Table 1 Rate and Rate Ratios (RR) of Central Line-Associated Bloodstream Infections by Race and Ethnicity

Race/Ethnicity	Total CLABSIs (n)[1]	Rate[2]	RR[3]	95% CI	p-value[4]
White	179	0.85	Reference	—	<0.001
Black	145	1.08	1.27	1.02-1.58	
Hispanic/Latino	27	1.21	1.43	0.95-2.14	
Asian	5	0.76	0.89	0.37-2.17	
American Indian/Alaska Native	1	0.26	0.31	0.04-2.22	
Native Hawaiian/Pacific Islander	1	1.87	2.20	0.31-15.71	
Other	92	1.52	1.79	1.39-2.30	

[1]Total number of CLABSIs over the surveillance period by race/ethnicity.
[2]Rates of central line-associated bloodstream infection per 1000 device days.
[3]White was the reference group for RR comparisons.
[4]Overall p-value by chi-square listed with the reference group.

Table 2 Rate and Rate Ratios (RR) of Catheter-Related Urinary Tract Infections by Race and Ethnicity

Race/Ethnicity	Total CAUTIs (n)[1]	Rate[2]	RR[3]	95% CI	p-value[4]
White	101	0.89	Reference	—	0.07
Black	74	1.26	1.42	1.05-1.92	
Hispanic/Latino	8	0.87	0.97	0.47-2.00	
Asian	7	2.21	2.49	1.16-5.36	
American Indian/Alaska Native	1	0.62	0.69	0.10-4.97	
Native Hawaiian/Pacific Islander	0	0	0	0	
Other	42	1.35	1.52	1.06-2.18	

[1]Total number of CAUTIs over the surveillance period by race/ethnicity.
[2]Rates of catheter-related urinary tract infection per 1000 device days.
[3]White was the reference group for RR comparisons.
[4]Overall p-value by chi-square listed with the reference group.

catheter-associated urinary tract infection (CAUTI) rates per 1,000 device days. Data for adult patients admitted to an academic medical center between 2018 and 2021 were stratified by 7 racial and ethnic groups: non-Hispanic White, non-Hispanic Black, Hispanic/Latino, Asian, American Indian/Alaska Native, Native Hawaiian/Pacific Islander, and othe. The "other" group was composed of bi- or multiracial patients, or those for whom no data were reported. We compared the CLABSI and CAUTI rates between the different racial and ethnic groups using Poisson regression. **Results:** Compared to non-Hispanic White patients, the rate of CLABSI was significantly higher in non-Hispanic Black patients (1.27; 95% CI, 1.02–1.58; $P < .03$) and those in the "other" race category (1.79; 95% CI, 1.39–2.30; $P < .001$, respectively), and these trends increased in Hispanic/Latino patients (Table 1). Similarly, Black patients had higher rates of CAUTI (1.42; 95% CI, 1.05–1.92; $P < .02$), as did Asian patients (2.49; 95% CI, 1.16–5.36; $P < .02$), and patients in the "other" category (1.52; 95% CI, 1.06–2.18; $P < .02$) (Table 2). **Conclusions:** Racial and ethnic minorities may be vulnerable to a higher rate of patient safety events, including CLABSIs and CAUTIs. Additional analyses controlling for potential confounding factors are needed to better understand the relationship between race or ethnicity, clinical management, and healthcare-associated infections. This evaluation is essential to inform mitigation strategies and to provide optimum, equitable care for all.

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Poster Presentation - Oral Presentation
Subject Category: Respiratory Viruses

Assessing alternatives to HEPA air purification requirements to reduce viral pathogen transmission in healthcare HVAC systems

