Results. 133 of 541 patients (25%) had been appropriately screened for HBV within six months prior to starting biologic therapy. 207 of 541 (38%) had been screened with appropriate serologies within ten years prior to starting a biologic. 23 providers participated in the survey, 7 each from the department of Rheumatology and Gastroenterology, and 9 from Dermatology. One-third of the providers were currently in training, another third were practicing for < 5 years, and the remainder had > 5 years of experience. 57% of the providers said they would screen everyone for HBV before starting a biologic. 78% of them chose the appropriate serologies. The time interval for rescreening was evenly spread amongst different providers, ranging from 3 months to 5 years. If a patient was switched to a new biologic, 48% of physicians would repeat screening only if the patient was determined to be at risk of reactivation or new acquisition of HBV. The major barrier to screening was uncertainty regarding who to screen and which tests to order.

Conclusion. This data reveals that there is inadequate screening for HBV prior to biologic therapy. The survey highlighted areas for quality improvement, including the need for wider dissemination of screening guidelines and development of a protocolized approach to ordering the correct tests.

Disclosures. **All Authors**: No reported disclosures

1075. Absolute Lymphocyte Count as a Predictor of Cytomegalovirus (CMV) Infection and Recurrence in Hematopoietic Stem Cell Transplant (HSCT) Recipients

Joanne Reekie, PhD[1]; Marie Helleberg, MD, PhD, DMSc[1]; Christina Ekenberg, MD, PhD[2]; Mark P. Khurana, MD[2]; Isabelle P. Lodding, MD, PhD[2]; Amanda Mocroft, PhD[3]; Jens Lundgren, MD, DMSc[1]; Henrik Sengeløv, MD, DMSc[1]; [1]Copenhagen University Hospital, Rigshospitalet, Copenhagen, Denmark, Copenhagen, Hovedstaden, Denmark; [2]Centre of Excellence for Health, Immunity and Infections (CHIP), Department of Infectious Diseases, Rigshospitalet, Copenhagen, Denmark, Copenhagen, Hovedstaden, Denmark; [3]CREME, Institute for Global Health, University College London, London, United Kingdom, London, England, United Kingdom

MATCH study group

Session: P-49. Infections in Immunocompromised Individuals

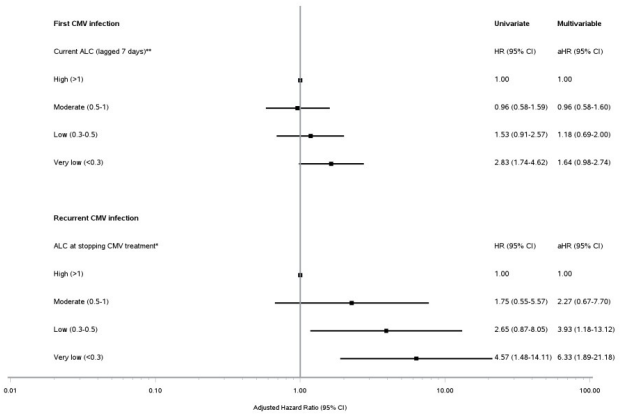
Background. Cytomegalovirus (CMV) is a serious complication following Hematopoietic Stem Cell Transplant (HSCT) and can lead to serious organ disease and mortality. This study aimed to investigate the association between absolute lymphocyte count (ALC) and CMV to determine whether ALC could help to identify those at an increased risk of CMV infection and recurrence

Methods. Adults undergoing HSCT between 2011 and 2016 at Rigshospitalet, Denmark were included. Cox proportional hazards models investigated risk factors, including ALC, for CMV infection in the first year post-transplant and recurrent CMV infection 6 months after clearance and stopping CMV treatment for the first infection. For the primary outcome ALC was investigated as a time-updated risk factor lagged by 7 days, and for recurrent CMV, ALC measured at the time at the time of stopping treatment for the first CMV infection was investigated (+/- 7 days).

