Table 2: Isolates of bacteremic donors with proportion of recipients treated.

| Donor | Blood Culture isolate               | Number of KTRs* who received PAT* | Number of KTRs who received PAT* | Number of KTRs Untreated |
|-------|-------------------------------------|-----------------------------------|----------------------------------|--------------------------|
| TMP-SMX | 36                                  | 9 (25%)                           | 27 (75%)                         |
| Bacitracin | 29                                  | 14 (78%)                          | 6 (39%)                          |
| Acinetobacter baumannii complex | 2                                   | 1                                 | 2                               |
| Enterobacter cloacae | 1                                   | 1                                 | 1                               |
| Enterococcus faecalis | 1                                   | 1                                 | 1                               |
| Escherichia coli | 2                                   | 2                                 | 2                               |
| Klebsiella pneumoniae | 2                                   | 2                                 | 2                               |
| Pseudomonas aeruginosa | 1                                   | 1                                 | 1                               |
| Staphylococcus aureus | 5                                   | 5                                 | 1                               |
| Streptococcus agalactiae | 1                                   | 1                                 | 1                               |

*Kidney Transplant Recipient (KTR)
* Prophylactic Antibiotic Therapy (PAT)
* Bacteria Adherent in culture growth of non-commensal organisms per the Center for Disease Control and Prevention’s National Healthcare Safety Network Organism List

Conclusion. KTR donors with bacteremia who were treated received a median of 8.5 days of PAT with no instances of breakthrough infection. In contrast, majority of donor blood cultures with organisms classified as common commensals were not treated and did well. Future studies are needed to assess whether perioperative antibiotics coupled with TMP/SMX prophylaxis post-transplantation are sufficient in select cases of transplantation from donors with bacteremia.

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211. Burkholderia Cenocepacia Infections at Sites Other Than the Respiratory Tract, a Large Case Series from a Tertiary Referral Hospital in Lebanon

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Session: P-10. Bacteremia

Background. Burkholderia cenocepacia has been described to cause mainly respiratory tract infections. We noticed an increased number of skin and soft tissue infections (SSTIs), bloodstream infections (BSIs) and osteomyelitis over the past years at our medical center.

Methods. This is a retrospective chart review of 44 patients with documented B. cenocepacia infection at sites other than the respiratory tract diagnosed between 2005 and 2020 at the American University of Beirut Medical Center, a tertiary referral hospital for the Middle East region.

Results. The nationalities of our patients were Iraqi (40.9%), Lebanese (34.1%), and Syrian (20.5%). Twenty-six of the infections (59.1%) were hospital-acquired infections (HAIs). The most common infections were BSIs (17/44, 38.6%), then SSTIs as 18/44 (40.9%). Half of the vertebral osteomyelitis were located in the lumbar, and 9/44 (20.5%) in the thoracic region. All the patients received directed therapy for an average duration of 23.48 days (IQR: 17.77–37.79) days, and for 60 days for those with osteomyelitis. Combination regimens of 2 antibiotics (cefazidime, quinolones, carbapenems, trimethoprim-sulfamethoxazole (TMP-SMX)) were used in 10 patients, whereas 24 received a single antibiotic. Thirty three patients (75%) were admitted to the hospital, 20 (45.5%) of which had an indwelling catheter and 12 (27.3%) were in the intensive care unit. Thirty two patients (96.9%) were discharged home. Susceptibility testing revealed 84.1%, 54.5%, 63.2%, and 65.9% susceptibility to ceftazidime, tetracycline, quinolones being the most common. All the patients received directed therapy for an average duration of 23.48 days (IQR: 17.77–37.79) days, and for 60 days for those with osteomyelitis. Combination regimens of 2 antibiotics (cefazidime, quinolones, carbapenems, trimethoprim-sulfamethoxazole (TMP-SMX)) were used in 10 patients, whereas 24 received a single antibiotic. Thirty three patients (75%) were admitted to the hospital, 20 (45.5%) of which had an indwelling catheter and 12 (27.3%) were in the intensive care unit. Thirty two patients (96.9%) were discharged home. Susceptibility testing revealed 84.1%, 54.5%, 63.2%, and 65.9% susceptibility to ceftazidime, tetracycline, quinolones, carbapenems respectively.

