Figure 1: Time and Rate of CMV-UL97-GCV-R resistance mutations

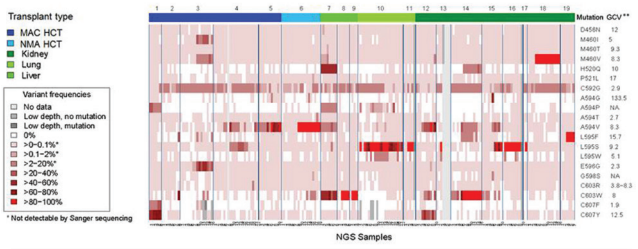
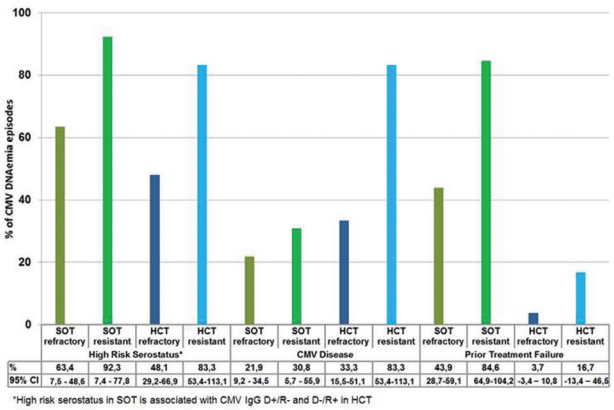


Figure. Heat map of the detected ganciclovir related mutations (GRMs) in CMV UL97. All available plasma samples with CMV loads >= 910 IU/mL per patient were sequenced from 19 patients with confirmed GRMs >10%.
*Indicate frequencies of quasispecies normally not detected by conventional Sanger Sequencing.
**Indicate GCV IC_{50} ratio of wildtype vs mutation.
Abbreviations: GCV; ganciclovir, HSCT; haematopoietic stem cell transplantation, SOT; solid organ transplantation, MAC; myeloablative conditioning, NGS; next generation sequencing, NMA; non myeloablative conditioning.

Figure 2: Comparison of clinical factors of CMV DNAemia between included refractory and resistant cases



*High risk serostatus in SOT is associated with CMV IgG D+/R- and D-/R+ in HCT

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

1585. Bloodstream Infection Survey in High-Risk Oncology Patients (BISHOP) with Fever and Neutropenia (FN): Correlation Between Initial Empiric Antibiotic Regimen Correlation and Susceptibility Patterns

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Background. The empiric initial antibiotic regimen (IAR) for treatment of febrile neutropenia (FN) relies on a knowledge of epidemiology and susceptibility patterns of bacterial bloodstream infections (BSI), especially in high-risk patient populations, i.e., those receiving chemotherapy for hematologic malignancies (HM) or undergoing hematopoietic stem cell transplant (HCT). As the last US national survey of BSI epidemiology in cancer patients was published in 2003, we sought to update these data focusing exclusively on high-risk patients with attention to IARs used and their concordance with susceptibilities of isolated bloodstream pathogens.

Methods. A prospective ongoing survey among 14 high-volume US cancer centers submitting clinical and microbiologic data from consecutive HM patients with BSI during first FN after cytotoxic chemotherapy or HCT. Concordance between antibiotic and BSI was determined by investigator (AZ, AF) interpretation of susceptibility reports provided by each center compared with IAR used, for single organism bacteremias only.

Results. Among 294 FN bacteremic episodes (93 HCT), there were 336 bacterial pathogens (48.5% Gram negative [GN] 46.5% Gram positive [GP] and 6% anaerobes), with 88% monomicrobial episodes. *E. coli* and viridans group Streptococci (VGS) were the most commonly isolated GN and GP, respectively, each accounting for nearly 25% of total organisms identified. IARs included cefepime 61%, piperacillin–tazobactam 24%, and meropenem 8%. Isolates were nonsusceptible to the IAR in 38/227 (17%) of FN episodes. Antibiotic mismatch was more likely to occur with a non-VGS GP (37%) vs. GN (13%) or VGS (2%) $P < 0.001$.

Conclusion. This is the first US national survey of high-risk BSI in FN. Although mismatch between BSI and IAR occurs in 17% of FN bacteremia episodes, this is driven primarily by non-VGS GP isolates such as CoNS and MRSA. Currently used IARs, comprised primarily of cefepime and piperacillin–tazobactam, generally provide reliable coverage for GN isolates across the United States (87%) but careful tracking of this rate is essential to identify further erosion of coverage in the current era of antimicrobial resistance.

