Efficacy Characteristics of MRSA Nares Screening by Culture Site

| Type | Number | Male | Age | Sensitivity | Specificity | Positive Predictive Value | Negative Predictive Value | P value MRSA |
|---|---|---|---|---|---|---|---|---|
| *Whole cohort* | | | | | | | | |
| Whole cohort | 447,579 | 430,356 (96.2%) | 68.3 +/- 12.4 | 67.4% 95% CI (67.0%-67.9%) | 83.0% 95% CI (82.8%-83.1%) | 31.4% 95% CI (31.2%-31.6%) | 95.7% 95% CI (95.6%-95.7%) | <0.0001 |
| *Blood* | | | | | | | | |
| Blood | 64,128 | 62,265 (97.1%) | 68.1 +/- 11.9 | 69.9% 95% CI (68.7%-71.0%) | 82.5% 95% CI (82.1%-82.8%) | 30.1% 95% CI (29.6%-30.6%) | 96.2% 95% CI (96.1%-96.3%) | <0.0001 |
| *Intra-abdominal* | | | | | | | | |
| Intra-abdominal | 8,071 | 7,754 (96.1%) | 65.0 +/- 11.4 | 64.0% 95% CI (59.1%-68.6%) | 90.9% 95% CI (90.2%-91.5%) | 27.2% 95% CI (25.2%-29.2%) | 97.9% 95% CI (97.7%-98.2%) | <0.0001 |
| Intra-abdominal sterile | 7,426 | 7,135 (96.1%) | 65.2 +/- 11.3 | 62.5% 95% CI (57.1%-67.8%) | 91.0% 95% CI (90.3%-91.7%) | 24.5% 95% CI (22.5%-26.7%) | 98.1% 95% CI (97.8%-98.4%) | <0.0001 |
| *Pulmonary* | | | | | | | | |
| Respiratory tract | 75,242 | 73,575 (97.8%) | 68.8 +/- 11.4 | 76.2% 95% CI (75.4%-77.0%) | 83.1% 95% CI (82.8%-83.4%) | 43.8% 95% CI (43.3%-44.3%) | 95.3% 95% CI (95.1%-95.4%) | <0.0001 |
| Sterile Respiratory | 15,583 | 15,204 (97.6%) | 67.0 +/- 11.0 | 74.6% 95% CI (72.7%-76.4%) | 84.7% 95% CI (84.1%-85.3%) | 44.7% 95% CI (43.6%-45.9%) | 95.2% 95% CI (94.9%-95.6%) | <0.0001 |
| *Renal System* | | | | | | | | |
| Renal system | 164,330 | 155,547 (94.7%) | 71.0 +/- 12.7 | 72.5% 95% CI (71.1%-73.8%) | 81.6% 95% CI (81.4%-81.8%) | 9.8% 95% CI (9.6%-10.0%) | 99.1% 95% CI (99.0%-99.1%) | <0.0001 |
| *Wound* | | | | | | | | |
| Wound | 95,832 | 92,816 (96.7%) | 64.7 +/- 11.9 | 59.7% 95% CI (59.0%-60.5%) | 85.5% 95% CI (85.2%-85.7%) | 48.1% 95% CI (47.5%-48.6%) | 90.4% 95% CI (90.3%-90.6%) | <0.0001 |
| Wound Sterile | 51,793 | 50,180 (96.9%) | 64.4 +/- 11.3 | 58.3% 95% CI (57.3%-59.3%) | 87.6% 95% CI (87.3%-88.0%) | 49.6% 95% CI (48.9%-50.4%) | 91.0% 95% CI (90.8%-91.2%) | <0.0001 |

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## 572. Relationship Between Chlorhexidine Gluconate (CHG) Skin Concentrations and Microbial Skin Colonization among Medical Intensive Care Unit (MICU) Patients

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***Background.*** CHG bathing is used to suppress patients' microbial skin colonization, in order to prevent infections and transmission of multidrug-resistant organisms. Prior work has suggested that microbial growth is inhibited when CHG skin concentrations exceed threshold levels.

***Methods.*** We conducted 6 single-day surveys from January 2018 to February 2019 in 7 academic hospital MICUs with established CHG patient bathing. Adult patients were eligible to have skin swabbed from adjacent 25 cm2 areas on the neck, axilla, and inguinal region for culture and CHG concentration determination. CHG skin concentrations were measured by a semi-quantitative colorimetric assay. Selective media were used to isolate targeted microorganisms (Table 1). Species were confirmed by matrix-assisted laser desorption ionization time-of-flight mass spectrometry; antibiotic susceptibility was determined by MicroScan (Beckman Coulter). We modeled the relationship between CHG skin concentrations (log2-transformed) and microorganism recovery (yes/no as primary outcome) using multilevel models controlling for clustering of body sites within patients and within ICUs, assessing slope and threshold effects.

