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transmission. Further surveillance and studies of measles vaccine failure are necessary to assess whether additional protective measures should be considered in these high exposure settings. It is clear, however, that unvaccinated HCWs pose a serious threat for nosocomial outbreaks, and that this group should be adequately vaccinated.

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Abstract No: 1565

Presentation at ESCV 2015: Poster 1

Monitoring the burden of respiratory syncytial virus in different age groups from 2011 to 2015 at National Influenza Centre in Slovenia

N. Berginc*, K. Prosenc

National Laboratory of Health, Environment and Food, Laboratory for Public Health Virology, Slovenia

Background: Respiratory syncytial virus (RSV), besides influenza, represents the leading cause of respiratory tract infections of varying severity in young children. RSV is becoming recognized as important cause of respiratory tract infections in the elderly. Nasal/throat swabs from patients with influenza like illness and acute respiratory tract infections, with personal, clinical, epidemiological data are collected all-year-round from a sentinel of 48 primary healthcare clinics (PHCs) and 2 hospitals (Hs) and tested for respiratory viruses. Data from seasons 2011/2012–2014/2015 were analyzed, to monitor the burden of RSV in different age groups (AGs).

Methods: From weeks 40/2011–20/2015 nucleic acids were extracted from 9371 specimens. Multiplex-RT-RT-PCRs were used for detection and subtyping of RSV (RSV-A, RSV-B) and influenza, adenoviruses, enteroviruses, rhinoviruses, metapneumoviruses, parainfluenza, bocaviruses, coronaviruses. AGs were formed: 0–2, 3–6, 7–14, 15–19, 20–64, ≥65 years of age (YA).

Results: In PHCs in AG of 0–2 YA RSV is present at similar rates as influenza and adenoviruses (19.5%, 22.3%, 20.2%, respectively), other viruses are present at lower rates (<8%). In other AGs, influenza is present at highest rates (46.0%–60.7%), RSV continuously decreases in rates (12.5%, 2.0%, 3.8%, 1.5%, 0% in AGs 3–6 YA, 7–14 YA, 15–19 YA, 20–64 YA, ≥65 YA, respectively). In Hs in AG of 0–2 YA RSV is present at similar rates as rhinoviruses and adenoviruses (14.2%, 16.5%, 19.3%, respectively), other viruses are present at lower rates (<10%). In other AGs, influenza is present at highest rates (10.9%–37.6%), rates of RSV continuously decrease in AGs 3–6 YA, 7–14 YA, 15–19 YA, 20–64 YA (6.8%, 2.6%, 1.5%, 2.7%, respectively), but increase again in AG ≥65 YA (7.4%). Young children (0–2 YA), positive for RSV, are more often diagnosed with bronchiolitis than pneumonia (48.8%, 6.8%, respectively). Patients of other AGs, positive for RSV, are more often diagnosed with pneumonia than bronchiolitis (27.6%, 18.4% in 3–6 YA; 18.8%, 0% in 7–14 YA; 33.3%, 0% in 15–19 YA; 13.0%, 8.7% in 20–64 YA; 22.1%, 18.9% in ≥65 YA, respectively). Acute respiratory distress was observed only in children and the elderly (0.2%, 1.1%, 1.1% in AGs 0–2 YA, 3–6 YA, ≥65 YA, respectively). A plot, representing all virus detections per week from weeks 40/2011–20/2015, shows that RSV usually starts to circulate just before or simultaneously with influenza and continues to circulate at significant rates during influenza season, when other viruses circulate in lower rates. In Slovenia: RSV-A predominated in 2011/2012, 2012/2013; RSV-B predominated in 2013/2014, 2014/2015.

Conclusion: Data collected trough an extended period confirmed seasonal burden of RSV that often coincides with influenza season. RSV represents the highest burden in young children (more often causing bronchiolitis) and the elderly (more often causing pneumonia).

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Presentation at ESCV 2015: Poster 1

Different transmission patterns of uncommon group A human rotavirus genotypes

S. Vila-Vicent*, M. Fernandez-Jimenez, C. Santiso-Bellon, N. Carmona-Vicente, J. Rodriguez-Diaz, J. Buesa

Department of Microbiology, University of Valencia, Spain

Background: Group A rotaviruses are one of the leading causes of acute gastroenteritis in young children worldwide. Rotavirus displays a seasonal pattern of infection in countries with temperate climate, with epidemic peaks occurring in winter and spring. Overall, 6 genotypes circulate in Europe with a prevalence >1% and included G1P[8], G4P[8], G2P[4], G3P[8], G9P[8] and G12P[8], making up these six genotypes to 91% of all characterized strains. However, uncommon genotypes are also sporadically detected.

Methods: Stool samples were analysed during several consecutive rotavirus seasons for group A rotavirus antigen in stool by enzyme immunoassay or by immunochromatographic assay. Viral RNA was extracted and G/P genotyping was performed by RT-multiplex PCR. Phylogenetic analyses of the VP7 and VP4 genes and full genome sequencing of selected uncommon G/P genotype strains were performed.

Results: Twenty-one G8 strains were found from 2008 to 2011, with a peak in March 2009. Sixty-nine G12 strains were detected from March 2011 to June 2012. G-type 8 was associated with P[6] in 13 samples, P[8] in 3 samples, P[4] in 6 samples and P[14] in 1 sample. G12 was always associated with P-type [P8]. Both emerging genotypes G8 and G12 were detected at the beginning and along the rotavirus annual season epidemic and apparently disappeared in summer. G12P[8] was not detected in the next rotavirus season and a few G8 strains were found later in combination with different P-types (P[4], P[8], P[14]). A notorious emergence of G12P[8] strains was detected in the Basque Country (Northern Spain), being the predominant genotype in the 2010–11 (65% of all strains) and 2011–12 seasons (81.6%). An increase of G12P[8] strains was detected during 2013–14 in other Spanish regions (Castile-Leon, Aragon, Catalonia, Valencia and Murcia), accounting overall for 15.3% of 466 typed strains. During the 2013-14 season, G12P[8] strains were detected in Valencia in 27.5% of rotavirus-positive samples.

Conclusions: Emerging G8 and G12 strains arose at the beginning of a rotavirus seasons and their transmission was extended to the whole epidemic season. G8 strains, although combined with different P-types, were detected during two more years. G12 strains, always combined with P[8], became one of the currently predominant genotypes in Spain. We hypothesize that G8P[6] rotavirus strains were less adapted to spread throughout our population than the common G1–G4 genotypes and the more recently emerged G9P[8] and G12P[8] genotypes.

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