Table 3. Logistic Regression Analysis of Outcomes Using CS-CMVi as Exposure

Risk Factor	OR	95% CI	p-value
A. Logistic Regression – Herpesviri	dae		
Letermovir primary ppx	1.24	0.34-4.5	.74
CS-CMVi	0.94	0.31-2.8	.90
ALL as primary malignancy	0.19	0.05-0.76	.02
Donor CMV seropositivity	0.24	0.07-0.84	.03
B. Logistic Regression – Non-CMV/	/Non-RVI		
Letermovir primary ppx	0.77	0.30-1.98	.60
CS-CMVi	0.94	0.39-2.25	.89
C. Logistic Regression – All Non-CM	//v		
Letermovir primary ppx	2.61	0.96-7.1	.06
CS-CMVi	1.44	0.55-3.72	.46
D. Logistic Regression – HHV-6			
Letermovir primary ppx	4.66	0.35-7.82	.52
CS-CMVI	1.67	0.48-5.88	.42
ALL as primary malignancy	0.17	0.03-0.84	.03
E. Logistic Regression – BKV			
Letermovir primary ppx	0.95	0.36-2.48	.91
CS-CMVI	1.31	0.54-3.14	.55
F. Logistic Regression – RVI			
Letermovir primary ppx	2.81	1.11-7.12	.03
CS-CMVi	2.07	0.85-5.04	.11
G. Logistic Regression – NRM Day	100		
Letermovir primary ppx	0.68	0.12-3.91	.67
CS-CMVI	1.90	0.41-8.88	.42
HCT source - Marrow	16.5	1.36-200	.03
H. Logistic Regression – NRM Wee	k 24		
Letermovir primary ppx	0.55	0.11-2.8	.47
CS-CMVi	4.83	1.14-20.4	.03
HCT source - Marrow	39.1	3.24-471	.004
I. Logistic Regression – NRM Wee	k 48		
Letermovir primary ppx	0.61	0.15-2.43	.48
CS-CMVI	5.30	1.44-19.4	.01
HCT source - Marrow	16.71	2.70-103.3	.002
Time to engraftment	1.16	1.02-1.33	.03

lymphoblastic leukemia; HHV-6, human herpes virus-6; BKV, BK virus; NRM, non-relapse mortality; HCT, hematopoletic cell transplant.

Conclusion. Our study showed that CS-CMVi is associated with higher 24- and 48-week non-relapse mortality but with no increase in the incidence of other non-respiratory viral infections in this matched cohort of allo-HCT recipients.

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923. Respiratory Syncytial and Parainfluenza Virus Infection Increase the Risk of Cytomegalovirus Reactivation in Allogeneic Hematopoietic Cell Transplant Recipients

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Background. Respiratory virus infections are associated with significant and specific local and systemic inflammatory response patterns, which may lead to reactivation of latent viruses. We examined whether viral upper (URTI) or lower respiratory tract infection (LRTI) with common respiratory viruses increased the risk of CMV viremia after allogeneic hematopoietic cell transplantation (HCT).

Methods. We retrospectively analyzed patients undergoing allogeneic HCT between 4/2008 and 9/2018. CMV surveillance was performed weekly and the presence of upper and lower respiratory symptoms were evaluated by multiplex respiratory viral PCR. We used Cox proportional hazards models to evaluate risk factors for development of any CMV viremia or high level CMV viremia in the first 100 days post-HCT. Each respiratory virus infection episode was considered positive for 30 days beginning the day of diagnosis.

Results. Among 2,545 patients (404 children, 2141 adults), 1,221 and 247 developed CMV viremia and high level CMV viremia, respectively, in the first 100 days post-HCT. Infections due to human rhinoviruses (HRV, N=476) were most frequent, followed by parainfluenza viruses 1-4 (PIV, N=139), seasonal human coronaviruses (COV, N=134), respiratory syncytial virus (RSV, N=77), influenza A/B (FLU, N=35), human metapneumovirus (MPV, N=37), and adenovirus (ADV, N=61). In adjusted models, RSV LRTI was associated with increased risk of developing CMV viremia at all levels (**Figures** 1 and 2), and PIV or RSV URTI increased the risk of high level CMV viremia; all other viruses showed no association in univariable models.

Model estimates for associations between LRTI and development of any CMV viremia‡



‡ Models were not performed with other viruses given limited number of outcome events. P values of LRTI with <0.05 in univariable models were included multivariable models. In univariable models

Adjusted for pre- and post-transplant factors if p<0.05 in univariable models. Adjustment factors: Pretransplant factors (age, sex, race, body habitus, donor type, stem cell source, CMV serostatus) + post-transplant factors (subsequent transplantation, lymphopenia and acute severe GVHD as time dependent covariates).

Abbreviation: LRTI = lower respiratory tract infection, CMV = cytomegalovirus, RSV = respiratory syncytial virus, HRV = human rhinovirus, PIV = parainfluenza virus, COV = seasonal human coronavirus, ADV = adenovirus, HR = hazard ratio, CI = confidence interval. GVHD = ordit-verus-bot disease.

Figure 1. Model estimates for associations between LRTI and development of any CMV viremia

Model estimates for associations between LRTI and development of high level CMV viremia‡



1 Models wave not performed with other viruses given limited number of outcome events. P values of LRTI with <0.05 in univariable models were included multivariable models. High level CMV viremia was defined as viral load >1,000 IU/m (PCR).

Adjusted for pre- and post-transplant factors if p<0.05 in univariable models Adjustment factors: Pretransplant factors (race, body habitus, stem cell source, CMV serostatus, and year of transplantation) + post-transplant factors (lymphopenia and acute severe GVHD as time dependent covariates).

Abbreviation: LRTI = lower respiratory tract infection, CMV = cytomegalowirus, RSV = respiratory syncytial virus, HRV = human rhinovirus, PIV = parainfluenza virus, HR = hazard ratio, CI = confidence interval, GVHD = graft-versus-host disease.

Figure 2. Model estimates for associations between LRTI and development of high level CMV viremia

Conclusion. We demonstrated that RSV and PIV infections are associated with an increased risk for development of CMV viremia after allogeneic HCT. This novel association provides the rationale to explore virus-specific inflammatory pathways that may trigger CMV reactivation. CMV viremia may also serve as an endpoint in clinical trials that assess new preventative or therapeutic interventions of RSV or PIV infection.

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924. Cytomegalovirus (CMV) Retinitis during Maintenance Chemotherapy for Acute Lymphoblastic Leukemia

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