Results. Of the 352 HSCT recipients included, 57% were male, 40% received myeloablative conditioning, 42% had high risk (D-R+) CMV IgG serostatus at transplant and the median age was 56 (IQR 43-63). 143 (40.6%) patients had an episode of CMV DNAemia a median of 47 days after transplant (IQR 35-62). A lower current ALC (≤ 0.3 x10^9/L) was associated with a higher risk of CMV infection in univariate analysis compared to a high current ALC (> 1 x10^9/L). However, this association was attenuated after adjustment, particularly for acute graft versus host disease (Figure). 102 HSCT recipients were investigated for risk of recurrent CMV of which 41 (40.2%) had a recurrent CMV episode a median of 27 days (IQR 16-50) after stopping CMV treatment for the first infection. A lower ALC (≤ 0.3 x10^9/L) at the time of stopping CMV treatment was associated with a significantly higher risk of recurrent CMV after adjustment (Figure). A higher peak viral load (> 1500 IU/ml) during the first episode of CMV infection was also associated with an increased risk of recurrent CMV (aHR 2.47, 95%CI 1.00-6.10 compared to < 750 IU/ml).

Association between absolute lymphocyte count (ALC) and risk of CMV infection and recurrent CMV within 6 months. **First CMV infection multivariable model also adjusted for sex, CMV serostatus, age, year of transplant, Charlson Comorbidity Index, Anti-thymocyte globulin (ATG) given, HLA donor-recipient matching, and acute graft versus host disease (time-updated) *Recurrent CMV infection multivariable model also adjusted for conditioning regimen, sex, CMV serostatus, age, year of transplant Anti-thymocyte globulin (ATG) given, HLA donor-recipient matching, and acute graft versus host disease and peak CMV viral load during the first CMV infection

Conclusion. A lower ALC at the time of stopping treatment for the first CMV infection was associated with an increased risk of recurrent CMV and could be used to help guide decisions for augmented CMV surveillance and clinical awareness of CMV disease symptoms in these patients.



Disclosures. **All Authors**: No reported disclosures

1076. Gaps in Measles and Mumps Seroprevalence Among Cancer Patients

Sara Marquis, MPH[1]; Jennifer Logue, BS[2]; Tillie Loeffelholz, BS[3]; ZZ Quinn, BA[3]; Catherine Liu, MD[3]; Marc Stewart, MD[4]; Helen Y. Chu, MD MPH[2]; Steven A. Pergam, MD, MPH[3]; Elizabeth M. Krantz, MS[5]; [1]Fred Hutch, Seattle, Washington; [2]University of Washington, Seattle, WA; [3]Fred Hutchinson Cancer Research Center; University of Washington, Seattle, WA; [4]Seattle Cancer Care Alliance, Seattle, Washington; [5]Fred Hutch Cancer Research Center, Seattle, Washington

Session: P-49. Infections in Immunocompromised Individuals

Background. Immunosuppressed cancer patients are at risk for morbidity and mortality from vaccine preventable diseases. Recent outbreaks and declining vaccination rates put cancer patients at increased risk for measles and mumps exposures. To assess the current status within our center, we measured measles and mumps seroprevalence among cancer patients.

Methods. Residual clinical plasma samples from patients seen at Seattle Cancer Care Alliance were collected between 8/11/2019 and 8/15/2019 and tested for measles and mumps IgG using ELISA (Genway Biotech); patients receiving intravenous immunoglobulin ≤16 weeks prior to collection date were excluded. Seroprevalence was calculated based on positive results; equivocal results were not considered protective. Demographic and clinical data were abstracted from medical records. Overall and subgroup seroprevalence were estimated with Wilson 95% confidence intervals (CI); Poisson regression with robust standard errors was used to compare subgroups and estimate prevalence ratios (PR).

Results. Of 1000 unique patients, 987 were eligible, with a median age of 61 years (range 2-97). More than half had a solid tumor (574 [58%]) while 376 (38%) had a hematologic malignancy (HM); 155 (16%) were hematopoietic cell transplant (HCT) recipients. The percentage of seropositive patients was 75% (95% confidence interval [CI]: 72%, 78%) for measles and 62% (95% CI: 59%, 65%) for mumps. Seropositivity was highest among older age groups, particularly those older than 63, who most likely have naturally acquired immunity (Figure 1-2). In multivariable analysis, patients aged 30-59 years were significantly less likely to be seropositive compared to patients ≥80 years of age. Patients with HM and those undergoing HCT were also less likely to be seropositive (Figure 3).