Werner Bischoff; David Ornelles; Lauren Ivey and Bill Payne

Background: High-efficiency particulate air (HEPA) filters are currently recommended when using recirculated air to eliminate the risk of pathogen transmission such as SARS-CoV-2 from one patient care area to the next. We tested the efficacy of lower-grade air filters in eliminating airborne virus transmission. **Methods:** We conducted an experiment in 2 adjacent exam rooms in an unoccupied hospital emergency unit. The HVAC system contained a 15,000-cubic-feet-per-minute rooftop air handler. All outside air and exhaust dampers were closed during the trial (full air recirculation). We conducted experiments in 3 tests arms with varying grades of MERV filters (AAF Flanders, Louisville, KY): (1) control without filters, (2) MERV8+14 filters, and (3) MERV8+16 filters. We repeated 20-minute virus challenge runs 3 times per test arm. Live attenuated influenza vaccine (2 mL LAIV, FluMist Quadrivalent 2020/21, AstraZeneca, Wilmington, DE), was aerosolized into the HVAC system via a commercial nebulizer. Air was sampled using 3 six-stage Andersen air samplers placed in the center of the adjacent room. Environmental particle counts were collected using a particle counter (PEC-PCO-1, PCE Americas). **Results:** Concentrations of viral RNA were determined by qPCR, and viral concentrations (vg/mL) in each stage of each arm were compared directly. Pairwise comparisons of the virus and particle burdens across each stage of each test arm were made using a general linear model. LAIV was detected in the control arm at a virus burden of 2,277 vg/mL, indicating a >6.5 log reduction of the virus released in the HVAC system (8.8×109 total vg). In the second arm, the MERV8+MERV14 filters demonstrated in a 13-fold decrease in viral burden compared to the control arm (mean virus burden: 169 vg/mL, p Our study demonstrates that viral containing particles can be transported via a hospital HVAC system from one patient room to the next. Considering the decrease in detectable virus within the HVAC system, the combination of MERV8+MERV16 filters reduced the virus burden reaching an adjacent room to levels well below the human infectious dosages for influenza and other highly infective viruses. **Conclusions:** Our findings indicate that MERV8+MERV16 filters provide protection against virus transmission through HVAC systems and are a cost-conscious alternative to HEPA filters.

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Clinical factors associated with antibiotic de-escalation after a positive multiplex molecular respiratory panel

Jonathan Baghdadi; Daniel Morgan; Anthony Harris and Katherine Goodman

Background: Under ideal circumstances, multiplex molecular respiratory panels can support early all discontinuation of unnecessary antibiotics by facilitating diagnosis of viral infection. Our goal was to identify clinic situations in which a positive respiratory panel was associated with antibiotic de-escalation. We focused on gram-negative antibiotics in recognition of the urgent threat posed by gram-negative resistance. **Methods:** The sample included hospitalized adults tested by respiratory panel while receiving gram-negative antibiotics at the University of Maryland Medical Center from 2015 to 2020. Only the first respiratory panel performed during hospitalization was included. The primary outcome was the combination of a positive result on respiratory panel indicating detection of a viral pathogen and de-escalation of gram-negative antibiotics. De-escalation was assessed

Table 1. Clinical Factors Associated with Detection of a Viral Pathogen on Respiratory Panel followed by De-Escalation of Gram-Negative Antibiotics

Clinical Variable	OR	95% Confidence Interval	p-value
Admission from home	1.34	(1.11, 1.63)	0.003
+10 years of age	0.94	(0.89, 0.99)	0.019
Admitting diagnosis of pneumonia	1.42	(1.12, 1.80)	0.003
Hematologic malignancy	0.64	(0.50, 0.81)	< 0.001
Chronic pulmonary disease	1.37	(1.15, 1.63)	< 0.001
Fluid and electrolyte disorder	0.94	(0.78, 1.14)	0.53
Substance abuse	1.39	(1.16, 1.68)	< 0.001
+1 Elixhauser comorbidity*	0.91	(0.88, 0.95)	< 0.001
ICU at time of testing	0.84	(0.67, 1.03)	0.10
Mechanical ventilation at time of testing	0.68	(0.52, 0.89)	0.006
Hypotension	0.77	(0.61, 0.97)	0.027
Leukocytosis	0.60	(0.49, 0.73)	< 0.001

OR, odds ratio; ICU, intensive care unit.
* Elixhauser Comorbidities were constructed based on present-on-admission ICD-10 diagnosis codes. The sum of Elixhauser comorbidities was included in the model as an ordinal variable ranging from 0 to 15.

based on antibiotics administered on day 3 after testing and was defined by discontinuation or switch to an agent with a narrower spectrum of activity. Least absolute shrinkage and selection operator (LASSO) regression was used to construct the multivariable logistic regression model. Classification and regression tree (CART) analysis was used to identify subgroups with a higher likelihood of the primary outcome. **Results:** Of 8,326 patients, 1,462 (17.6%) tested positive by respiratory panel. The most common pathogen was rhinovirus (7.9% of the sample). Gram-negative–targeted antibiotics were de-escalated in 4,456 cases (53.5% of the sample), including 887 patients with a positive result on respiratory panel indicating a viral pathogen (60.7% of patients with a positive viral result). LASSO regression was used to select 12 variables (Table 1). Admitting diagnosis of pneumonia (OR, 1.42), comorbid substance abuse (OR, 1.39), chronic pulmonary disease (OR, 1.39), and admission from home (OR, 1.34) were associated with antibiotic de-escalation in conjunction with a positive respiratory panel. Leukocytosis (OR, 0.59), hematologic malignancy (OR, 0.64), mechanical ventilation at time of testing (OR, 0.68), and hypotension (OR, 0.77) were associated with decreased likelihood of antibiotic de-escalation in conjunction with a positive respiratory panel. CART analysis identified patients tested within 40 hours of admission as having a higher likelihood of a positive result in conjunction with antibiotic de-escalation. Among patients tested within 40 hours of admission, the probability of a positive result followed by antibiotic de-escalation was 11.9% (95% CI, 11.1%–12.8%). For patients tested >40 hours after admission, the probability was 6.0% (95% CI, 4.8%–7.2%). **Conclusions**: Targeted use of respiratory panel testing may increase the likelihood of an informative result that can drive decision making related to antibiotic use. Our exploratory analysis suggests that respiratory panel testing in the first 2 days

