Figure 2. Measles and mumps seroprevalence by age

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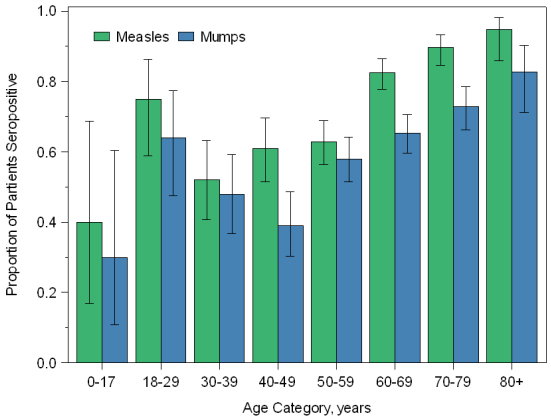

Estimates for measles and mumps seroprevalence by age category at time of sample collection. Height of the filled bars represents the prevalence estimate and capped bars represent the 95% confidence interval for those estimates.

Figure 3. Multivariable model estimates for measles and mumps seroprevalence

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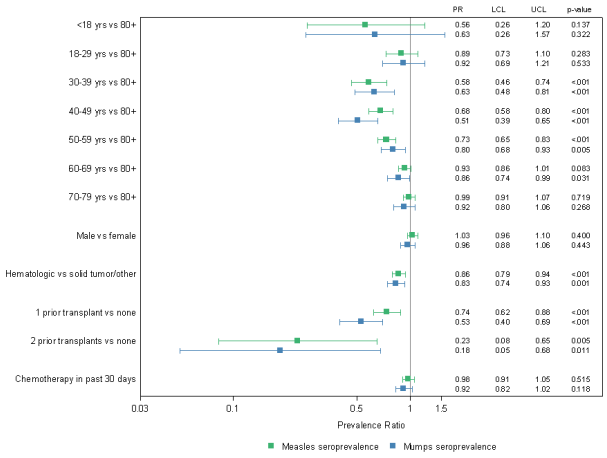

Forest plot of multivariable model estimates for measles (green) and mumps (blue) seroprevalence. Squares represent the prevalence ratio (PR) estimate and brackets extend to the lower (LCL) and upper (UCL) limits of the 95% confidence interval. Estimates are adjusted for all variables shown.

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.

Disclosures. **Helen Y. Chu, MD MPH**, **Cepheid** (Grant/Research Support)**Ellume** (Grant/Research Support)**Glaxo Smith Kline** (Consultant)**Merck** (Consultant)**Sanofi-Pasteur** (Grant/Research Support) **Steven A. Pergam, MD, MPH**, **Chimerix, Inc** (Scientific Research Study Investigator)**Global Life Technologies, Inc.** (Research Grant or Support)**Merck & Co.** (Scientific Research Study Investigator)**Sanofi-Aventis** (Other Financial or Material Support, Participate in clinical trial sponsored by NIAID (U01-AI132004); vaccines for this trial are provided by Sanofi-Aventis)

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

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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.

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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

of AR genes per patient metagenome was 48.5 (range 23 to 87 genes). The median number of AR genes per control metagenome was 24 (range 16 to 25 genes). We detected 97 unique AR genes across all samples, 63 of which (65%) were detected in patient samples but not controls. All AR genes found in control metagenomes were present in at least one patient metagenome. No AR genes detected in patients were common to all patients. Subsets of clinically relevant genes corresponded with patient stool AR bacteria culture results.

Antimicrobial resistance gene detection heatmap for renal transplant recipient stool samples after antibiotic treatment for ESBL infection.

Conclusion. Viable AR bacteria and diverse AR gene profiles were frequently detected from renal transplant recipient stool samples after antibiotic treatment for infection. These data suggest that AR bacterial colonization and AR gene profiles may require distinct treatments other than systemic antibiotics for eradication.

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

1079. The Risk of Cytomegalovirus (CMV) Infection and Recurrence Among Solid Organ Transplant Recipients

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MATCH Study Group

Session: P-49. Infections in Immunocompromised Individuals

Background. Solid organ transplant (SOT) recipients are at a high risk of developing cytomegalovirus (CMV) post-transplant (tx) with many experiencing a recurrence shortly after clearing the first episode. We aimed to identify risk factors associated with CMV infection and recurrence.