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1586. Prevalence and Significance of Pre-transplant BK Viremia and Viruria in Deceased and Living Kidney Donors and Kidney Transplant Recipients

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Background. BK virus (BKV) is a major cause of nephropathy in kidney transplantation. Pre-transplant BKV shedding in the donor or recipient may increase the risk for developing BKV viremia in kidney transplant recipients.

Methods. From August 2016 to December 2017, we prospectively performed pre-transplant BKV DNA PCR testing on plasma and urine samples from deceased kidney donors procured through Donor Network West, our local organ procurement organization and third largest in the country. We also simultaneously performed pre-transplant BKV DNA PCR testing of plasma and urine from living kidney donors and adult kidney transplant recipients as well as post-transplant surveillance testing of recipients at Stanford University Medical Center.

Results. BKV DNA PCR testing of plasma and urine samples from 212 deceased kidney donors revealed 17 donors that were positive (16 in urine, 1 in plasma; 8.02% BKV DNA detection). Fifty of these specimens went to Stanford kidney transplant recipients, including four donors with BKV viruria (8.00%). During the study period, we obtained complete pre-transplant donor and recipient pairings for 47 deceased and 39 living adult kidney transplant recipients. Of these 86 kidney recipients, none had detectable BKV DNA in pre-transplant donor or recipient plasma specimens, while 10 (four deceased, six living) had BKV DNA detected in the urine. The majority (9/10) were positive in the donor urine, with one positive in the recipient and one in both the recipient and donor. After a minimum follow-up of 5 months, three (30%) had developed BKV viremia, compared with three of the 76 (3.9%, $P = 0.009$) with negative pre-transplant BKV DNA. The rate of BKV viruria was not significantly different between deceased and living kidney donors (4/47 (8.5%) vs. 6/39 (15.4%), $P = 0.32$).

Conclusion. In one of the largest cohorts in the United States that also includes deceased donor testing, we demonstrate that pre-transplant BKV viruria, particularly

of the donor, is associated with development of BKV viremia in kidney transplant recipients. Pre-transplant BKV DNA screening in the urine of kidney donors (deceased and living) may be useful in predicting risk for BKV viremia.

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

1587. Analysis of Breakthrough Blood Stream Infections in Left Ventricular Assist Device Recipients Managed With Chronic Antimicrobial Suppressive Therapy

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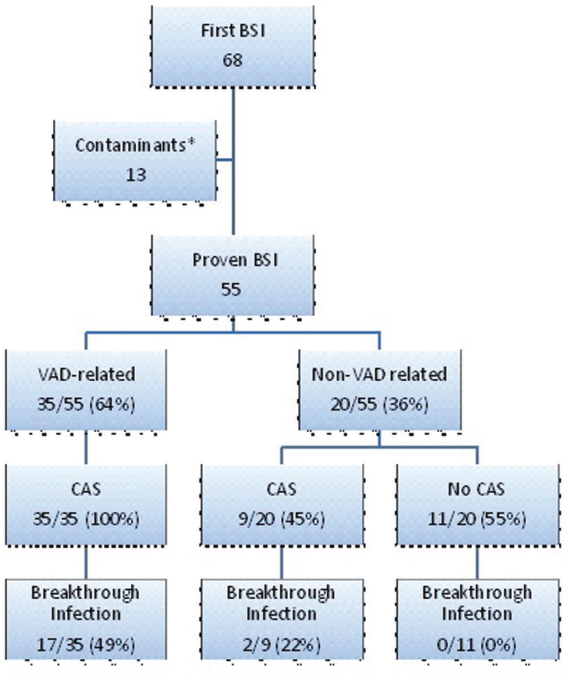
Background. Left ventricular assist devices (LVAD)-associated infections are associated with fivefold higher 1-year mortality. Published literature is insufficient to inform clinicians regarding optimal management of bloodstream infection (BSI) in patients LVAD recipients. In particular, it is unclear which episodes of BSI may result in occult hematogenous seeding of the device surfaces, and therefore should be managed with chronic suppressive therapy (CAS). We aim to describe BSI, CAS, and breakthrough BSI in our LVAD population.

Methods. We retrospectively reviewed 332 episodes of all LVAD infections at Mayo Clinic from 2007 to 2015. We categorized BSI as LVAD related/associated and LVAD nonrelated as defined by established criteria in the cardiac device literature. Our primary outcome was to describe breakthrough BSI in LVAD related and nonrelated infections in patients receiving CAS and those who were not.

