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.

for HAdV DNAemia (HR 9.7; 95% CI 3.4–27.4; p = 0.000). HadV DNAemia was a predictor for allo-reactive disease (HR 2.6; 95% CI 1.2–5.4; p = 0.013).
Conclusions: HAdV positivity in NPA pre-HSCT is a very strong predictor for the development of HAdV DNAemia after HSCT. Early detection and intervention might contribute to prevent HAdV-disease after HSCT.

Oral presentations 4

OP4-1
Surveillance and oseltamivir resistance of human influenza A virus in Turkey during the 2007–2008 season

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Monitoring the activity of influenza viruses is important for establishing the circulating types and for detection of the emergence of novel sub-types and antiviral resistant strains. This is the first report from Turkey on the surveillance and oseltamivir resistance of influenza viruses in 2007–2008. Five hundred and twenty four nasal swabs were tested from different geographical regions in Turkey during November 2007 – April 2008. One hundred and sixty three (31%) samples were positive for influenza viruses of which 111 (68%) were influenza A, 52 (31%) influenza B using an immuno-capture ELISA. Forty isolates were selected at random from influenza A positive samples and grown in MDCK cell cultures. The supernatant of the cell cultures was used for RNA extraction followed by RT-PCR to detect the sub-types. Sub-typing revealed all samples as A/H1N1. The N1 gene segment of 30 A/H1N1 samples was sequenced in part, from the 201st to 365th residue, which included the critical region for oseltamivir resistance. Then resulting sequences were analyzed with oseltamivir sensitive and resistant strains obtained from National Center for Biotechnology Information (NCBI) GeneBank by CLC Main Workbench Software. H275Y (H274Y according to N2 numbering) mutation, which is known to confer resistance to oseltamivir, was detected in 6 out of 30 (20%) H1N1 isolates. The D354G mutation was observed in all oseltamivir resistant H1N1 isolates but not in the oseltamivir sensitive isolates. Assay of neurominidase activity revealed that these isolates were resistant to oseltamivir, but sensitive to zanamivir.

OP4-2
Timely diagnosis of respiratory tract infections: evaluation of the performance of the respifinder assay compared to the RVP assay

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Lower respiratory tract infections are a common cause of hospitalization in infants and young children and are typically caused by viral or bacterial pathogens. Diagnostic methods such as culture and serology are time consuming and have several other drawbacks such as limited sensitivity, long turn-a-round time and limited number of detected pathogens. Nucleic acid amplification methods can increase sensitivity and enable the initiation of appropriate interventions without delay.
Broad-spectrum detection and identification circumvent the use of individual diagnostic DNA or RNA based assays. At present, several commercial assays are available for broad-spectrum detection. We compared the performance of the Respiratory Virus Panel assay (RVP) (Luminex Molecular Diagnostics) with that of the Respifinder assay (Pathofinder) for the detection of respiratory pathogens. A total of 106 EQC samples of 9 QCMD Quality Control panels were analysed, of which 95 samples were expected to be positive.
RVP was positive in only 31 samples. For 8 samples an inconclusive result was obtained. All samples containing adenovirus, Coronavirus NL63, Coronavirus OC43 and Coronavirus 229E were false negative with RVP. No false positive results were found. Hence, sensitivity was 32.6% and specificity 100%.
A positive result was found with the Respifinder assay in 75 samples. For 3 weak positive samples an inconclusive result was obtained. For 2 adenovirus type 31 samples the analysis was also false negative. No false positive results were found. Hence, sensitivity was 79% and specificity 100%.
In conclusion, the results of our study seem to indicate a better sensitivity for the Respifinder.

OP4-3
Molecular detection of respiratory viruses: routine application on 522 samples taken in children less than 2 year old

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We describe the development of two multiplex RT-PCR methods for the detection of respiratory viruses in a routine laboratory which tests about 3000 respiratory samples per year. We specifically targeted children less than two years of age. The detection of hRSV, Influenza A, Influenza B was performed every day by multiplex real time RT-PCR (ProFlu-1 Real Time Assay from Prodesse, Argène, Verniolle, France) and the detection of Rhinovirus was performed twice a week by real time RT-PCR (Andeweg et al., J Clin Microb 1999). Between January and April 2008, 522 respiratory specimens were tested, 309 were positive (59.2%). Single infections were detected in 272 samples: 126 rhinovirus, 109 hRSV, 20 influenza B and 17 influenza A. Dual or triple infections were detected in 37 samples, mainly with hRSV and rhinovirus (29 cases). Ct values were comparable for all 4 viruses between single and multiple infections. Clinical data were collected for 133 patients. Concerning children below 42 days of age (38 patients), 17 presented with bronchiolitis and 14 were positive (82%). Regarding children over 42 days of age (95 patients), 38 presented with bronchiolitis and 29 were positive (76%). Implementation of molecular detection of hRSV, influenza A, influenza B and rhinovirus largely improved virus detection compared to classical technics: +15% for hRSV and +93% for rhinovirus. Nethertheless, about 40% of the samples remain negative which emphasizes the need of a broader detection of other respiratory viruses.

OP4-4
Prevalence, quantification and cut-off level of parvovirus B19 DNA in endomyocardial biopsies of cardiac patients and non-cardiac control subjects

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Purpose: Parvovirus B19 (PVB19) persistence has been linked to acute myocarditis and dilated cardiomyopathy. Unfortunately, previous studies lack detailed research on virus presence in normal hearts and various forms of heart failure. Therefore, we evaluated in detail viral DNA prevalence in hearts of cardiac patients and controls.
Methods: Endomyocardial biopsies (EMBs) were collected from patients with diseased hearts and compared to controls. Real-time PCR reactions for PVB19, adenovirus, human herpesvirus-6 and Epstein-Barr virus were performed using ABI prism 7000 and standard curves were included in each run.
Results: A high prevalence of viral genome could be amplified in both groups, up to 84%. Importantly, a significant higher PVB19 DNA load was detected in patients with diseased hearts compared to control subjects, whereas other viruses did not reveal any significant differences in DNA loads. In cardiac patients, mean PVB19 DNA load was 450 copies/ug DNA with a lower 3SD range of 273 copies/ug DNA. In control subjects, mean PVB19 DNA load was 144 copies/ug DNA with an upper 3SD range of 231 copies/ug DNA. Therefore a cut-off value of 250 copies/ug DNA was most optimal to indicate increased PVB19 loads associated with cardiac disease.
Conclusions: The present study demonstrates high virus prevalence in various forms of heart failure and healthy hearts. Importantly, high PVB19 loads in EMBs are associated with cardiac disease. We propose the use of a cut-off value of 250 copies/ug DNA to discriminate between normal PVB19 DNA levels and increased PVB19 DNA levels associated with cardiac disease.

OP4-5
Genetic variants of human parvovirus B19 in South Africa: co-circulation of three genotypes and identification of a novel subtype of genotype 1.

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Background: Three distinct genotypes of parvovirus B19 are now recognized (1, 2 & 3), which differ in overall DNA sequence by ~10%. The