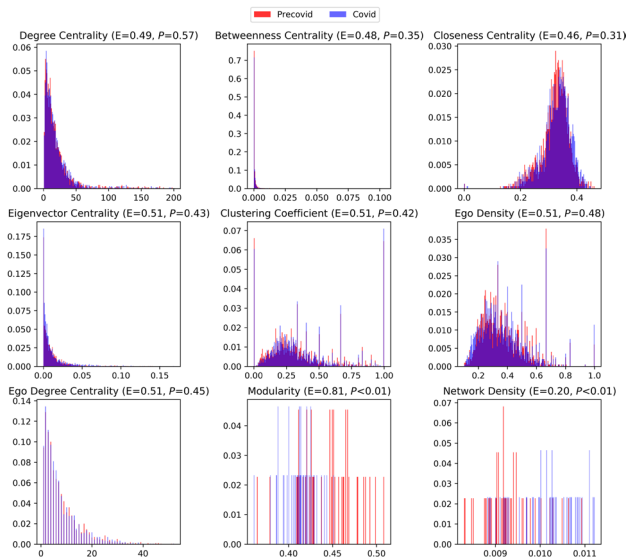


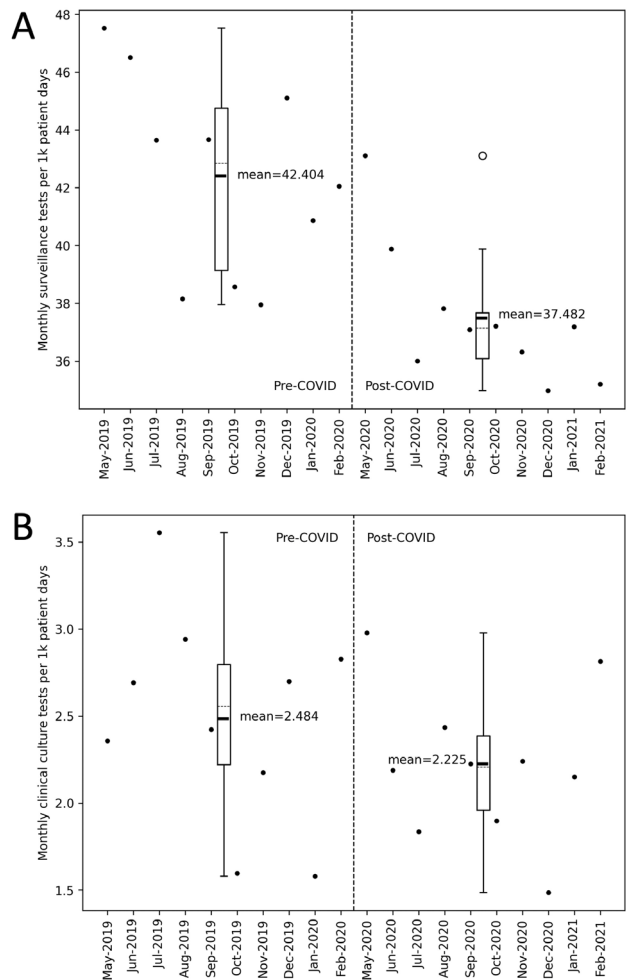
Figure 5. Social Network Properties and Analysis (Effect Size, P-Value)



We analyzed three major types of network properties for this analysis: (1) Node properties of the pre- and post-COVID-19 networks consisted of all the edges in the pre- and post-COVID-19 periods, respectively. We considered a number of standard properties used in social network analysis to quantify opportunities for patient-patient transmission: degree centrality (links held by each node), betweenness centrality (times each node acts as the shortest 'bridge' between two other nodes), closeness centrality (how close each node is to other nodes in network), Eigenvector centrality (node's relative influence on the network), and clustering coefficient (degree to which nodes cluster together) in the first five panels (left to right, top to bottom); (Newman, Networks: An Introduction, 2010). Each panel shows the frequency distributions of these properties. These properties generally did not have a normal distribution and therefore we used a Mann Whitney U test on random subsets of nodes in these networks to compare pre- and post-COVID properties. The mean effect size (E) and P-values are shown for each metric in parenthesis. We concluded that all of these pre- versus post-COVID-19 network properties were statistically similar. (2) Properties of the ego networks (networks induced by each node and its 'one-hop' neighbors). We considered density (average number of neighbors for each node; higher density generally favors lower outbreak threshold) and degree centrality (number of links held by each node) of ego networks (middle right and bottom left panels). The mean effect size and p-values using the Mann Whitney test are shown in parenthesis; there were no statistically significant differences in these properties in the pre- and post-COVID networks. (3) Aggregate properties of the weekly networks, consisting of all the interactions within a week. We considered modularity (measure of how the community structure differs from a random network; higher modularity means a stronger community structure and lower likelihood of transmission) and density (average number of neighbors each node; higher density generally favors lower outbreak threshold) of the weekly networks (bottom middle and bottom right panels). The modularity in the post-COVID weekly networks was slightly lower (i.e., it has a weaker community structure, and the network is more well mixed), while density was slightly higher, the differences of which were statistically significant; a caveat is that these are relatively small datasets (about 40 weeks). These differences (higher density, and better connectivity) both increase the risk of transmission in the post-COVID networks. In summary, the post-COVID networks either have similar properties as the pre-COVID networks, or had changes which are unlikely to have played a role in reducing MRSA transmission.