Characteristics of patients

**Patients' Characteristics**

| Age | Gender | Nationality | Smoking history | Past medical history | Chronic kidney disease | Malignancy | Diabetes Mellitus | Chronic liver disease | Prior surgical history on affected site | History of trauma | Atherosclerotic cardiovascular disease | Cerebral vascular accident |
|-----|--------|-------------|----------------|---------------------|------------------------|------------|------------------|----------------------|----------------------------------------|----------------------|-------------------------------|--------------------------|
| 50.54 ± 9.048 | Males | Lebanese | Smoker | None | 6 | 19 | 7 | 2 | 19 | 4 | 8 | 3.68 |

Conclusion. B. cenocepacia BSIs, SSTIs, abscesses, and osteomyelitis were noted to be more common at our medical center as HAIs particularly in Iraqi and Syrian patients, raising the concern that countries at war might be at increased risk for such infections. Our susceptibilities results were consistent with the literature. Although B. cenocepacia is a resistant bacteria, the majority of our patients were successfully treated.

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212. Measuring the Morbidity of Infectious Complications of the Opiate Epidemic: A Retrospective Cohort Study

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Session: P-10. Bacteremia

Background. Many states have reported that the incidence of invasive bacterial and viral infections has risen alongside rates of opiate use and injection drug use. The aim of this exploratory project is to characterize the incidence of invasive bacterial infections (IBI) over time in a national Veteran population, describe screening for substance use among Veterans with IBI, and assess engagement in harm reduction services.

Methods. A national, multicenter, retrospective cohort of Veterans admitted to the Veterans Health Administration (VA) between 10/1/2008 – 9/30/2018 with a positive blood culture was created using electronic health record (EHR) data. Patients' demographics, clinical characteristics, microbiologic cultures, prescription history, laboratory values, and administrative coding data were extracted from the EHR. All analyses were performed in Microsoft Excel.

Results. Among 5,158,137 inpatient admissions during the study period, we identified 257,926 unique patients with bacteremia (5.0%). The incidence of bacteremia/sepsis increased consistently during the study period, rising from 2.29 per 10,000 patient-days to 5.97 per 10,000 patient-days across the national VA healthcare system (Figure 1). Among Veterans with bacteremia, 17,436 (6.8%) had prior history of substance use and 24,927 (9.7%) had a history of hepatitis C virus infection. In 196,295 cases (76.1%), no urine toxicology screening was completed or the result was negative. Among Veterans with bacteremia, 17,436 (6.8%) had prior history of substance use and 24,927 (9.7%) had a history of hepatitis C virus infection. In 196,295 cases (76.1%), no urine toxicology screening was completed or the result was negative. In 196,295 cases (76.1%), no urine toxicology screening was completed or the result was negative.

Conclusion. Similar to findings in other populations, the incidence of IBI has steadily increased within the national VA. Despite limited screening, a high proportion of Veterans with bacteremia had prior history of substance use and 24,927 (9.7%) had a history of hepatitis C virus infection. In 196,295 cases (76.1%), no urine toxicology screening was completed or the result was negative. In 196,295 cases (76.1%), no urine toxicology screening was completed or the result was negative.

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213. Assessment of Compliance with Order Set and Bundle for Management of Staphylococcus aureus Bacteremia

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Session: P-10. Bacteremia

Background. Staphylococcus aureus (S. aureus) is an aerobic gram-positive coccus that causes a variety of infections. S. aureus bloodstream infections, also known as bacteremias, have significant morbidity and mortality and are difficult to eradicate. A single-center study showed a 9.4% recurrence rate for S. aureus bacteremia, despite adequate treatment. The Infectious Disease Society of America (IDSA) recognizes the seriousness of S. aureus infections, particularly methicillin-resistant S. aureus (MRSA), and has released guidance for treatment of these infections. Guidance for S. aureus bacteremias includes identification and removal of the source and early optimization of antibiotics. Serial imaging and laboratory monitoring, including repeat blood cultures, are also necessary to establish the duration of treatment, ensure microbiologic
eradication, and reduce the risk of long-term complications. Due to the complexity of *S. aureus* bacteremia, early involvement of infectious diseases (ID) specialists is strongly recommended.

**Methods.** This retrospective, single-center study was designed to evaluate the current management of *S. aureus* bacteremias, including compliance to the elements of the ID high order bundle. Patients 18 years and older who had a positive blood culture for *S. aureus* were included in this study. Recurrence of *S. aureus* infection was assessed at 6 months. Data was analyzed to compare patients with and without ID consults.

