and was analyzed by in-house real-time PCRs for a panel of 16 respiratory viruses.

Results: NPS was positive for at least one virus in 42.5% of the cases, of which 30.6% had one virus and 11.9% had two or more viruses. Rhinovirus was detected in 24.2% of the samples, enterovirus in 11.7% and parechovirus in 8.7%. Adenovirus, human bocavirus, coronavirus-OC43/NL63/229E, influenza A and B virus, human metapneumovirus, parainfluenza virus type 1–4 and RSV were each detected in 0.3–2.6% of the samples. In two-thirds of the examinations, the children had clinically signs of a RTI. Children with clear signs of a RTI had frequently 1 or more viruses (70%), compared to children with a milder RTI (40%) and children without signs of RTI (28%) (p < 0.001).

Conclusions: This is the first Norwegian study screening kindergarten children with an extensive panel of respiratory viruses along with clinical examination. Surprisingly two-thirds of children attending Norwegian kindergartens had mild or clear signs of an upper respiratory tract infection. Our results furthermore showed a high prevalence of picornaviruses (rhino-, entero- and parechovirus) in children with RTI, but even children without signs of RTI had often a positive PCR-test for picornaviruses.

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Impact of the implementation of a respiratory TaqMan® Array Card syndromic based diagnostic approach on clinical management of pediatric inpatients

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Background: Viral respiratory infections are a leading cause of hospitalization and death in children. Despite the viral origin antibiotics are often prescribed. In this study, we report the impact of implementing an in house TaqMan® Array Card (TAC) based respiratory panel in the diagnostic care of pediatric inpatients. We examined if TAC implementation was associated with consequent changes in clinical management: awareness of viral pathogens possibly causing severe LRTI’s, ordering molecular based tests instead of culture, and reduction of antibiotic use.

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Methods: Pediatric inpatients (0–5 year) were identified between January 1st, 2013 and December 31st, 2014 for whom a respiratory TAC analysis was ordered within 24 hours of admission. Patients with respiratory symptoms, were selected by All Patient Refined Diagnosis Related Group (APR-DRG). The TAC panel (implemented January, 2013) included testing for following 34 respiratory pathogens: influenza A virus (H1, H3, H7), influenza B virus, RSV A, RSV B, parainfluenza viruses 1 to 4, adenovirus, rhinovirus, enterovirus, bHPV, coronavirus (229E, HKU1, OC43, NL63, MERS), bacovirus, cytomegalovirus, paracovirus, mumps virus, measles virus, Mycoplasma pneumoniae, Chlamydia pneumoniae, Chlamydia psittaci, Bordetella pertussis, Bordetella parapertussis, Bordetella holmesii/bronchiseptica, Coxiella burnetti, Legionella pneumophila, Pneumocystis jiroveci, and Aspergillus species.

Results: During the study period, 875 pediatric patients were admitted among who 298 (34.1%) were diagnosed with respiratory pathology and received antibiotic therapy (180 in 2013, 118 in 2014). In 2013, 192 tests of different respiratory episodes were performed. Based on the results of this novel test, clinicians only prescribed antibiotics for 63 episodes (32.8%) reflecting a possible slight overconsumption linked to the introduction period. However, only 69 results (42%) led to antibiotic use. 95 (58%) results did not evoke antibiotics prescription.

Conclusion: A change in clinical management based on TAC results was observed. Awareness of potential viral pathogens causing LRTI's resulted in reduction of antibiotic use. Implementation of respiratory TAC had following potential benefits: early, highly sensitive and specific appropriate broad pathogen diagnosis, improved management of the individual child, reduced selection of resistant bacteria, considering co-infections, treatment adaptation options, transmission prevention opportunity, expanding view on respiratory epidemiology, reduced need for further laboratory evaluation, and possibly reducing the overall costs of care. In conclusion, the use of respiratory TAC guides clinical decision making and reduces inadequate antibiotic use for viral infections.

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Seroprevalence of hepatitis E virus differs significantly among first and second generation migrant groups in Amsterdam, the Netherlands

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Background: Hepatitis E virus (HEV) is transmitted via the faecal-oral route. Genotypes 1, 2 and 4 are present in areas with poor hygiene conditions and may be imported in Western countries by migrants originating from HEV endemic countries. HEV genotypes 3 and 4 may be transmitted in Western countries by eating contaminated food such as meat from pigs and wild animals. Amsterdam has a multi-ethnic population, including people originating from (sub)tropical regions. Their various cultures reflect different dietary patterns, which in turn may result in different exposures to HEV. Therefore, we studied HEV seroprevalence among 6 different ethnic groups living in Amsterdam to get more insight in the origin of HEV infections in the Netherlands.

Methods: From January 2011 to June 2014, over 13,000 individuals participated in HELIUS (Healthy Life In an Urban Setting), a multi-ethnic population cohort study in which blood samples and questionnaires were collected. For this HEV study we selected 200 individuals aged 18–44 years per ethnicity, associated with the following countries: Surinam (African- and South Asian ethnicities), Morocco, Ghana, Turkey and the Netherlands. Per participant a plasma sample was tested by HEV IgM and IgG assays detecting antibodies to all 4 genotypes (Wantai BPE, Beijing, China). Logistic regression was performed to analyse the association between ethnicity and the presence of HEV antibodies.

Results: Plasma samples from a total of 1199 participants were tested for HEV antibodies. The overall seroprevalence of anti-HEV IgM was 0.4% (n = 5), indicating very few acute HEV infections. The overall HEV IgG seroprevalence was 8% (n = 91) and increased with age, as expected (P = 0.001 for trend). There were no significant differences for gender but there were significant differences between ethnicities (P < 0.001). Compared to the Dutch (9%), the Ghanaian group (22%) had a significant higher HEV IgG seroprevalence (OR 3.0; 95%CI 1.7–5.5). Moroccans (10%) had a comparable whereas South-Asian Surinamese (1%), African Surinamese (2%) and Turkish people (3%) had a significantly lower HEV IgG seroprevalence compared to the Dutch. A lower educational level was significantly associated with HEV IgG seropositivity (P < 0.001). The HEV IgG seroprevalence was significantly higher in first generation (11%) versus 2nd generation (1%) migrants (P < 0.001). There was no relation of HEV IgG seroprevalence with eating meat frequently.

Conclusions: HEV infection in the Netherlands differs across different ethnic groups and generation of migration status. Seroprevalence in first generation migrants may reflect the level of infection in their native countries.

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Re-emergence of HIV in the PWID population of Glasgow

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Background: People who inject drugs (PWIDs) are at high risk of acquiring HIV from sharing injecting equipment and also from high risk sexual activity while under the influence of drugs or in exchange for drugs [1]. There are around 16 million PWIDs worldwide and an estimated 3 million are infected with HIV, 32% in Eastern Europe and 22% in East and South East Asia [2]. Since the introduction of harm reduction measures in the early 1990s the prevalence of HIV in PWIDs in Glasgow and elsewhere in Scotland has remained low. However in the first 5 months of 2015 we detected 13 new cases of HIV in this population with 7 identified as recent infections using our avidity assay. All the cases were found to have subtype C virus with the resistance mutations V179E and E138A.

Methods: We carried out a retrospective study to determine the prevalence of this virus within the HIV community in Greater Glasgow and Clyde (GGC). Clinical and laboratory details were collected...