Conclusion. A significant reduction in post-COVID-19 MRSA transmission may have been an unintended positive effect of enhanced infection control measures, particularly hand hygiene and increased mask use. A modest (11.6%) post-COVID-19 reduction in surveillance testing may have also played a role. Despite pandemic-related cohorting and census fluctuations, most network properties were not significantly different post-COVID-19, except for aggregate density and modularity which varied in a direction that instead favored transmission; therefore, HCP-based networks did not play a significant role in reducing MRSA transmission. Multivariate modeling to isolate relative contributions of these factors is underway.

Figure 6. Surveillance Testing and Clinical Culturing



Post-COVID-19, there was a modest (11.6%) but statistically significant reduction in surveillance PCR testing (42.4 mean tests per 1,000 patient days pre- versus 37.5 post-COVID-19; $P < 0.002$). There was not a statistically significant difference in rates of clinical cultures sent (2.48 cultures per 1,000 patient days pre- versus 2.23 post-COVID-19; $P = 0.288$).

Disclosures. All Authors: No reported disclosures

174. Increase in *Candida auris* cases in New Jersey healthcare facilities during the COVID-19 pandemic — 2017–2020

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Session: O-34. The Interplay Between COVID and other Infections

Background. *Candida auris* is a fungal pathogen associated with multidrug resistance, high mortality, and healthcare transmission. Since its U.S. emergence in 2017, to March 19, 2021, 1708 clinical infections were reported nationwide, of which 235 (13.8%) were reported in New Jersey. The New Jersey Department of Health (NJDOH) maintains *C. auris* surveillance in healthcare facilities (HCF) such as acute care hospitals, long-term acute care hospitals (LTACHs), and skilled nursing facilities, to monitor

clinical infections and patient colonization. We aimed to characterize the epidemiology of *C. auris* infection and colonization among HCF patients during 2017–2020.

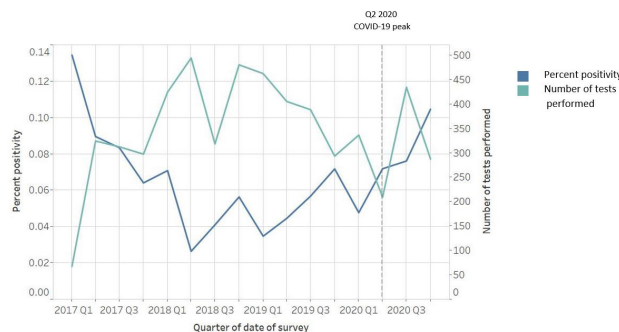
Methods. HCFs report *C. auris* cases identified from clinical specimens and surveillance activities such as admission screenings and point prevalence surveys (PPS) to NJDOH. Cases are classified as either infection or colonization using National Notifiable Diseases Surveillance System case definitions. We analyzed cases reported during 2017–2020 to describe types of cases, facilities reporting cases, and demographics of affected patients. We analyzed PPS results to calculate percent positivity of tests from patients without previously identified infection and compared percent positivity between types of facilities. We examined quarterly trends for all variables before and after the COVID-19 pandemic peak in the second quarter of 2020.