Figure 1. Distribution of age at sample collection and measles antibody test results

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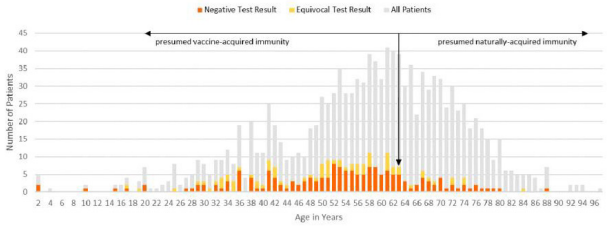
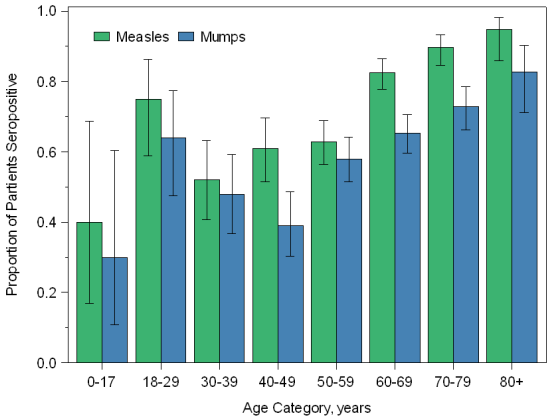


Distribution of negative and equivocal measles antibody test results by age at time of sample collection. The height of the stacked columns represents total eligible patients (grey), those with equivocal IgG measles test results (yellow) and those negative for measles IgG (orange). The vertical arrow indicates those born in 1957, prior to which naturally-acquired immunity can be presumed.

Figure 2. Measles and mumps seroprevalence by age

Figure 2. Measles and mumps seroprevalence by age



Estimates for measles and mumps seroprevalence by age category at time of sample collection. Height of the filled bars represents the prevalence estimate and capped bars represent the 95% confidence interval for those estimates.

Figure 3. Multivariable model estimates for measles and mumps seroprevalence

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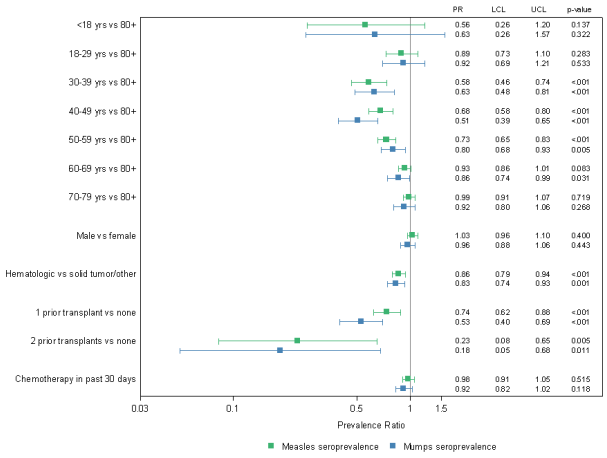

Forest plot of multivariable model estimates for measles (green) and mumps (blue) seroprevalence. Squares represent the prevalence ratio (PR) estimate and brackets extend to the lower (LCL) and upper (UCL) limits of the 95% confidence interval. Estimates are adjusted for all variables shown.

Conclusion. One-quarter of cancer patients tested did not have evidence of seroprotection for measles and mumps. Seronegative and equivocal responses were observed primarily among younger patients and those with hematologic malignancies. Deficits in protective antibody seen in this study are common among cancer patients and underscore the need for population/community-based efforts to increase herd immunity and protect vulnerable populations.

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1077. Infectious complications after second allogeneic hematopoietic cell transplant (allo-HCT) in adult patients with hematological malignancies

Stephen Maurer, MD[1]; Kathleen A. Linder, MD[2]; Carol A. Kauffman, MD, FIDSA, FSHEA[3]; Philip McDonald, MD[4]; Jonathan T. Arcobello, MD[5]; Jon Karl D. Velasco, MD[6]; Pranatharthi Chandrasekar, md[7]; Sanjay Revankar, MD[6]; Marisa H. Miceli, MD, FIDSA[2]; [1]Univeristy of Michigan, Ann Arbor, Michigan; [2]University of Michigan, Ann Arbor, MI; [3]Ann Arbor VA Healthcare System, Ann Arbor, MI; [4]Hurley Medical Center, Detroit, Michigan; [5]Wayne State, Detroit, Michigan; [6]Wayne State University, Bradenton, Florida; [7]wayne state university, detroit, MI

Session: P-49. Infections in Immunocompromised Individuals

Background. A 2nd allo-HCT is received by some adults after relapse of their underlying malignancy, development of a second malignancy, or graft failure. Few studies have reported on infectious complications in adults given a 2nd HCT

Methods. This is a retrospective review of infectious complications and overall mortality of 60 adult patients who received a 2nd HCT from Jan. 2010 - Dec. 2015. Data were collected for 2 years post-HCT for each patient. Infections were separated into < 30 days (d) post-HCT, 30-100d post-HCT, and >100d post-HCT.

