



**Figure 2.** Taxonomic identifications using Metaxa2 resulting from metagenomic sequencing of samples subjected to different processing methods. 1) List of abbreviations. IN: internal standard added, not PMA treated. NP: no internal standard added, PMA treated. IPF: internal standard added, PMA treated, filtered. IPN: internal standard added, PMA treated, unfiltered. NPF: no internal standard added, PMA treated, filtered. Samples generated from the filter retentate are marked with "F" followed by the pore size of the filter. Samples starting with "S" represent the ZymoBIOMICS Microbial Community Standard only. 2) All taxa claimed as components by the ZymoBIOMICS Microbial Community Standard are in gray. 3) Taxa labeled with an asterisk in the legend were detected by cultivation coupled with MALDI-TOF MS. *Pantoea agglomerans*, *Pseudodescherichia vulneris*, *Pseudomonas fluorescens*, *Pseudomonas putida*, *Psychrobacter faecalis*, *Erwinia rhapontici*, *Bacillus simplex*, *Cultibacterium Avidum* were detected by cultivation but not seen by metagenomic sequencing.

**Fig. 2.**

### Presentation Type:

Poster Presentation

### Blood Culturing Practices at an Academic Medical Center

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**Background:** Blood cultures are part of the evaluation of hospital patients with fever. Patients with central lines in place, frequently have blood samples for culture drawn through lines. We sought to assess blood culturing practices at our institution. **Methods:** Retrospective review of BCs performed in hospitalized patients over a 12-month period (August 2018–July 2019) at an academic, tertiary-care center with 1,297 licensed beds and >62,000

admissions a year. A specialized phlebotomy team is involved in all peripherally drawn blood samples; however, the patient's nurse obtains a blood sample through a central line. **Results:** Overall, 35,121 blood cultures were performed for an incidence rate of 106 BC per 1,000 patient days or 566 blood cultures per 1,000 admissions. Most blood samples (67%) were collected via peripheral venipuncture. We detected significant variation in culturing rates and the proportion of blood samples obtained through central lines among collecting units (Table 1). Overall, the blood culture contamination rate was 1.6%. Blood samples obtained through a central line had a higher contamination rate (2.2%) compared to samples obtained through peripheral venipuncture (1.3%;  $P < .0001$ ). Blood culture rates were highest in intensive care units (ICUs) compared with other types of patient care units (Table 1). The blood

**Table 1.** Blood Culture Patterns in Different Patient Populations

Unit	No. of Blood Cultures (BC)	BC per 1,000 Patient Days	Positivity Rate, %	Contamination Rate, %	BC Proportion Drawn Through Lines, %
Hospital-wide	35,121	106	10	1.6	23
ICUs	11,315	246	8.8	1.3	30
Hematology-oncology units	6,965	217	10	2	40
General care medical units	5,160	108	10	1.5	2.7
General care surgical units	2,799	45	9	1.4	5
General care pediatrics	603	49	12	2.6	71

culture positivity rate was significantly lower in ICUs (8.8%) compared with hematology-oncology (10%; HR, 0.88; CI, 0.80–0.96;  $P = .006$ ), general medicine (10%; HR, 0.88; CI, 0.80–0.97;  $P = .013$ ), and pediatrics (12%; HR, 0.74; CI, 0.59–0.92;  $P = .008$ ). The ICUs had the lowest rate of BC contamination at 1.3%. **Conclusions:** Blood samples obtained through central lines for culture are more likely to be contaminated than peripherally drawn blood samples. Despite a relatively high rate of line-drawn blood samples for culture, ICUs had the lowest BC contamination rate, possibly reflecting high familiarity of ICU nurses with line draws. Blood samples collected through lines were most frequently performed in pediatrics and hematology-oncology, and these units had correspondingly higher rates of contamination. This information will be used to inform institutional guidelines on blood culturing and to identify ways to minimize blood culture contamination, which often results in additional testing and/or unnecessary antimicrobial use.

