Table 3: Adjusted Multinomial logistic regression

	Transient vs Uncolonized RRR (95% CI)	P value	Persistent vs Uncolonized RRR (95% CI)	P value	Persist vs Transient RRR (95% CI)	P value
Age	0.99 (0.97-1.01)	0.331	**0.98 (0.96-0.99)**	**0.007**	0.98 (0.96-1.01)	0.186
Male gender	0.74 (0.41-1.36)	0.335	0.89 (0.55-1.45)	0.641	1.20 (0.62-2.31)	0.593
Nonwhite race	1.65 (0.77-3.52)	0.199	1.59 (0.66-3.85)	0.304	0.97 (0.61-1.53)	0.881
Charlson	1.00 (0.94-1.07)	0.962	1.00 (0.92-1.09)	0.981	1.00 (0.90-1.11)	0.993
PSMS score	**1.09 (1.00-1.19)**	**0.048**	**1.13 (1.04-1.23)**	**0.003**	1.04 (0.94-1.14)	0.442
Open Wounds	1.54 (0.57-4.11)	0.392	2.77 (0.94-8.13)	0.064	1.80 (0.57-5.73)	0.318
Duration of study follow-up, mean (SD)	1.01 (1.00-1.01)	0.063	**1.02 (1.01-1.02)**	**<0.001**	**1.01 (1.00-1.01)**	**0.003**
Antibiotics	1.21 (0.64-2.30)	0.559	0.78 (0.38-1.60)	0.505	0.65 (0.33-1.28)	0.210

:
R-GNB colonization in vulnerable NH patients is common (407 [45.5%] of 896 and often persistent (94 [55%] of 171 patients with sufficient follow-up to assess persistence). Patients with persistent R-GNB had lower functional status, longer LOS, and higher readmission rates than those without. R-GNB decolonization should be investigated as a strategy to potentially improve outcomes among NH patients.

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: MDR GNR
Inpatient point-prevalence screening of New Delhi Metallo-β-lactamase (NDM)–producing Enterobacaterales and *Candida auris*

Christian Greco; Heather Smith; Candice Fearon; Jennifer Flaherty; Simona Kendrick; Kimberly Malcolm; Marcy McGinnis; Manisha Shah; Kadiatu Banjoko; Anjali Zedek; Justin Smyer; Shandra Day; Nora Colburn; Christina Liscynesky and Michael Haden

Background: Carbapenem-resistant Enterobacterales (CRE) are an increasing threat to patient safety but only a small percentage of CRE identified are NDMs. Since 2018, clinical CRE isolates have been submitted to the Ohio Department of Health for sequencing and NDM cases have notably increased since that time. *Candida auris* is an emerging pathogen with similar risk factors for colonization as CRE. **Methods:** A point-prevalence study was initiated after an index patient was identified with NDM CRE infection or colonization during their inpatient admission. Two patient populations were included in the study: current patients on the same unit as the index patient and currently hospitalized patients who overlapped on any unit with the index patient for at least 72 hours. Patients had perirectal screening for CRE (via PCR) and axilla or groin screening for *C. auris* (via Xpert Carba-R Assay). Patients were excluded if they had been discharged, expired, or refused testing. **Results:** We completed 5 point-prevalence studies from March 21, 2021, to October 15, 2021. The index patients were admitted at different times and across 2 campuses including medical, cardiac, and surgical ICUs as well as medical-surgical and inpatient rehabilitation units. Moreover, 3 species of NDM were identified from urine and 2 species were identified from bronchoalveolar lavage: *Enterobacter hormaechei*, *Citrobacter freundii*, and *Enterobacter cloacae* complex. *C. freundii* and *E. cloacae* complex both had dual mechanisms of NDM and KPC. Although some of the index patients overlapped temporally within the health system, none overlapped in the same unit or building. None of the patients had recently received health care outside the United States, although 1 patient had emigrated from Togo >5 years prior and 4 had had prior local healthcare exposure within 12 months of admission. Also, 147 patients were identified for screening; 105 consented, 32 declined, and 10 were excluded due to being discharged, deceased, or unable to consent. Inpatient point-prevalence screening tests for all patients tested (n = 105) were negative for NDM CRE and *C. auris*. **Conclusions:** Despite an increase of inpatients with NDM CRE, evidence of patient-to-patient transmission was not identified, likely resulting from adherence to standard precautions. The diversity of species and lack of international travel suggests that these patients likely acquired NDM