***Results.*** We enrolled 736/759 (97%) patients and sampled 2176 skin sites. Gram-positive bacteria were detected most frequently (Table 1). The adjusted odds of identifying gram-positive organisms decreased linearly as CHG skin levels increased (Figure 1a), without evidence of a threshold effect. We also found significant negative linear slopes without evidence of threshold effects for other pathogens tested (Table 2; Figure 1), with the exception of gram-negative bacteria and vancomycin-resistant enterococci. When modeling quantitative culture results (colony-forming units) for gram-positive organisms as a continuous outcome variable, a similar relationship was found.

***Conclusion.*** Higher concentrations of CHG were associated with less frequent recovery of gram-positive bacteria and Candida species on the skin of MICU patients who were bathed routinely with CHG. For microbial inhibition, we did not identify a threshold concentration of CHG on the skin; rather, increasing CHG skin concentrations led to additional gains in inhibition. For infection prevention, aiming for high CHG skin levels may be beneficial.

**Table 1:** Prevalence of Microorganisms Recovered by Culture from Skin of Medical Intensive Care Unit Patients at 7 Hospitals

| Organism | Neck | Axilla | Inguinal | Total |
|---|---|---|---|---|
| Gram-Positive Bacteria | 612/729 (84) | 461/728 (63) | 456/709 (64) | 1529/2166 (71) |
| *Staphylococcus aureus* | 64/732 (9) | 24/730 (3) | 32/714 (5) | 12/2176 (6) |
| Methicillin-resistant *S. aureus* | 21/730 (3) | 8/727 (1) | 12/709 (2) | 41/2166 (2) |
| *Enterococcus* species | 63/732 (9) | 38/730 (5) | 118/714 (17) | 219/2176 (10) |
| Vancomycin-resistant enterococci | 26/729 (4) | 16/727 (2) | 50/708 (7) | 92/2164 (4) |
| Gram-Negative Bacteria | 63/731 (9) | 47/729 (7) | 93/713 (13) | 203/2173 (9) |
| *Candida* species | 77/721 (11) | 62/722 (34) | 118/704 (17) | 257/2147 (12) |
| *Candida auris* | 0/721 (0) | 2/722 (0.3) | 0/704 (0) | 2/2147 (0.1) |

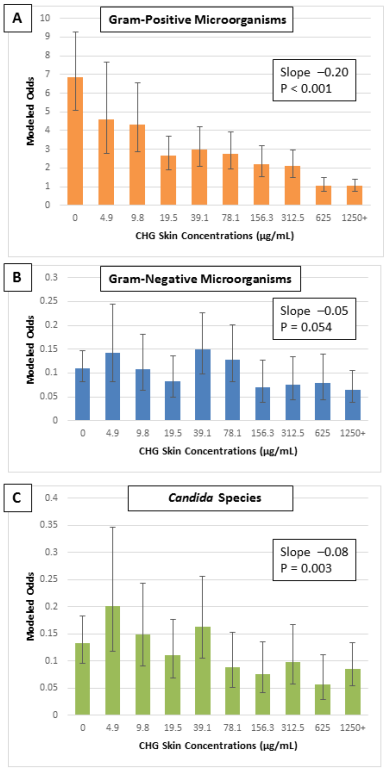
Note. Cells represent n/N (%) = number of positive skin sites / number of skin sites sampled for target microorganism. Total represents all three body sites combined.

**Table 2:** Linear Effects of Chlorhexidine Gluconate Skin Concentration on Microbial Recovery by Culture from Skin

| Organism | Change in odds/log2 CHG unit | *P* value |
|---|---|---|
| Gram-Positive Bacteria | -0.20 | <0.001 |
| *Staphylococcus aureus* | -0.18 | <0.001 |
| Methicillin-resistant *S. aureus* | -0.19 | 0.003 |
| *Enterococcus* species | -0.07 | 0.003 |
| Vancomycin-resistant enterococci | -0.06 | 0.12 |
| Gram-Negative Bacteria | -0.05 | 0.054 |
| *Candida* species | -0.08 | 0.003 |

Note. Slope represents change in microorganism recovery by culture from patient skin for every unit increase in log2-CHG skin concentration (i.e., for each doubling of CHG skin concentration).

**Figure 1. Relationship Between Chlorhexidine Gluconate (CHG) Skin Concentrations and Modeled Odds of Microorganism Culture Detection Among Medical Intensive Care Unit Patients**




Note. Odds of microorganism culture detection on the skin at each CHG skin concentration were estimated using mixed effects models that controlled for body site clustered within patients and within ICUs. Bars represent 95% confidence intervals. Slope represents change in odds of microorganism recovery for every unit increase in CHG skin concentration.