Results. Mean age at 2nd HCT was 49+13; 60% were men. The most common reason for the 1st HCT was acute myeloid leukemia (AML) or myelodysplastic syndrome (MDS) (73%,n= 44) The 2nd HCT was for relapse of original malignancy (62%,n=37), graft failure (27%,n=16), and new malignancy (10%,n=6). The 2nd HCT was received a median of 344d (range 29-8248) after 1st HCT. Neutrophil engraftment occurred by 13+4d in 50/60 patients.

Fifty-eight patients (97%) had at least one infection during the study period. A total of 183 infections were reported: 75 (41%) were < 30d, 56 (31%) 30-100d, and 52 (28%) >100d post-HCT. Bacterial infections, primarily *C. difficile*, vancomycin-resistant *Enterococcus*, and coagulase (-) *Staphylococcus* caused 90 (49%) infections and were seen throughout the post-HCT period. Viral infections, predominantly CMV and BK virus, caused 60 (33%) of infections, peaking at 30-100d post-HCT. Only 19 (10%) infections were fungal, most of which were mold infections and occurred >30d post-HCT.

Thirty-nine (65%) patients died by 2 years post-HCT, 27 within the first year. Cause of death was infection in 16 (41%), graft failure, relapse, or GVHD in 16 (41%), other in 7 (18%). At < 30d post-HCT, 5 deaths (71%) were from infection 4 of which were bacterial. At 30-100d post-HCT, 6/9 (69%) deaths were from relapse/graft failure/GVHD. All 6 deaths from fungal infections were >100d post-HCT. Bacterial Infections and engraftment failure within 100d post-HCT were associated with increased mortality (p .05 and < .001, respectively).

Conclusion. All but 2 patients receiving a 2nd allo-HCT developed an infection. Most deaths at < 30d post-HCT were from infection. Overall 2-year mortality was 65% and 41% of deaths were related to infection.

Disclosures. Marisa H. Miceli, MD, FIDSA, SCYNEXIS, Inc. (Advisor or Review Panel member)

1078. Renal Transplant Recipient Resistomes Reveal Expansive Sub-Clinical Burden of Resistance After Treatment for ESBL-Producing Bacterial Infections.

Michael Woodworth, MD, MSc[1]; Roth Conrad, n/a[2]; Amanda F. Strudwick, BSN[1]; Ahmed Babiker, MBBS[1]; Stephanie M. Pouch, MD, MS, FAST[1]; Stephanie M. Pouch, MD, MS, FAST[1]; Aneesh Mehta, MD[1]; Rachel Friedman-Moraco, MD[1]; Max W. Adelman, MD, MSc[1]; Kostas Konstantinidis, PhD[2]; Colleen Kraft, MD, MSc[1]; [1]Emory University School of Medicine, Atlanta, Georgia; [2]Georgia Institute of Technology, Atlanta, Georgia

Session: P-49. Infections in Immunocompromised Individuals

Background. Renal transplant recipients have frequent infection and colonization with antibiotic resistant (AR) bacteria. However, little is known about the burden of AR following targeted antibiotic treatment.

Methods. This was a prospective study conducted as part of a single center clinical trial at Emory University. Demographic and clinical data regarding transplant and AR bacterial infection were abstracted. Stool samples were collected from renal transplant recipients treated with antibiotics for ESBL-producing gram negative infections. Bacterial cultures with AR-selective media and Illumina short-read sequencing were performed on stool samples. Confirmatory phenotypic isolate AR testing was performed with the Vitek2 platform. Resistome profiles were produced by assembling short reads into scaffolds using MetaSPAdes, predicting protein coding sequences using Prodigal and classifying proteins as antimicrobial resistance determinants using AMRFinderPlus. AMRFinderPlus results for patients were then compared to fecal metagenomes from 3 healthy Human Microbiome Project controls. Differences in AR genes in renal transplant patients vs controls were compared.

Results. Metagenome sequencing was performed for 6 (5 female) patient stool samples. Stools were collected a median of 30 days after infection. The median number