proportion of male cases and controls was 60%. Length of stay for cases was longer than controls (median 39 days [range 1-539 days] vs. 3 days [range 1 – 136 days]), P < 0.001) and 82% of cases died within 30 days vs. 21% of controls (P < 0.001). In adjusted analyses, patient-level predictors of VRE bacteremia included: organ transplant (OR 18.83 [95% CI 8.37 – 42.79], cancer (OR 9.56 [95% CI 6.61 – 15.97]), ICU admission (OR 7.45 [95% CI 3.57 – 15.54]), heart disease (OR 5.95 [95% CI 1.92 – 13.18]) and length of stay (OR 1.08 per day [95% CI 1.03 – 1.12]); COPD (OR 3.10 [95% CI 0.86 – 11.20]) and diabetes (OR 2.35 [95% CI 0.72 – 7.64]) were not significant predictors. Hospital-level predictors included hospital size ≥800 beds (OR 10.64 [95% CI 3.84 – 34.25]), teaching hospitals (OR 4.20 [95% CI 1.65 – 10.74]).

Conclusion. Immunocompromised and patients admitted to ICU are at highest risk of VRE bacteremia, particularly at large hospitals and teaching hospitals. These results may help inform clinical decisions and infection prevention programs.

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2189. Case–control Study of VRE Acquisition in a Tertiary Care Hospital: Testing the Roles of Antibiotic use, Proton Pump Inhibitor Use and Colonization Pressure

Rishi Chanderraj, MD; Twisha Patel, PharmD; Clare Kinnear, PhD MPH; Andrew Read, DPhil; Laraine L. Washler, MD; Keith S. Kaye, MD, MPH and Robert Woods, MD PhD; 1University of Michigan Health System, Ann Arbor, Michigan, 2Michigan Medicine, Ann Arbor, Michigan, 3Pennsylvania State University, University Park, Pennsylvania, 4Division of Infectious Diseases, University of Michigan Medical School, Ann Arbor, Michigan, 5Infection Prevention and Epidemiology, Michigan Medicine, Ann Arbor, Michigan, 6University of Michigan Medical School, Ann Arbor, Michigan

Session: 242. HAI: MRSA, MSSA, and Other Gram-positives
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Background. Vancomycin-resistant Enterococcus (VRE) is a leading cause of healthcare associated infections. VRE can asymptptomatically colonize the gastrointestinal tract and colonization is a risk factor for subsequent sterile site infection. Active surveillance for colonization using rectal swabbing and contact precautions of colonized patients has been pursued by multiple institutions. In this setting, risk factors for converting from swab negative to swab positive have not been assessed.

Methods. We performed a retrospective matched case control study from June 2013 through December 2016 in a single institution. Patients admitted to eight units were routinely screened on admission and weekly thereafter. Cases had a positive swab followed by positive swab more than 3 days after admission. Controls were matched to time of admission to second swab (±5%), unit on which the second swab was performed, and date of admittance ±365 days. Co-morbidity data, culture data, and antibiotic and proton pump inhibitor (PPI) days on therapy (DOT) were abstracted from the electronic medical record and verified by manual checking 5% of the cohort. A comorbidity risk factor model was generated using conditional logistic regression and backward stepwise removal by AIC criterion to identify comorbidities significantly associated with conversion. With the best fit comorbidity model, colonization pressure, antibiotic use and PPI use were tested.

Results. We identified 551 cases with matched controls. The comorbidities conferring significantly increased odds ratio (OR) of converting from swab negative to swab positive include age (OR 1.01 per year, P = 0.035), time to index swab (OR 1.5, P = 0.026), neutropenia (OR 1.62, P = 0.001) and renal failure (OR 4.20 [95% CI 1.65 – 10.74]). Having one or more DOT of any systemic antibiotic was the largest effect on conversion to VRE positivity (OR 5.6, P < 0.001), but total antibiotic DOT was not significant. Each PPI DOT conferred an OR of 1.06 (P < 0.001). Colonization pressures from patients identified to be carriers and placed in contact precautions did not confer and increased risk.

