Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: MDR GNR

A retrospective longitudinal observational study of natural history of ESBL/MDR gram negative organisms in patients hospitalized in a tertiary hospital

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Background: The IDSA recommends that when determining empiric treatment for a given patient, clinicians should consider previous organisms and associated antibiotic susceptibility data in the prior 6 months when multidrug-resistant/extended-spectrum β-lactamase gram-negative rods (MDR /ESBL GNR) is suspected. The presence of MDR GN in cultures on previous hospitalization or in surveillance cultures leads to use of broader-spectrum empiric antibiotic in subsequent admissions. We sought to determine whether the presence of an MDRO in 1 hospital admission dictates the need for broader-spectrum antibiotic use in subsequent hospitalizations when a different site is considered the source of infection. **Methods:** The study was conducted at a 700-bed tertiary-care level I trauma center. Infection control records were reviewed for patients aged 21–99 years admitted between July 1, 2013, through January 31, 2014, who had any ESBL or MDR GNR at any site including surveillance culture. The charts were surveyed until January 31, 2016, for ESBL or MDR gram-negative organisms at any site during subsequent hospitalizations. The CDC definition of MDR/ESBL was applied. **Results:** Of the 50 people followed, 34 patients (68%) had ESBL/MDR recovered at a single sentinel site, 6 patients (12%) had ESBL/MDR in multiple sites, and in 10 patients (20%) had ESBL/MDR only in surveillance cultures during their primary hospitalization. In 34 patients with a single sentinel site MDRO/ESBL in their primary hospitalization, 16 (47%) were identified in urine, 13 (38%) were identified by bronchoalveolar lavage (lung), 4 (12%) were identified on skin or MS, and 1 (3%) was identified at another site. When lung and urine were the sole sites of recovery of MDRO/ESBL in primary hospitalization, respectively, 3 patients (23%) and 2 patients (12.5%) subsequently developed MDROs in a secondary site on subsequent admissions. Overall, 10 bacteremia episodes occurred in 8 patients among 189 total admissions. MDRO/ESBL *Klebsiella* spp were identified in the cultures of 5 patients (50%), MDRO *Acinetobacter* spp were identified in the cultures of 3 patients (30%), and ESBL *E. coli* was identified in the cultures of 2 patients (20%). The organism causing bacteremia was present at a different sites during the same admission in only 3 (30%) of these cases: 2 were cultured from urine and 1 was cultured from a pulmonary source. **Conclusions:** The presence of MDRO at 1 site in a previous hospitalization may not be sufficient evidence to justify very broad antibiotics for patients during subsequent admissions, especially when another site is considered the source of infection. More studies are needed on natural history of MDRO in different patient populations with different risk factors.

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Low function and frequent readmission in nursing home patients with persistent resistant gram-negative bacterial colonization

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Background: Persistent colonization with resistant gram-negative bacteria (R-GNB) increases risk of clinical infection and intra-facility transmission among nursing home (NH) patients. Limited data exist on the roles of age and function on duration of R-GNB colonization. **Methods:** Secondary data analysis was performed from a cohort study of patients admitted to 6 Michigan NHs between November 2013 and May 2018. Swabs obtained upon enrollment, day 14, day 30, then monthly until NH discharge from 6 anatomical sites were cultured for GNB. R-GNB were defined as resistant to ciprofloxacin, ceftazidime, or imipenem. Positive R-GNB culture from a single visit followed by negative cultures for the same organism from ≥2 subsequent visits were defined as transient R-GNB colonization. All other patients with positive R-GNB cultures from multiple visits were considered persistently colonized. Demographic data, antibiotic use, device use, and physical self-maintenance scales (PSMSs) were obtained upon enrollment. Characteristics were compared between patients with transient versus persistent R-GNB and uncolonized patients using multinomial logistic regression. **Results:** We recruited 896 patients (median age, 75 years; 41% male; 46% nonwhite) and followed them for 2,437 total visits. Of 896 patients, 407 (45.4%) were colonized with ≥1 R-GNB during their stay. Of 171 patients with ≥ 2 follow-up visits after R-GNB detection, 94 (55%) remained persistently colonized with the same R-GNB (Table 1). *Escherichia coli* (30%) and *Proteus mirabilis* (22%) were the most frequently identified R-GNB. The most common anatomical colonization sites were perirectal (368 [24.3%] of 1,147) groin (340 [14.3%] of 2,046), and hands (115 [4.8%] of 2283). Compared to uncolonized patients, patients with persistent (1.09; 95% CI, 1.00–1.19, $P = .048$) and transient R-GNB colonization (1.13; 95% CI, 1.04–1.23; $P = .003$) had lower PSMS (Tables 2 and 3). Compared to uncolonized and transiently colonized patients, patients with persistent R-GNB colonization had prolonged