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## 573. Enterococcal Bacteremia in a Tertiary Care Center in Mexico: A Retrospective Analysis Focus on Vancomycin-Resistant *E. faecium* and Ampicillin-Resistant *E. faecalis*

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***Background.*** The primary pathogens in genera enterococcus are *E. faecalis* and *E. faecium*, increasing acquired resistance to glycopeptides and β lactamic has done the management more challenging. We aimed to describe the risk factors for acquisition of bacteremia for vancomycin-resistant *E. faecium* (VRE) and ampicillin-resistant *E. faecalis* (ARE) and the 30-day mortality in comparison to susceptible enterococcal bloodstream infection (BSI)

***Methods.*** From 2007- 2017 medical records of all BSI for *E. faecalis* and *E. faecium* were evaluated. Risk factor for acquisition of VRE and ARE as well as the significant variables associated with 30-day mortality for enterococcal BSI were determined by univariate and multivariate analysis. The molecular mechanism of VRE was performed by PCR

***Results.*** There were 192 patients with *E. faecium* BSI of which 107(56%) patients had VRE BSI with 94% VRE strains expressing *vanA* gene. The index bacteremic episodes were classified as nosocomial o healthcare associated in 99%, 102(95%) had hospitalization 1 year before and 101(94%) history of use of antibiotics 3 months earlier, the multivariate analysis showed duration of the previous hospitalization >10 days (OR, 80.18; 95% CI, 1.81–634), use of central venous catheter [OR, 11.15; 95% CI, 2.48–50.2), and endotracheal cannula [OR, 17.91; 95% CI, 1.22–262) as significant associated variables. The mortality for VRE was greater than susceptible *E. faecium* (60% vs. 24%, $P < 0.001$). The only factors for 30-day mortality for *E. faecium* BSI in the multivariate analysis was APACHE ll score [OR,1.45; 95% CI, 1.26–1.66) and patients with chemotherapy of cancer. (OR, 3.52; 95% CI, 1.09–11.39). 147 patients had *E. faecalis* BSI of which 18 (11%) patients had ARE, we did not find relevant clinical differences of ARE in comparison with ampicillin-susceptible *E. faecalis*, neither in risk factors for acquisition of ARE nor 30-day mortality [7(39%) vs. 38(29%), $P = 0.58$] in uni and multivariate analysis

***Conclusion.*** Our evaluation showed in a period of 10 years that VRE expressing *vanA* gene had a strong association with patients with previous nosocomial exposure. Severely ill patients and cancer patients on chemotherapy during the bacteremic episode were the variables more associated with 30-day mortality. ARE is yet of low prevalence and less known, constant surveillance about it is warranted

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## 574. Reporting of Vancomycin-Resistant *Enterococcus* Bacteremia among National Healthcare Safety Network Acute Care Hospitals

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***Background.*** The National Healthcare Safety Network's (NHSN's) Multidrug-resistant Organism/Clostridioides difficile (MDRO/CDI) Module serves as a surveillance platform for tracking antibiotic-resistant laboratory-identified (LabID) organisms. LabID event surveillance, which does not require submission of clinical data to NHSN, provides proxy measures for MDRO burden. While surveillance of some organisms is federally mandated, these requirements do not extend to vancomycin-resistant Enterococcus (VRE). We sought to describe the extent of acute care hospital (ACH) participation in NHSN VRE surveillance and identify facility-level factors associated with VRE bacteremia. These could explain differences in VRE incidence and be used in preparation for a national risk-adjusted benchmark.

***Methods.*** ACHs that reported at least one month of facility-wide inpatient (FacWideIN) VRE bacteremia LabID Event data to NHSN in 2017 were included in the analysis. LabID events were categorized as healthcare facility-onset (HO), defined as a laboratory result for a specimen collected ≥4 days after admission, or community-onset (CO), defined as a specimen collected < 4 days after admission. Monthly patient day and admission denominators were used to calculate FacWideIN HO incidence and CO prevalence rates. Univariate analyses were performed on facility-level factors from NHSN's annual hospital survey to assess their relationship with HO VRE bacteremia.

***Results.*** A total of 544 HO VRE bacteremia events were reported by 498 hospitals in 37 states. About 67% of reporting hospitals were located in California. The national rate of HO VRE bacteremia was 0.27 per 10,000 patient-days and the CO VRE bacteremia rate was 0.58 per 10,000 admissions. Major medical school affiliation, hospital type, larger number of beds and ICU beds, longer average length of stay and the presence of an oncology unit were significantly associated with HO VRE bacteremia (Table 1).

