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.

P131 Human herpesvirus-6 viraemia in children with primary immunodeficiency undergoing stem-cell-transplantation

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Background: Human herpesvirus-6 (HHV-6) is known to infect or reactivate in immunocompromised children. This is a cohort study of HHV-6 infection in children with primary immunodeficiency (PI) who underwent haematopoietic-stem-cell transplantation (HSCT) in a single centre between July 1998 and June 2005.

Aims: Determine the prevalence of HHV-6 infection, risk factors and clinical features.

Methods: A total of 126 children with PI (SCID/CID 54, CGD 12, CD40-ligand deficiency 11, Omenn's 10, WAS 9, XLP 5, Osteopetrosis 4 and others 21) received allogeneic HSCT. Quantitative HHV-6 PCR in whole blood was performed weekly for up to 3 months posttransplant. All patients received prophylactic aciclovir.

Results: HHV-6 viraemia (all subtype-B) was detected in 39/126 (31%) children. No significant difference in prevalence between matched-related (16/43), matched-unrelated (15/36) and parental-haploidentical HSCT (8/32). None of 15 recipients of Cord matched-unrelated HSCT had viraemia ($p = 0.005$). Constant viraemia with stable high viral-load was detected in two cases. HHV-6 occurred less frequently in infants than children older than 1 year (14/77 vs. 25/49, $p = 0.0001$). Concurrent CMV viraemia was detected in 22/39 (56.4%). Observed occurrence of GVHD (54%), fever (43.6%), pneumonitis (38.5%), hepatitis (28.2%) and a median engraftment interval of 22 days were similar to reported rates in comparable cohorts. No cases of encephalitis seen.

Conclusions and Discussion: HHV-6B viraemia is common in PI children receiving HSCT. Risk of infection appears to be less in infants and Cord-matched HSCT. Persistent viraemia raises the possibility of chromosomally-integrated HHV-6. Evaluation of clinical findings in comparison to HHV-6 non-viraemic primary-immunodeficient HSCT recipients is required.

P132 Intragenic variations in the HCMV RL11-family

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Human cytomegalovirus (HCMV) exhibits one of the largest genomes among herpesviruses. The HCMV genome comprises 12 multigene families. One of those families is the RL11-family which encodes a characteristic domain, termed RL11D. This domain is predicted to be located on the surface of the RL11 proteins and is supposed to play an essential role in pathogenicity and cell tropism. The aim of this study was to assess the sequence variability of the RL11D in HCMV wild-type strains by focusing on the RL11-family members UL1, UL4, UL6, UL7 and UL10.

Therefore, 60 routinely collected HCMV-DNA positive samples from 32 solid organ transplant recipients and from 28 other patients were analysed. The clinical material originated from different compartments including lavage, urine and serum. DNA sequences were aligned and compared with published data of four passaged laboratory strains. Phylogenetic tree analyses were performed on the basis of individual sequence alignments of the five investigated RL11D.

This analysis showed that investigated HCMV wild-type strains could be divided into 4 groups (UL4) and 3 groups (UL1, UL6, UL7, UL10), respectively. Within each group, the amino acid sequences were 100%–96% identical, whereas pairwise comparisons between distinct groups of each RL11D revealed 94%–54% identity. In addition, our data revealed that there was no significant linkage between the newly defined groups of the different RL11-family members.

The results of our study highlight the variability between HCMV wild-type strains and thus underline the complexity of the viral influence on virus-host interactions.

P133 Cytomegalovirus monitoring in allogeneic haemopoietic stem cell transplant recipients

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Aim: We reviewed the patterns of cytomegalovirus (CMV) reactivation/infection in 112 haematopoietic stem cell transplantation (HSCT) recipients.

Method: 112 allogeneic HSCT were performed between September 2003 and June 2005: 86 received reduced intensity conditioning (RIC) HSCT and 26 received myeloablative (MA) conditioning. Weekly quantitative CMV DNA monitoring was carried out for at least 6 months post transplantation. Pre-emptive therapy with ganciclovir or valganciclovir was started after two consecutive detectable CMV DNA results.

Results: The median follow up period was 237 days. CMV viremia occurred in 22/23[95.7%] D−R+, 27/40[67.5%] D+R+ and 3/13[23.1%] D+R− transplantations at a median of 36 days [first episode = 52 patients], 132[second = 14], 195[third = 5], 257[fourth = 3] and 315[fifth = 1 patient]. The median peak CMV load was 4.06 $\log_{10}$ for the first viremia.

Treatment history was available in 27 episodes of CMV viremia of which 4 died. 13 received ganciclovir, 2 valganciclovir and one ganciclovir followed by valganciclovir. In 7 episodes, treatment was changed to include foscarnet due to a lack response to treatment. Median CMV loads in those who responded to the first line treatment was significantly lower than those who required foscarnet (3.25 $\log_{10}$ vs 4.29 $\log_{10}$; $p = 0.003$).

Conclusions: D−R+ transplants were at most risk of CMV viremia. There was no difference in CMV viraemic episodes between RI/MA conditioning. There was no difference in duration of viremia/peak CMV viremia between those with one or more episodes of viremia. Treatment was successful with ganciclovir/valganciclovir when the CMV load was below 4.0 $\log_{10}$ at the beginning of treatment.

P134 The detection of human papilloma virus in infant respiratory tract papillomas

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Objective: To investigate the relationship between patients with infant respiratory tract papillomas and human papilloma virus (HPV6.11) and to study the changes of different sub-groups of T lymphocytes in the peripheral blood. Methods Fluorescence quantitative PCR (FQ-PCR) which combines PCR and fluorescence probe hybridization was used to detect DNA of HPV6.11. Using Flow Cytometry to detective the quantity of different T lymphocytes' subgroups.

Results: 115 of 130 cases were HPV6.11 DNA positive, the average was 105.68±2.65 copies/mg. The percent of CD3+ T lymphocytes, CD4+ T lymphocytes and CD8+ T lymphocytes in the peripheral blood of patient group are 62.73±8.63, 30.54±7.05, 26.08±6.93.

Conclusions: FQ-PCR is a convenient**,** accurate and specific method which detected the infection degree of the pathogenic germs. However, there was no significant difference between the patient group and the control group in the result of CD3+ T lymphocytes, CD4+ T lymphocytes and CD8+ T lymphocytes in the peripheral blood.

P135 The changes of sub-group of T-lymphocyte in the peripheral blood of the SARS patients

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Objective: To study the changes of different sub-groups of T lymphocytes in the peripheral blood of the Severe Acute Respiratory Syndrome (SARS) patients.