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); (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) and degree centrality (number of links held by each node) 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.

Disclosures. All Authors: No reported disclosures
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 demographic characteristics 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 (52.2%) 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%.

**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

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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 Enterobacteriaceae (Citrobacter, Escherichia coli, Enterobacter, Klebsiella, Morganella, Proteus mirabilis, Serratia marcescens) collected from patients hospitalized at Veterans Affairs (VA) Medical Centers nationally from 2011 to 2020. Time trends were assessed with jointpoint 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 for E. coli and CR for P. mirabilis which remained stable, and CR for 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.

**Conclusion.** The COVID-19 pandemic significantly impacted antibiotic resistance trends in Gram-negative bacteria which may be beneficial for antibiotic stewardship in VA Medical Centers.

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