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Subject Category: SSI
Characterization of MRSA and ESBL pathogens from patients with surgical-site infections in Accra, Ghana
Terrel Sanders; Jeannette Bentum; Anne Fox; Beverly Egyir and Chaselynn Watters

Background: In Ghana, treatment of surgical site infections (SSIs) is often empirical and not based on targeted therapy (ie, knowledge of the organisms infecting surgical sites or their susceptibility profiles). This empirical approach most often leads to inappropriate prescription, which is a major driver of antimicrobial resistance. Using phenotypic and molecular tools, we investigated *S. aureus*, *E. coli*, *K. pneumoniae*, and *P. aeruginosa* recovered from patients with SSIs. **Methods:** Identification of bacteria species recovered from wound swabs and aspirates was performed using matrix-assisted laser desorption/ionization time-of-flight mass spectroscopy (MALDI-TOF MS). Antimicrobial susceptibility testing (AST) was done using the Kirby-Bauer disk diffusion method. Results were interpreted according to the CLSI 2018 guidelines. Extended-spectrum β-lactamase (ESBL) positivity was detected among the gram-negative isolates using the double disk-diffusion method and PCR amplification of ESBL genes (*bla*SHV, *bla*TEM, and *bla*CTX-M). *Staphylococcus aureus* isolates resistant to cefoxitin were further tested for the presence of *mecA* using PCR. **Results:** In total, 312 patients were enrolled in this prospective study. The 243 bacteria species identified comprised *Escherichia coli* (34%; 107 of 312), *Klebsiella pneumoniae* (20%; 62 of 312), *Pseudomonas aeruginosa* (16%; 49 of 312), and *S. aureus* (8%; 25 of 312). *S. aureus* isolates were susceptible to clindamycin, erythromycin, gentamicin, linezolid, rifampicin, and norfloxacin, but 10 *S. aureus* isolates were resistant to cefoxitin and were positive for the *mecA* gene (MRSA). Among the 169 isolates in the Enterobactericae category (*E. coli* and *K. pneumoniae*), 143 (85%) were resistant to tetracycline; 141 (83%) were resistant to trimethoprim–sulfamethoxazole; 118 (70%) were resistant to cefotaxime; 111 (66%) were resistant to cefuroxime; 98 (58%) were resistant to ciprofloxacin; 86 (51%) were resistant to gentamicin; and 81 (48%) were resistant to chloramphenicol. However, 161 (95%) were sensitive to amikacin and 159 (94%) were sensitive to meropenem. Among the 49 *P. aeruginosa* isolates, 45 (92%) showed sensitivity to amikacin, 43 (88%) showed sensitivity to meropenem, 35 (71%) showed sensitivity to gentamicin, and 35 (71%) showed sensitivity to ciprofloxacin. ESBL was detected in 59 (55%) of 107 *E. coli* isolates, and 48 (77%) of 62 *K. pneumoniae* isolates. *bla*CTX-M was the dominant ESBL gene in *E. coli* isolates (34 of 59, 58%). For *K. pneumoniae* isolates, *bla*CTX-M genes were detected in 45 (94%) of 48 isolates and *bla*SHV genes were detected in 44 (92%) of 48 isolates. Among the 49 *P. aeruginosa* isolates, 3 harbored the *bla*TEM gene. **Conclusions:** The findings of high proportions of ESBL-producing bacteria species in Ghana is a grave public health concern. Data generated in this study will inform treatment decisions and policies and appropriate antibiogram development and will support antimicrobial stewardship programs at the respective healthcare facilities in Ghana.

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Subject Category: Surveillance/Public Health
Bacterial contamination on used face masks in healthcare personnel
Madison Nightingale; Manali Mody; Alexander Rickard and Marco Cassone

Background: Face masks have been worn universally and for long periods of time by healthcare personnel during the COVID-19 pandemic. They are frequently touched or adjusted with the hands and may come in contact with various surfaces and high-touch sites when taken off and on even briefly. These activities present opportunities for face masks to become contaminated with microorganisms. Nursing homes have high rates of multidrug-resistant bacteria and low PPE compliance; therefore, contamination of face masks in this setting may be of great interest. We investigated bacterial colonization status on used face masks in healthcare personnel, including assessing the presence of clinically important and multidrug-resistant bacteria. **Methods:** At a nursing home serving mostly