**Results.** Eighty-four patients met inclusion criteria. ID consultation resulted in a higher percentage of patients achieving 100% compliance with the bundle elements compared to patients without ID consults (73% vs 25%, respectively; p=0.009). For further breakdown of compliance see Table 1. No statistical difference was detected in recurrence rates (11% vs 33%, respectively; p=0.18) or mortality (8% vs 25%, respectively; p= 0.17) due to the small sample size.

**Conclusion.** ID specialist involvement for the treatment of *S. aureus* bacteremia resulted in greater compliance with the *S. aureus* bacteremia bundle. No statistical difference in recurrence or mortality rates was detected.

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**214. Prospective Evaluation of the GenMark Dx ePlex® Blood Culture Identification Gram Negative Panel**

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**Session:** P-10. Bacteremia

**Background.** The ePlex BCID Gram-Negative (GN) panel utilizes electrowetting technology to detect the most common causes of GN bacteremia (21 targets) and 6 antimicrobial resistance genes from positive blood culture bottles. Rapid detection of extended spectrum β-lactamas (ESBL; CTX-M), carbapenemases (KPC, NDM, IMP, VIM, OXA 23/48), and highly resistant bacteria such as *Acinetobacter baumannii*, *Stenotrophomonas maltophilia* enables early optimization of antimicrobial therapy.

**Methods.** In this prospective study, we evaluated the performance of the BCID-GN panel compared to traditional standard of care culture and susceptibility testing with organism identification using the BioMerieux Vitek MS Matrix Assisted Laser Desorption Ionization (MALDI) Time of Flight mass spectrometry. Samples submitted for standard of care testing in BioMerieux BacT/Alert resin FA/FN blood culture bottles on the BacT/Alert VIRTUO automated blood culture system with GN panel (105/105, 100%). Consistent with alternative resistance mechanisms, only 8/12 (66.7%) of Enterobacterales with resistance to 3rd generation cephalosporins harbored the CTX-M gene. In contrast, 8/8 (100%) of isolates from samples harboring the CTX-M gene were resistant to 3rd generation cephalosporins.

**Conclusion.** Detection of *S. maltophilia*, *Acinetobacter baumannii* expressing OXA 23/48, and 8 Enterobacterales expressing CTX-M represent opportunities for early optimization of antimicrobial therapy in 10/108 (9.3%) of samples. The BCID-GN Panel provides rapid accurate detection of resistant gram negative bacteria enabling high quality data driven optimization of antimicrobial therapy.

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215. *Candida glabrata* (CG) Bloodstream Infections (BSIs) Are Characterized by Genetically Diverse Populations of Strain Variants Recovered from Positive Blood Cultures (BCs)

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**Session:** P-10. Bacteremia

**Background.** The long-standing paradigm is that almost all BSIs stem from a single, clonal organism ("single-organism" hypothesis). We hypothesized that CG-positive BCs were comprised of genetically diverse strain variants.

**Methods.** Five to ten CG colonies were isolated from positive BC bottles from ten distinct patients (pts) for a total of 94 clones, which underwent NextGen short-read sequencing (Illumina). Variants were analyzed using SNPeff, and a phylogeny was constructed with Maximum Likelihood method.

**Results.** BCs harbored a diverse population of CG strains that were unique to each pt ([Fig. 1]). All strains were genetically distinct, differing by unique SNPs and insertions-deletions (indelo) [Fig. 2-3]. SNPs were ~8-fold more common than indels. Individual genomes from the same time point in the same pt exhibited consistent magnitude of variations relative to reference genome; however, variations were unique, pointing to significant genomic variability that could be both intra- and interclonal. The number of variant sites for within-pt pairwise clone comparisons ranged from 1924-8500. There were 124.145 variant sites when all clones are compared. Roughly half of all SNPs were identical in different samples from a given pt; the remainder were present/absent in at least one sample per pt. Long-read WGS revealed strains with structural variants in each pt, including chromosomal recombinations and gene duplications that were not evident by short-read WGS. A genomic phylogeny construction showed that 94 clones spanned 3 distinct clades that were distinct from the reference strain. Finally, comparison of non-synonymous mutations among intra-pt clones showed overwhelming overrepresentation of adhesin and adhesin-like genes, pointing to possible importance in host adaptation.