Methods. SOT recipients (≥ 18 years) transplanted between 2011-2016 were investigated for factors associated with CMV infection within 1 year from baseline and recurrent CMV within 6 months of stopping CMV treatment for the first infection using cumulative incidence curves and Cox proportional hazards models. Baseline was defined as either tx date or date of stopping CMV prophylaxis for those initiating CMV prophylaxis within 7 days of tx. Individuals with breakthrough CMV while on prophylaxis were excluded (n=29).

Figure 1 Risk of CMV infection in 755 SOT recipients in the first year from baseline, stratified by CMV serostatus. Baseline was defined either the date of transplant (n=285) or stopping CMV prophylaxis (n=470).

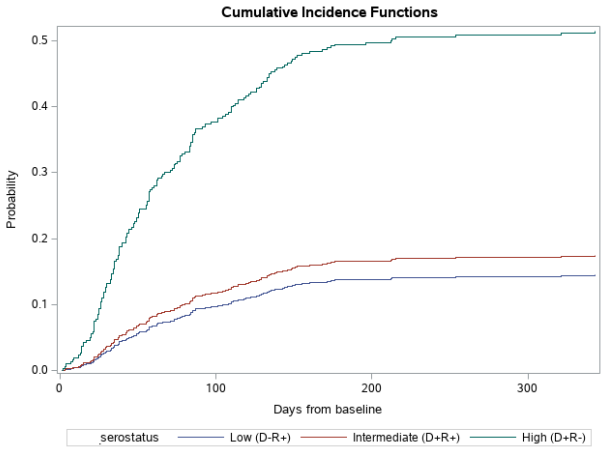
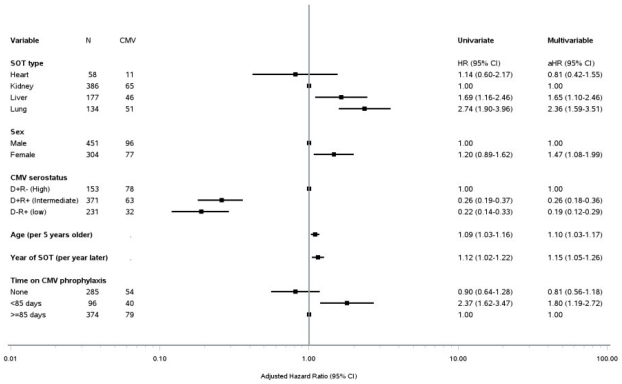


Figure 2 Factors associated with CMV infection in the first year from baseline. Baseline was defined either the date of transplant (n=285) or stopping CMV prophylaxis (n=470).



Results. We included 755 SOT recipients, 173(23%) developed CMV infection within one year of baseline with CMV disease present at diagnosis in 17% of the cases. The risk of CMV infection was lower in patients with low (aHR 0.19, 95%CI 0.12-0.29) and intermediate (aHR 0.26, 95%CI 0.18-0.36) risk CMV IgG serostatus compared to high risk (Figure1). Liver and lung tx, female sex, older age and year of tx were also associated with an increased risk of CMV infection (Figure 2). Among the 470 (62%) patients who received CMV prophylaxis those who received < 85 days had a higher risk of CMV infection than those receiving ≥ 85 days (aHR 1.80, 95%CI 1.19-2.72).

99 recipients were investigated for recurrent CMV; 40 (40%) experienced relapse within 6 months of stopping treatment for their first infection. The risk of recurrent CMV was significantly lower in those with low (aHR 0.20, 95%CI 0.06-0.74) and intermediate risk serostatus (aHR 0.40, 95%CI 0.19-0.84) (Figure 3). Older age (aHR 1.23 per 5 years older, 95%CI 1.06-1.44) was also significantly associated with recurrent CMV infection (Figure 4).

Figure 3 Risk of recurrent CMV infection in the 6 months following clearance and stopping of treatment for the first CMV infection (N=99), stratified by CMV serostatus at the time of transplant