Results. During 2017–2020, 614 *C. auris* cases identified from clinical specimens were reported to NJDOH [243 (39.6%) infection, 371 (60.4%) colonization]; of these, 139 (57.2%) and 301 (81.1%), respectively, were identified at long-term acute care hospitals (LTACHs). PPS percent positivity was higher at LTACHs (mean 7.6%) compared with all other facility types (mean 3.6%) for 13 of 16 quarters during 2017–2020. Case reports increased 2.6-fold from the Q2 2020 peak of the COVID-19 pandemic to Q3 2020. From Q1 to Q4 2020, PPS percent positivity increased from 4.8% to 10.5%.

Figure 1. *Candida auris* cases reported to New Jersey Department of Health, 2017–2020

| Characteristic | All (n = 614) n (%) | Infection (n = 243) n (%) | Colonization (n = 371) n (%) |
|--|---------------------|---------------------------|------------------------------|
| Median age at first positive specimen collection date, years (IQR) | 71 (62-80) | 69 (60.5-79) | 72 (63-80) |
| Year reported | | | |
| 2017 | 150 (24.4) | 75 (30.9) | 75 (20.2) |
| 2018 | 136 (23.0) | 56 (23.0) | 80 (21.6) |
| 2019 | 149 (24.5) | 54 (22.2) | 95 (25.6) |
| 2020 | 179 (28.1) | 58 (23.9) | 121 (32.6) |
| Facility type | | | |
| Acute care hospital | 100 (16.3) | 86 (35.4) | 14 (3.8) |
| Long-term acute care hospital (LTACH) | 440 (71.7) | 139 (57.2) | 301 (81.1) |
| Ventilator-capable skilled nursing facility | 62 (10.1) | 8 (3.3) | 54 (14.6) |
| Other facility type * | 7 (1.1) | 5 (2.1) | 2 (0.5) |
| Unknown facility type | 5 (0.8) | 5 (2.1) | 0 (0.0) |
| Source of first positive specimen | | | |
| Axilla/groin composite swab | 332 (54.1) | 0 (0.0) | 332 (89.5) |
| Blood | 77 (12.5) | 87 (34.0) | 0 (0.0) |
| Respiratory | 27 (4.4) | 27 (10.5) | 0 (0.0) |
| Urine | 69 (11.2) | 70 (27.3) | 0 (0.0) |
| Wound | 20 (3.3) | 20 (7.8) | 0 (0.0) |
| Other source | 9 (1.5) | 10 (3.9) | 0 (0.0) |
| Unknown source | 80 (13.0) | 42 (16.4) | 39 (10.5) |

Figure 2. *Candida auris* test percent positivity among healthcare facility patients sampled for point prevalence surveys* and total number of *C. auris* point prevalence tests performed, New Jersey, 2017–2020. *Excluding individuals already known to be cases



Conclusion. The COVID-19 pandemic may have exacerbated *C. auris* transmission in HCF and potential causes should be further explored. LTACHs carry a disproportionate burden of patients colonized with *C. auris* and should be prioritized for surveillance and containment efforts.

Disclosures. All Authors: No reported disclosures

175. Antibiotic Resistance in Select Gram-negative Bacteria Over the Past Decade Among Hospitalized Veterans Nationally

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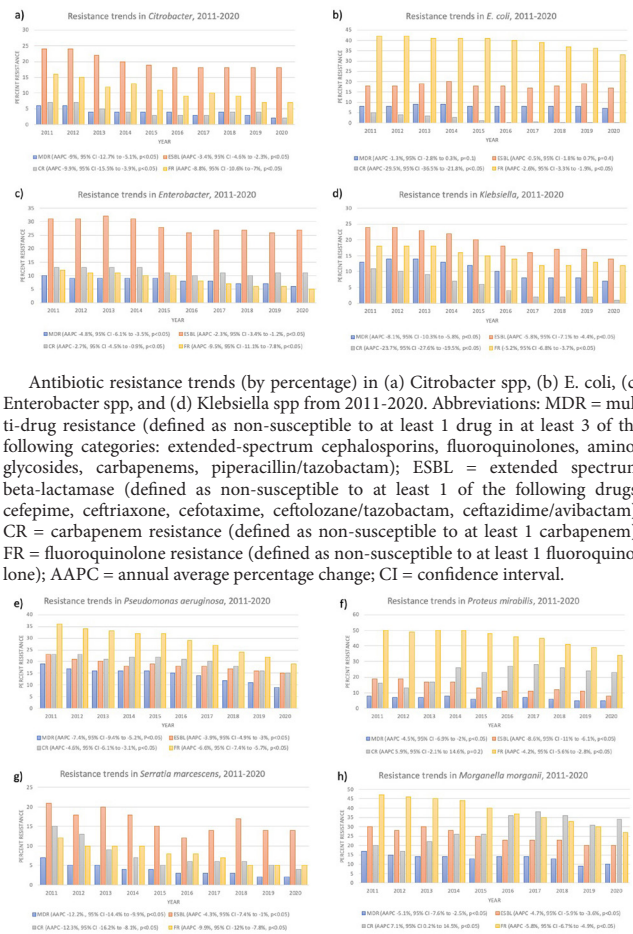
Session: O-35. Trends in Gram-negative Resistance

