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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 were 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 viraemia occurred in 22/23[95.7%] D+R+, 27/40[67.5%] D+R+ and 31/33[23.1%] D+R– transplants 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 viremic 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 detect 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/μg. 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.

P136 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.
Methods and Materials: The blood samples came from three groups: the SARS patients group, the suspected group and the healthy persons group. All the samples were analyzed with the Flow Cytometry and Blood Corpuscle Analysis Apparatus to determine the quantities of different T lymphocytes sub-groups, and then the results of the patients were compared with those of the suspected and the healthy persons.

Results: The total lymphocytes, CD3+ T lymphocytes, CD4+ T lymphocytes and CD8+ T lymphocytes in the peripheral blood of the SARS patients were all lower than those of the healthy persons in early proceeding. As contrast, there were no differences between samples of the suspected and the healthy persons.

Conclusions: The total lymphocytes, CD3+ T lymphocytes, CD4+ T lymphocytes and CD8+ T lymphocytes in the peripheral blood of the SARS patients were destroyed in early proceeding, so the quantities of these cells could be used as one adjuvant criterion for diagnosis.

Blood donors viral profile at Menoufiya Governorate – Egypt

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Background: Transmission risks of Hepatitis and HIV viruses has decreased, tests becoming more sensitive. CMV and EBV can be primary or reactivation of the endogenous latent infection.

Aim of the Study: Evaluate viral profile in donors, to implement protection measures for safer blood supply.

Methods: Blood donors (114 males and 6 females) were included mean age 27.27 SD 6.89 yrs; viral markers measured by (MIA). They included (Total -HCV IgG, (HBsAg), (Total Anti-Hbc), (Anti-HIV type 1 & 2), and (CMV Ig G) while, (5) EBV- VCA-IgG by ELISA.

Results: revealed CMV-IgG (86.7%), EBV-VCA-IgG (53.3%), anti-HBc (23.3%) and anti-HCV (15%) while; both HBsAg and anti-HIV were negative. (13.3%) were query EBV-VCA-IgG, seroconversion may occur. Coexisting infections of CMV and EBV were (50%). Significance was revealed for association of Hbc and CMV Abs (20%), with EBV Abs (11.7%) 31.7% for both (p < 0.05). Coinfection of HCV with either CMV or EBV were (3.3%) and (6.7%) respectively 23.3% for both. Combined HCV, HCV Abs were (5%) and found at age >25yrs (28.6%), (20%) while, for <25yrs (16%), (8%) respectively revealed insignificance (P > 0.05). First donation represents 23.3% for both. Combined CMV and HCV Abs were (5%) and found at age >25yrs (58.3%) first donation while, (41.7%) for second revealed exacerbation of infection (P < 0.05).

Conclusion: CMV infection was the highest so; blood units should be leuko-reduced. The significant coinfection of CMV and HCV gives the message about liver affection. Our recommendation was once blood donation at age <25yrs.

Hepatitis B vaccine uptake and response in a London regional dialysis unit

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Background: Hepatitis B(HBV) vaccination for all patients likely to require dialysis was recommended in the revised guidelines published in 2002 by the Department of Health (DoH). A prelimiary cohort of the 980–2000 haemodialysis cohort in the dialysis programme based at King’s College Hospital, London showed that 35 of 158 (22%) patients had prior exposure to HBV, 4 of whom were carriers. We studied the impact on HBV vaccine uptake and response in the unit after DoH guidelines were implemented in 2002.

Methods: Between 2002–2004 there were 233 pre-dialysis, 157 peritoneal dialysis and 236 haemodialysis patients. Hepatitis B surface antigen (HBsAg), hepatitis B core total antibody (anti-HBc) status were noted along with vaccination history and hepatitis B surface antibody (anti-HBs) response.

Results: In the 1998–2000 haemodialysis cohort, 20 of 40 (50%) patients with available HBV vaccination history received 3 doses of vaccine. Vaccine uptake was better in the 2002–2004 cohort with 96 of 126(76.8%) vaccinated pre-dialysis patients having received 3 doses. Analysis of the 2002–2004 pre- and post-dialysis, haemodialysis cohorts with 3 doses of HBV vaccination showed an anti-HBs response of >100UI/U in 36/95 (37.5%), 13/23 (56.2%), 6/17 (35.29%) and 10–100UI/U in 19/96(19.7%), 7/23/30(43.4%), 5/17(29.41%) patients respectively. If >100UI/U is taken as vaccine response, the respective rates are 57.29%, 87%, and 64.7%. In the 1998–2000 haemodialysis cohort, 9/20(45%) and 1/20(5%) patients had anti-HBs response of >100UI/U and 10–100UI/U respectively.

Conclusion: These are encouraging results following implementation of DoH guidelines that show improvement in vaccine uptake and response as compared with other reports of post-immunisation response in similar groups.

Varicella zoster vaccination of health care workers is cost-effective

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Background: Nosocomial varicella continues to be a problem for hospitals, occupational health and virology departments across the UK. Although cost-effectiveness studies have not been performed, in December 2003, the Chief Medical Officer recommended that all health care workers (HCWs) susceptible to varicella zoster virus (VZV) should be immunised.

Methods: Our institution implemented this new policy from April 2004 onwards. Additionally, from April 2005 each vaccinee was provided with a questionnaire which assessed the tolerability of vaccination, asked if the vaccinees had had any contact with VZV after immunisation and whether they had developed a rash illness.

Results: Since April 2004 a total of 200 HCWs have been immunized, of whom 156 have completed the schedule. Of 85 questionnaires so far adminstered, 55 have been returned up to the end of April 2006. Forty-seven respondents (85.5%) had received both doses. Fourteen (25.5%) reported any adverse reaction, ranging from pain/irritation at the injection site (6/55, 10.9%) to a vesicular rash in three individuals (5.4%). Vesicular fluid was obtained and showed vaccine strain DNA in two and wild-type virus in one. This particular HCW had had contact with chickenpox around the time of vaccination. Of note, of the 7/55 respondents (12.7%) who had contact with VZV after vaccination, none subsequently developed chickenpox.

Conclusions: Although the CMO anticipated that VZV vaccination of HCWs would be cost neutral, in our cohort, at least seven potential transmissions to HCWs were prevented by vaccination in one year.

We believe the cost savings from this are self-evident.

Real-time NASBA assay for the detection of influenza A and B

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Objectives: bioMérieux is developing a real-time NASBA assay to detect Influenza A and B RNA in different kind of respiratory clinical samples, by using the NucliSens® EasyQ basic kit V2 in combination with specific primers and molecular beacons.

Methods: Influenza RNA is isolated using the NucliSens® miniMAG or EasyMAG extraction. An internal control is added to the sample prior to nucleic acid extraction. The assay is designed to detect in a single tube, using a three-label approach, the internal control and both Influenza A and Influenza B RNA. Targeted regions are MP and NS for Influenza A and B respectively. Amplification reactions were performed in a NucliSens® EasyQ Analyser allowing real-time detection.

Results: Various human and animal Influenza strains were tested with this new assay. Analytical sensitivity studies showed a threshold at 10 copies in direct amplification. Furthermore, a study based on 89 Nasal/throat swabs in transport medium from hospitalised