Conclusion: Decreasing PPI use and preventing the initiation of antibiotic when possible should be considered to decrease VRE transmission in the hospital.

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2190. Single Nucleotide Polymorphisms (SNPs) Analyses Reveal Potential Vancomycin-Resistant Enterococci (VRE) Transmission Networks Between Rooms and Patients in a Hospital Setting

Lynn El Haddad, PhD; Samuel Scarponi, PhD; Glen Otero, PhD; Shaashank S. Ghantothi, MD, PhD; Mark Stibich, PhD, MHS; and Roy F. Chemaly, MD, MPH, FIDSA, FACP; 1Infectious Diseases, Infection Control, and Employee Health, The University of Texas MD Anderson Cancer Center, Houston, Texas, 2Department of Mathematics and Statistics, University of Vermont, Burlington, VT, 3Independent researcher, San Diego, California, 4Infectious Diseases, Infection Control and Employee Health, The University of Texas MD Anderson Cancer Ctr, Houston, Texas, 5Xerox Healthcare Services, LLC, Houston, Texas, 6Department of Infectious Diseases, Infection Control, and Employee Health, The University of Texas MD Anderson Cancer Center, Houston, Texas

Session: 242. HAI: MRSA, MSSA, and Other Gram-positives
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Background. The transmission of pathogens in a hospital setting is important for tracking and controlling the spread of multi-drug resistant organisms, VRE in particular. The transmission of pathogens may occur through direct patient contact or through the surrounding environment including medical equipment.

Methods. In this study, 90 VRE isolates were selected for Whole Genome Sequencing (WGS) including 55 VRE-positive rectal swabs (S) from hematopoietic cell transplant recipients, 29 environmental swabs from these patients' bathrooms (B), and 26 swabs from their main rooms (M). We used SNPs analyses of 100 ortholog concatenated genes to identify VRE clusters and transmission networks between patients and rooms. We categorized isolates into hospital-acquired (HA) VRE (after ≥ 48h from admission) and community-acquired (CA) VRE (≤48h). Patient location and VRE sequence types (STs) were identified.

Results. HA and CA VRE isolates did not group into distinct clades. Eight different STs were observed, all belonging to the clonal complex CC17. Interestingly, 1 strain belonged to ST194 which is rarely found in the US and bacteremia was observed in patients with VRE belonging to ST736 and ST664 (Fig1). Some VRE strains isolated from patients and their room environment (pairs) were only 40% identical whereas different pairs were 99% identical based on the SNPs found in 100 ortholog concatenated genes. Two pairs were isolated from distinct rooms and time period and were highly genetically identical (Fig1, in pink).

Conclusion. To our knowledge, this is the first study that compares numerous HA and CA VRE as well as VRE strains derived from the environment and immunocompromised patients. Due to the high frequency of mobile genetic elements’ gain/loss in VRE, “hybrid” genomes are emerging resulting in a fusion of HA and CA VRE. We showed the potential presence of transmission networks between rooms and VRE transfer to patients. This data will aid in implementing efficient infection control strategies to prevent and control the spread of this opportunistic organism in the hospital setting.

Figure 1. Phylogenetic tree showing the genetic relatedness of the 90 VRE isolates according to SNPs found in 100 ortholog concatenated genes.

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2191. Characteristics of Tedizolid Non-susceptible Enterococcal Clinical Isolates

Abhay Dhand, M.D.; Leslie Lee, PharmD; Stephen Lobo, MD and Guiqing Wang, MD/PhD; 1Transplant Infectious Diseases, Westchester Medical Center, Valhalla, New York, 2Westchester Medical Center/New York Medical College, Valhalla, New York

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Background. Tedizolid is a novel oxazolidinone antibiotic with activity across a broad range of gram-positive pathogens. The aim of this study was to describe the characteristics of tedizolid (TZD) resistant enterococcal clinical isolates.