***Conclusion.*** Based on the VRE data reported to NHSN, certain facility-level factors may contribute to a higher incidence of HO VRE bacteremia. Future analyses can allow us to determine whether these factors are independently associated with VRE. Risk-adjusted surveillance data can help guide facilities and states to compare their burden of VRE to a national benchmark.

Table 1: Facility factors associated with healthcare facility-onset VRE bacteremia

| Facility factors | Healthcare facility onset VRE Bacteremia Incidence Rate, per 10,000 patient days | 95% Confidence Interval | P-value |
|---|---|---|---|
| Hospital type | | | |
| General acute care | 0.276 | 0.253, 0.300 | 0.0088 |
| Pediatrics or other specialty | 0.076 | 0.035, 0.145 | Referent |
| Total bed size | | | |
| < 75 beds | 0.106 | 0.052, 0.195 | 0.0045 |
| 75–157 beds | 0.131 | 0.093, 0.180 | 0.0002 |
| 158–283 beds | 0.205 | 0.169, 0.246 | 0.0245 |
| ≥ 284 beds | 0.337 | 0.305, 0.372 | Referent |
| ICU bed size | | | |
| < 8 beds | 0.074 | 0.030, 0.154 | 0.0015 |
| 8–17 beds | 0.157 | 0.115, 0.207 | 0.0007 |
| 18–40 beds | 0.179 | 0.145, 0.218 | 0.0044 |
| ≥ 41 beds | 0.347 | 0.314, 0.382 | Referent |
| Average length of stay | | | |
| < 3.4 days | 0.107 | 0.073, 0.151 | < 0.0001 |
| 3.4–4.0 days | 0.139 | 0.107, 0.177 | < 0.0001 |
| 4.1–5.0 days | 0.243 | 0.208, 0.283 | 0.026 |
| > 5.0 days | 0.431 | 0.384, 0.482 | Referent |
| Medical school affiliation | | | |
| Major teaching | 0.361 | 0.324, 0.401 | 0.0155 |
| Graduate teaching | 0.164 | 0.128, 0.209 | 0.4460 |
| Undergraduate teaching | 0.144 | 0.094, 0.213 | 0.1648 |
| None | 0.211 | 0.177, 0.252 | Referent |
| Oncology Unit | | | |
| Present | 0.396 | 0.353, 0.442 | < 0.0001 |
| Absent | 0.187 | 0.164, 0.212 | Referent |

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## 575. Evaluation of Risk Factors and Clinical Outcomes of Patients with Vancomycin-Resistant *Enterococcus* Infections

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***Background.*** Vancomycin-resistant *Enterococci* (VRE) occurs with enhanced frequency in hospitalized patients and are usually associated with poor clinical outcomes. The purpose of this study was to evaluate the risk factors and clinical outcomes of patients with VRE infections.

***Methods.*** This study was an IRB-approved multi-center retrospective chart review conducted at a three-hospital health system between August 2016-November 2018. Inclusion criteria were patients ≥18 years and admitted for ≥24 hours with cultures positive for VRE. Patients pregnant or colonized with VRE were excluded. The primary endpoint was to analyze the association of potential risk factors with all-cause in-hospital mortality (ACM) and 30-day readmission. The subgroup analysis focused on the association of risk factors with VRE bacteremia. The secondary endpoint was to evaluate the impact of different treatment groups of high dose daptomycin (HDD) (≥10 mg/kg/day) vs. low dose daptomycin (LDD) (< 10 mg/kg/day) vs. linezolid (LZD) on ACM and 30-day readmission. Subgroup analysis focused on the difference of length of stay (LOS), length of therapy (LOT), duration of bacteremia (DOB) and clinical success (CS) between the treatment groups.

***Results.*** There were 81 patients included for analysis; overall mortality was observed at 16%. Utilizing multivariate logistic regression analyses, patients presenting from long-term care facilities (LTCF) were found to have increased risk for mortality (OR 4.125, 95% CI 1.149–14.814). No specific risk factors were associated with 30-day readmission. Patients with previous exposure to fluoroquinolones (FQ) and cephalosporins (CPS), nosocomial exposure and history of heart failure (HF) showed association with VRE bacteremia. ACM was similar between HDD vs. LDD vs. LZD (16.7% vs. 15.4% vs. 0%, $P = 0.52$). No differences were seen between LOS, LOT, CS, and DOB between the groups.

***Conclusion.*** Admission from LTCFs was a risk factor associated with in-hospital mortality in VRE patients. Individuals with history of FQ, CPS and nosocomial exposure as well as history of HF showed increased risk of acquiring VRE bacteremia. There was no difference in ACM, LOS, LOT, and DOB between HDD, LDD and LZD.

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## 576. A Multicenter Epidemiology Study on Risk Factors of Vancomycin-Resistant *Enterococcus* Infections in China: Results from the China Antimicrobial Surveillance Network (CHINET) in 2016

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