Table 1: Patient Demographics by R-GNB Colonization Status

	Total Cohort (n=318)	Never R-GNB Colonization (n=147)	Transient R-GNB Colonization (n=77)	Persistent R-GNB Colonization (n=94)	P value
Age, median (IQR)	75 (65-85)	77 (66-86)	75 (64-85)	74 (65-82)	0.396
Male gender	130 (40.9%)	65 (44.2%)	29 (37.7%)	36 (38.3%)	0.531
Non-white race	145 (45.6%)	59 (40.1%)	38 (49.4%)	48 (51.1%)	0.189
Charlson Score, median (IQR)	2 (1-4)	2 (1-4)	2 (1-4)	2 (1-4)	0.9057
Dementia	69/317 (21.8%)	23/146 (15.8%)	20/77 (26.0%)	26/94 (28.0%)	0.055
PSMS score, median (IQR)	**14 (11-19)**	**13 (11-17)**	**16 (12-19)**	**17 (14-21)**	**<0.001**
Indwelling Device Upon Admission	**58 (18.2%)**	**17 (11.6%)**	**18 (23.4%)**	**23 (24.5%)**	**0.017**
Open Wounds	**61/317 (19.2%)**	**19/146 (13.0%)**	**14/77 (18.2%)**	**28 (29.8%)**	**0.005**
Hospital LOS Prior to NH admission, median (IQR)	6 (3-10)	6 (4-10)	5 (3-11)	6 (3-10)	0.3912
Duration of study follow-up, median (IQR)	**28.5 (27-62)**	**28 (22-33)**	**29 (27-61)**	**61 (28-175)**	**<0.001**
Duration prior to first colonization/study exit, median (IQR)	**14 (0-28)**	**28 (22-33)**	**0 (0-9)**	**0 (0-6)**	**<0.001**
Antibiotics upon enrollment (any)	175/303 (57.8%)	78/142 (54.9%)	44/72 (61.1%)	53/89 (59.6%)	0.633
Outcomes					
Re-hospitalization	**86 (27.0%)**	**28 (19.1%)**	**20 (26.0%)**	**38 (40.4%)**	**0.001**
Clinical Infection (after first colonization), any	100 (31.5%)	37 (25.2%)	27 (35.1%)	36 (38.3%)	0.074
UTI	54 (17.0%)	21 (14.3%)	12 (15.6%)	21 (22.3%)	0.249
Pneumonia	16 (5.0%)	6 (4.1%)	4 (5.2%)	6 (6.4%)	0.726
SSTI	20 (6.3%)	7 (4.8%)	4 (5.2%)	9 (9.65)	0.292
C. difficile	5 (1.6%)	2 (1.4%)	1 (1.3%)	2 (2.1%)	0.875

Table 2: Unadjusted Multinomial Analysis of Patient Characteristics Associated with Colonization Status