Background. Public health institutions including the World Health Organization and the United States Centers for Disease Control and Prevention (CDC) have recognized the threat of antibiotic resistant infections caused by Gram-negative bacteria. These bacteria are particularly concerning as they can demonstrate resistance to all available antibiotic classes through various mechanisms. We set out to assess antibiotic resistance trends in Gram-negative bacteria to optimize antimicrobial stewardship and infection control initiatives in our health system.

Methods. We identified positive cultures (1st per patient per month) of *P. aeruginosa* and select *Enterobacteriales* (*Citrobacter*, *Escherichia coli*, *Enterobacter*, *Klebsiella*, *Morganella morganii*, *Proteus mirabilis*, *Serratia marcescens*) collected from patients hospitalized at Veterans Affairs (VA) Medical Centers nationally from 2011 to 2020. Time trends were assessed with joinpoint regression to estimate average annual percent changes (AAPC) with 95% confidence intervals (CIs) for the following resistance phenotypes utilizing CDC definitions: multi-drug resistance (MDR), extended-spectrum beta-lactamase (ESBL), and carbapenem (CR) and fluoroquinolone (FR) resistance.

Results. We included 496,384 isolates in our study: *E. coli* (32.6%), *Klebsiella* (20%), *P. aeruginosa* (18.9%), *P. mirabilis* (11.5%), *Enterobacter* (7.8%), *Citrobacter* (3.7%), *S. marcescens* (2.9%), and *M. morganii* (2.6%). Trends in resistance are shown in the figures. MDR, ESBL, CR, and FR decreased significantly ($p < 0.05$) over the study period for most of the organisms assessed, with the exception of MDR and ESBL *E. coli* and CR *P. mirabilis* which remained stable, and CR *M. morganii* which increased significantly by 7.1% per year (95% CI 0.2% to 14.5%). The largest decreases were in CR *E. coli* by 29.5% per year (95% CI -36.5% to -21.8%), CR *Klebsiella* by 23.7% per year (95% CI -27.6% to -19.5%), and MDR and CR *S. marcescens* by 12.2% (95% CI -14.4% to -9.9%) and 12.3% per year (95% CI -16.2% to -8.1%), respectively.

Figure 1. Antibiotic resistance trends in *Citrobacter* spp., *E. coli*, *Enterobacter* spp., and *Klebsiella* spp.



Antibiotic resistance trends (by percentage) in (a) *Citrobacter* spp., (b) *E. coli*, (c) *Enterobacter* spp., and (d) *Klebsiella* spp from 2011-2020. Abbreviations: MDR = multi-drug resistance (defined as non-susceptible to at least 1 drug in at least 3 of the following categories: extended-spectrum cephalosporins, fluoroquinolones, aminoglycosides, carbapenems, piperacillin/tazobactam); ESBL = extended spectrum beta-lactamase (defined as non-susceptible to at least 1 of the following drugs: cefepime, ceftriaxone, cefotaxime, ceftolozane/tazobactam, ceftazidime/avibactam); CR = carbapenem resistance (defined as non-susceptible to at least 1 carbapenem); FR = fluoroquinolone resistance (defined as non-susceptible to at least 1 fluoroquinolone); AAPC = annual average percentage change; CI = confidence interval.

Figure 2. Antibiotic resistance trends in *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Serratia marcescens*, and *Morganella morganii*. Antibiotic resistance trends (by percentage) in (e) *Pseudomonas aeruginosa*, (f) *Proteus mirabilis*, (g) *Serratia marcescens*, and (h) *Morganella morganii* from 2011-2020. Abbreviations: MDR = multi-drug resistance (defined as non-susceptible to at least 1 drug in at least 3 of the following categories: extended-spectrum cephalosporins, fluoroquinolones, aminoglycosides, carbapenems, piperacillin/tazobactam); ESBL = extended spectrum beta-lactamase