CRE from a local reservoir in the community or healthcare settings. Given the continued increase in NDM CRE without traditional risk factors, it is critical for hospitals and public health agencies to collaborate to identify these organisms and that they develop surveillance programs to clarify risk factors for colonization.

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Molecular Epidemiology
Whole-genome sequencing to assess clonality in a series of prosthetic joint *Staphylococcus epidermidis* isolates

Samantha Simon; Mohamad Sater; Ian Herriott; Miriam Huntley and Brian Hollenbeck

Background: Prosthetic joint infections (PJIs) are costly and cause increased morbidity and mortality for patients. *Staphylococcus epidermidis* is a common cause of both early postoperative and late-presenting PJIs. Although *S. epidermidis* is a normal part of the human skin microflora, its ability to form biofilm on implanted medical devices make it an important causative pathogen of PJIs. We investigated genetic, epidemiologic, and environmental factors contributing to *S. epidermidis* PJIs by performing whole-genome sequencing and clinical epidemiologic investigation of isolates collected from infected patients between 2017 and 2020. **Methods:** Patients with *S. epidermidis* isolated from a prosthetic joint that was placed at our orthopedic specialty hospital were identified using the microbiology laboratory records and electronic medical records. Whole-genome sequencing and single-nucleotide polymorphism (SNP)–based clonality analyses were performed using the epiXact service at Day Zero Diagnostics. These analyses included species identification, in silico MLST typing, phylogenomic analysis, as well as genotypic assessment of the prevalence of specific antibiotic resistance genes, virulence genes, and other relevant genes. For clonal isolates, additional reviews of surgical history and clinical data were performed. **Results:** In total, 62 *S. epidermidis* joint isolates were identified from 46 patients. Among these isolates, 52 were of sufficient purity to be used for genomic analysis (Fig. 1). A number of genes appeared in every isolate including *sepA*, *smr*, *cap*, *sesB*, *sesG*, and *embp*. Also, 6 *S. epidermidis* samples had a discrepancy between phenotypic resistance to oxacillin and the presence of the *mecA* resistance gene. We also identified 6 distinct clusters of isolates, all of which had SNP distances <10 base pairs (Fig. 2). Each cluster consisted of 2–4 patients. Cluster isolates accounted for 29.8% of all *S. epidermidis* prosthetic joint isolates. Most clonal isolates occurred in patients who were heavily exposed to different healthcare settings. Further epidemiologic investigation showed that some of these clonal isolates had ties to aspirations or procedures, whereas no clear connection could be determined for others. **Conclusions:** *S. epidermidis* isolated from clinical prosthetic joint samples
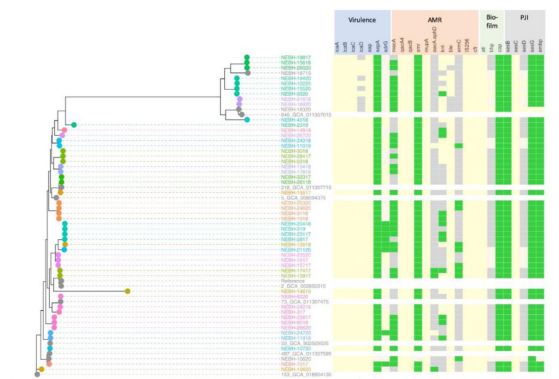

Fig. 1.