	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 (0.98-1.01)	0.452	0.99 (0.97-1.00)	0.127	0.99 (0.97-1.01)	0.334
Male gender	0.76 (0.40-1.44)	0.401	0.78 (0.52-1.18)	0.239	1.03 (0.57-1.84)	0.928
Nonwhite race	1.45 (0.77-2.76)	0.253	1.56 (0.76-3.21)	0.230	1.07 (0.71-1.62)	0.745
Charlson	1.00 (0.94-1.07)	0.941	1.02 (0.98-1.07)	0.361	1.02 (0.96-1.08)	0.530
Dementia	0.175 (0.76-4.66)	0.175	2.04 (0.96-4.37)	0.065	1.09 (0.52-2.28)	0.819
PSMS score	**1.09 (1.03-1.16)**	**0.004**	**1.16 (1.09-1.22)**	**<0.001**	1.06 (0.99-1.13)	0.081
Indwelling Device on admission	**2.33 (1.27-4.30)**	**0.007**	**2.48 (1.37-4.48)**	**0.003**	1.06 (0.64-1.75)	0.815
Open Wounds	1.49 (0.68-3.24)	0.319	**2.84 (1.27-6.36)**	**0.011**	1.91 (0.66-5.53)	0.234
Hospital LOS Prior to NH	1.01 (0.97-1.05)	0.705	1.01 (0.98-1.04)	0.547	1.00 (0.97-1.03)	0.942
Duration of study follow-up	**1.01 (1.00-1.02)**	**0.003**	**1.02 (1.01-1.03)**	**<0.001**	**1.01 (1.00-1.01)**	**<0.001**
Days to 1st Positive Cx or DC	**0.91 (0.87-0.97)**	**0.002**	**0.91 (0.86-0.96)**	**0.001**	0.99 (0.95-1.04)	0.805
Antibiotics Upon Enrollment (any)	1.29 (0.72-2.32)	0.398	1.21 (0.56-2.59)	0.627	0.94 (0.68-1.30)	0.694
Outcomes						
Re-hospitalization	1.49 (0.81-2.74)	0.198	**2.88 (1.78-4.68)**	**<0.001**	**1.93 (1.01-3.72)**	**0.048**
Clinical Infection (after first colonization), dichot	1.61 (0.82-3.15)	0.169	1.85 (0.89-3.82)	0.099	1.15 (0.53-2.50)	0.725
UTI	1.11 (0.62-1.99)	0.731	**1.73 (1.08-2.76)**	**0.023**	1.56 (0.89-2.73)	0.121
Pneumonia	1.29 (0.72-2.30)	0.391	1.60 (0.38-6.68)	0.517	1.24 (0.36-4.25)	0.727
SSTI	1.10 (0.38-2.17)	0.866	2.12 (0.66-6.85)	0.210	1.93 (0.72-5.18)	0.191
C. difficile	0.95 (0.08-11.19)	0.970	1.58 (0.42-5.92)	0.500	1.65 (0.32-8.64)	0.552

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

lengths of NH stay (1.01; 95% CI, 1.00–1.01; P = .003). **Conclusions:** 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.

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Inpatient point-prevalence screening of New Delhi Metallo-β-lactamase (NDM)–producing Enterobacterales and *Candida auris*

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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.

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Whole-genome sequencing to assess clonality in a series of prosthetic joint *Staphylococcus epidermidis* isolates

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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

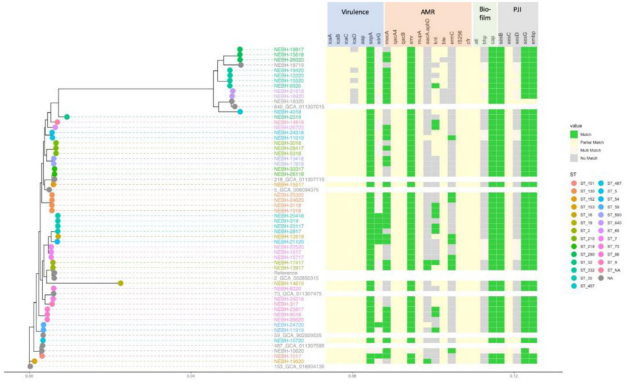

Fig. 1.