**Funding:** None

**Disclosures:** Consulting fee- Merck (Priya Sampathkumar)  
Doi:10.1017/ice.2020.657

#### **Presentation Type:**

Poster Presentation

#### **Bloodstream Infections Caused by *S. aureus*: Daptomycin Nonsusceptibility and Clinical Aspects**

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**Background:** *Staphylococcus aureus* is one of the leading pathogens isolated from bloodstream infections (BSIs), and vancomycin has been the main choice to treat MRSA (methicillin-resistant *S. aureus*) infections. Vancomycin-intermediate *S. aureus* (VISA) and heteroresistant-VISA (hVISA) have been described, limiting this antibiotic use. We evaluated aspects associated with the resistance and its clonality of the *S. aureus* isolated from BSIs, and we determined their association with clinical aspects of patients attended at Rio de Janeiro between 2016 and 2018. The detection of MRSA and trimethoprim-sulfamethoxazole resistant isolates was performed using the disk diffusion test, while the minimum inhibitory concentrations (MICs) were evaluated for 5 antimicrobials using the broth microdilution method. The MICs for ceftaroline and vancomycin of the MRSA isolates were determined using the E test. The presence of hVISA isolates was evaluated for isolates with vancomycin MICs of 1 and 2 µg/mL by screening on BHI agar

added with vancomycin. The population profile was divided by the area under the curve (ie, PAP/AUC test). SCC *mec* was evaluated by PCR and the clonal profile by PFGE method. Among 123 *S. aureus* isolates from BSI, 31% were MRSA. MIC<sub>50</sub> and MIC<sub>90</sub> were daptomycin 2 and 2 µg/mL; linezolid, 1 and 1 µg/mL; oxacillin 1 and 256 µg/mL; teicoplanin, 0.5 and 0.5 µg/mL and vancomycin 1 and 1 µg/mL. MIC values for ceftaroline and vancomycin were 0.75 and 2 µg/mL. The frequency of isolates not susceptible to daptomycin was 75%. The clonal lineages and SCC*mec* types found were USA100/ST5-II (50%), USA800/ST5-IV (22%), USA300/ST8-IV (15.8%), USA1100/ST30-IV (5.3%), BEC/ST239-III (5.3%), and 1 isolate carrying SCC*mecV*/ST1. We found 1 VISA isolate, and the PAP/AUC analysis detected 3 hVISA isolates that were associated with the USA100 and USA300 lineages. Overall, 85% of patients had a vascular catheter. More advanced age was associated with MRSA infection as was higher mortality. Patients with end-stage renal disease were more affected by MSSA infection. Daptomycin nonsusceptibility and VISA and hVISA phenotypes associated with prevalent clonal lineages were described. In addition, MRSA infections presented higher mortality, which emphasizes the importance of epidemiological studies.

**Funding:** None

**Disclosures:** None

Doi:10.1017/ice.2020.658

#### **Presentation Type:**

Poster Presentation

#### **Boots and Bugs: The Beginning of an Intervention for Firefighters**

Christine McGuire-Wolfe, Pasco County Fire Rescue

**Background:** Multiple studies have demonstrated that pathogens are present in both apparatus and stations within the fire service. Pasco County Fire Rescue's (PCFR's) 500+ firefighters routinely wear boots to trauma scenes and into patient's residences and then into the dormitory and living areas of the fire stations. Pasco County Fire Rescue (PCFR) recently participated in a larger effort to identify the bacteria, yeast, and mold that firefighters, emergency medical technicians, and paramedics are exposed to on apparatuses and the station living environment during a typical shift. During these efforts to swab multiple touch points within apparatus (ambulances and engines) and common areas of the stations, firefighters' boots were identified as a significant source of bacterial contamination. **Methods:** Swabs of 191 surfaces in 23 vehicles and 5 fire stations were collected, including 3 swabs from the bottom of firefighter boots. **Results:** Firefighter boots had the highest bacterial CFUs of all locations swabbed, with >900,000 and 378,000 CFUs per boot. Disinfection with a quaternary