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
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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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Bacterial contamination on used face masks in healthcare personnel
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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