Results. We identified 68 episodes of bacteremia in our LVAD population. Of these, 55 were proven BSI (see Fig 1). In our study cohort, 45/55 (82%) were male and median patient age was 62 years. A majority of LVAD implants were destination therapy 34/55 (62%) and 35/55(64%) had a central line in place at the time of BSI. Twenty patients had non-VAD-related BSI and nine of these (9/20, 45%) patients were placed on CAS with two of these (2/9, 22%) had subsequent breakthrough BSI, whereas 11/20 (55%) were not placed on CAS with no breakthrough infections seen (Figure 1).

Conclusion. Our preliminary data suggest that routine use of CAS for non-VAD-related BSI is not necessary as only a minority go on to have breakthrough BSI. Limiting unnecessary use of antibiotics will have significant implications for stewardship and preventing emergence of resistance.

Figure 1: Breakthrough Infections by CAS



*Contaminants=blood cultures that are deemed non-virulent/contaminated by chart review; CAS= chronic antimicrobial suppression; VAD=ventricular assist device; BSI=blood stream infection

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1588. Clinical Prediction Tool for Extended-Spectrum B Lactamase-Producing *Enterobacteriaceae* as the Etiology of Bacteremia in Solid Organ Transplant Recipients

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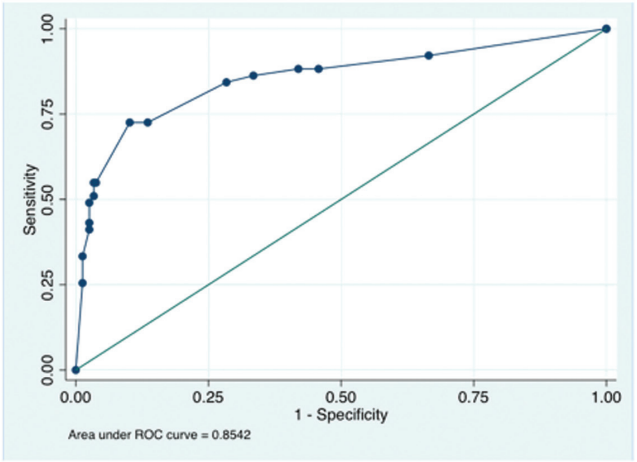
Background. Multidrug-resistant Gram-negative bacterial infections have emerged as a significant cause of morbidity among solid-organ transplant (SOT) recipients, leading to challenges in selection of empiric antibiotic therapy. As such, we developed a predictive tool to determine whether these patients are high or low risk for extended-spectrum β-lactamase (ESBL)-producing *Enterobacteriaceae* (EB) bacteremia at the time of positive blood culture.

Methods. All SOT recipients admitted to the Hospital of the University of Pennsylvania with blood cultures positive for EB between January 2007 and July 2016 were included in the source cohort. Multivariate logistic regression was used to determine predictors of ESBL-EB bacteremia. Manual forward selection was utilized to maximize area under the receiver operating characteristic curve (AUC), with sequential addition of covariates until achieving an AUC increase of <1%. A scoring system was developed based on the adjusted odds ratios for each covariate. Interval validity was assessed using the Hosmer-Lemeshow statistic, sensitivity, specificity, and the bootstrapping technique.

Results. Over the study period, there were 287 SOT recipients admitted with an EB bacteremia, of which 51 were due to an ESBL-producing organism. The final model that predicted presentation with ESBL-EB bacteremia included: identification of an ESBL-EB on culture in the previous 12 months, trimethoprim-sulfamethoxazole exposure in the prior 6 months, receipt of a kidney transplant, and fluoroquinolone exposure in the prior 6 months. This model achieved an AUC of 0.85, sensitivity of 54.9%, specificity of 96.6%, and Hosmer–Lemeshow statistic of 0.26 (Figure 1). Based on the adjusted odds ratios for each factor, scores of +3, +1, −1, and +1 were assigned to each covariate, respectively. With this scoring system, the maximum attainable score was 5, with any score of ≥3 deemed to be predictive of ESBL-EB bacteremia. After bootstrapping, the adjusted AUC remained at 0.85.

Conclusion. **The** presence of ESBL-EB organism as the etiology of bacteremia in SOT recipients can be predicted using the above scoring system. This tool will inform judicious empiric antibiotic use in this population at the time of positive blood culture.

Figure 1: Receiver operating characteristic (ROC) curve for predictive model



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

1589. Increased Detection of Diarrheal Pathogens in Hematopoietic Stem Cell Transplant Recipients Using a Multiplexed PCR Panel

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