Methods. Tedizolid resistant isolates were recovered from patients at Westchester Medical Center, New York from 2012 to 2016. In vitro susceptibility of tedizolid isolates was performed by broth microdilution using the Sensititre™ panel
in accordance with the guidelines of the Clinical and Laboratory Standards Institute. The sequence type (ST) of enterococci was determined based on multilocus sequence typing (MLST) data derived from assembled next-generation sequencing.

**Results.** During the study period, we identified 8 clinical isolates which were resistant to Tedizolid. Clinical characteristics, genomic, treatment and outcome data are summarized in Table 1. 7/8 isolates were *E. faecium* belonging to a unique ST736 which predominates in our hospital. 7/8 isolates showed G2567T mutation of 23S rRNA. Only one patient had prior receipt of Linezolid. None of the patients had received Tedizolid in past.

**Conclusion.** There is de-novo emergence of Tedizolid resistant enterococcal isolates. This along with higher incidence daptomycin non-susceptibility in our institution is of significant concern. This highlights the need for further improvement in infection control practices and newer options for the treatment of enterococcal infections.

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2192. Emergence of Alarming Clindamycin and Erythromycin-resistant Streptococcus Group B over 2004–2016 in Kuwait

**Neera Al-Sweih, MD, FRCPath1; Aisha Al-Haqqan, MD2 and Hessa Al-Otaibi, MD**

1Maternity Hospital / Ministry of Health, Kuwait, Kuwait; Microbiology, Faculty of Medicine, Kuwait University, Kuwait, 2Kuwait Board CMKB, Maternity Hospital, Ministry of Health, Kuwait; 3Kuwait Board CMKB, Maternity hospital, Ministry of Health, Kuwait

**Session:** 242. HAI: MRSA, MSSA, and Other Gram-positives

**Background.** Group B streptococcus (GBS) is an important neonatal pathogen known to be associated with high morbidity and mortality. GBS is a well-known etiology of postpartum infection and recently is considered to be an emerging pathogen in adult patients causes severe sepsis and invasive infections. The aim of this study was to evaluate the rate of clindamycin and erythromycin resistance among GBS isolated from invasive and noninvasive clinical specimens over the past 13 years.

**Methods.** From 2004 to 2016, 134 invasive and 2,660 noninvasive, non-repeat isolates were included in the study. The identification was done by Vitek-2 and MIC was determined by E test.

**Results.** Among 134 invasive isolates, 124 were from blood. 94 from neonates and 30 from adults and 10 were from GSE. Clindamycin resistance rate for invasive GBS isolates were 5.3% in 2004–2006, 5.7% in 2011–2014, 23.7% in 2011–2014 and 43.5% in 2015–2016 with 23 (17.2%) overall resistant rate. The overall resistance rate to erythromycin among invasive strains was (29.4%, n = 42), however, it was 13.2% in 2004–2006, 25.7% in 2007–2010, 55.3% in 2011–2014 and 30.4% in 2015–2016. Resistance pattern to clindamycin and erythromycin of noninvasive GBS isolates were as follow: (4.4% and 8.1%) in 2004–2010 (21.6% and 33.8%) in 2010–2014 and (52.5% and 49.4%) in 2015–2016, respectively. All isolates were sensitive to penicillin, ampicillin, vancomycin and teicoplanin. However, 94.6% and 95.3% were highly resistant to gentamicin and tetracycline, respectively. Six serotypes were identified in invasive GBS isolates, III (28.8%) was the most prevalent, followed by V (20.7%), Ia and II (15.3%), Ib (8.1%), IV (7.2%), VII (0.9%) and 4 (3.6%) were NT. Serotype distribution of the noninvasive GBS was as follow: serotype V (31.4%), III (23.7%) and II (12.7%) were the predominant. A high level clindamycin and - erythromycin resistant invasive GBS strains with MIC > 256 µg/ml were (61.5% and 28%) respectively.

**Conclusion.** Rate of GBS resistance to clindamycin and erythromycin are significantly increased after the study period. These findings should strongly support ACOG recommendations that clindamycin use for intrapartum prophylaxis to be restricted to penicillin allergic women and it necessitates that all GBS isolates to be tested for clindamycin.

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