reasonable sensitivity is preferred to limit the impact of false-positive results on the assessment of intervention effectiveness. Using information from the prior tools, we aimed to determine whether an algorithm using data available in the Veterans Affairs (VA) EMR could accurately and efficiently identify deep incisional or organ-space SSIs found in the VA Surgical Quality Improvement Program (VASQIP) data set for cardiac and orthopedic surgery patients. **Methods:** We conducted a retrospective cohort study of patients who underwent cardiac surgery or total joint arthroplasty (TJA) at 11 VA hospitals between January 1, 2007, and April 30, 2017. We used EMR data that were recorded in the 30 days after surgery on inflammatory markers; microbiology; antibiotics prescribed after surgery; *International Classification of Diseases* (ICD) and current procedural terminology (CPT) codes for reoperation for an infection related purpose; and ICD codes for mediastinitis, prosthetic joint infection, and other SSIs. These metrics were used in an algorithm to determine whether a patient had a deep or organ-space SSI. Sensitivity, specificity, PPV and negative predictive values (NPV) were calculated for accuracy of the algorithm through comparison with 30-day SSI outcomes collected by nurse chart review in the VASQIP data set. **Results:** Among the 11 VA hospitals, there were 18,224 cardiac surgeries and 16,592 TJA during the study period. Of these, 20,043 were evaluated by VASQIP nurses and were included in our final cohort. Of the 8,803 cardiac surgeries included, manual review identified 44 (0.50%) mediastinitis cases. Of the 11,240 TJAs, manual review identified 71 (0.63%) deep or organ-space SSIs. Our algorithm identified 32 of the mediastinitis cases (73%) and 58 of the deep or organ-space SSI cases (82%). Sensitivity, specificity, PPV, and NPV are shown in Table 1. Of the patients that our algorithm identified as having a deep or organ-space SSI, only 21% (PPV) actually had an SSI after cardiac surgery or TJA. **Conclusions:** Use of the algorithm can identify most complex SSIs (73%–82%), but other data are necessary to separate false-positive from true-positive cases and to improve the efficiency of case detection to support research questions.

Cardiac surgery	Mediastinitis present by chart review	Mediastinitis absent	Total	
Algorithm flagged as mediastinitis	32	118	150	PPV = 21.3%
Algorithm did not flag	12	8641	8653	NPV = 99.9%
Total	44	8759	8803	
	Sensitivity = 72.7%	Specificity = 98.7%		

Orthopedic surgery	Deep/organ-space SSI present by chart review	Deep/organ-space SSI absent	Total	
Algorithm flagged as Deep/organ-space SSI	58	222	280	PPV = 20.7%
Algorithm did not flag	13	10947	10960	NPV = 99.9%
Total	71	11169	11240	
	Sensitivity = 81.7%	Specificity = 98.0%		

Fig. 1.

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Presentation Type:
Oral Presentation

Variation in Hospitalist-Specific Antibiotic Prescribing at Four Hospitals: A Novel Tool for Antibiotic Stewardship

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Background: Hospitalists play a critical role in antimicrobial stewardship as the primary antibiotic prescriber for many inpatients. We sought to describe antibiotic prescribing variation among hospitalists within a healthcare system. **Methods:** We created a novel metric of hospitalist-specific antibiotic prescribing by linking hospitalist billing data to hospital medication administration records in 4 hospitals (two 500-bed academic (AMC1 and AMC2), one 400-bed community (CH1), and one 100-bed community (CH2)) from January 2016 to December 2018. We attributed dates that a hospitalist electronically billed for a given patient as billed patient days (bPD) and mapped an antibiotic day of therapy (DOT) to a bPD. Each DOT was classified according to National Healthcare Safety Network antibiotic categories: broad-spectrum hospital-onset (BS-HO), broad-spectrum community-onset (BS-CO), anti-MRSA, and highest risk for *Clostridioides difficile* infection (CDI). DOT and bPD were pooled to calculate hospitalist-specific DOT per 1,000 bPD. Best subsets regression was performed to assess model fit and generate hospital and antibiotic category-specific models adjusting for patient-level factors (eg, age ≥65, ICD-10 codes for comorbidities and infections). The models were used to calculate predicted hospitalist-specific DOT and observed-to-expected ratios (O:E) for each antibiotic category. Kruskal-Wallis tests and pairwise Wilcoxon rank-sum tests were used to determine significant differences between median DOT per 1,000 bPD and O:E between hospitals for each antibiotic category. **Results:** During the study period, 116 hospitalists across 4 hospitals contributed a total of 437,303 bPD. Median DOT per 1,000 bPD varied between hospitals (BS-HO range, 46.7–84.2; BS-CO range, 63.3–100; anti-MRSA range, 48.4–65.4; CDI range, 82.0–129.4). CH2 had a significantly higher median DOT per 1,000 bPD compared to the academic hospitals (all antibiotic categories $P < .001$) and CH1 (BS-HO, $P = .01$; anti-MRSA, $P = .02$) (Fig. 1A). The 4 antibiotic groups at 4 hospitals resulted in 16 models, with good model fit for CH2 ($R^2 > 0.55$ for all models), modest model fit for AMC2 ($R^2 = 0.46$–0.55), fair model fit for CH1 ($R^2 = 0.19$–0.35), and poor model fit for AMC1 ($R^2 < 0.12$ for all models). Variation in hospitalist-specific O:E was moderate (IQR, 0.9–1.1). AMC1 showed greater variation than other hospitals,

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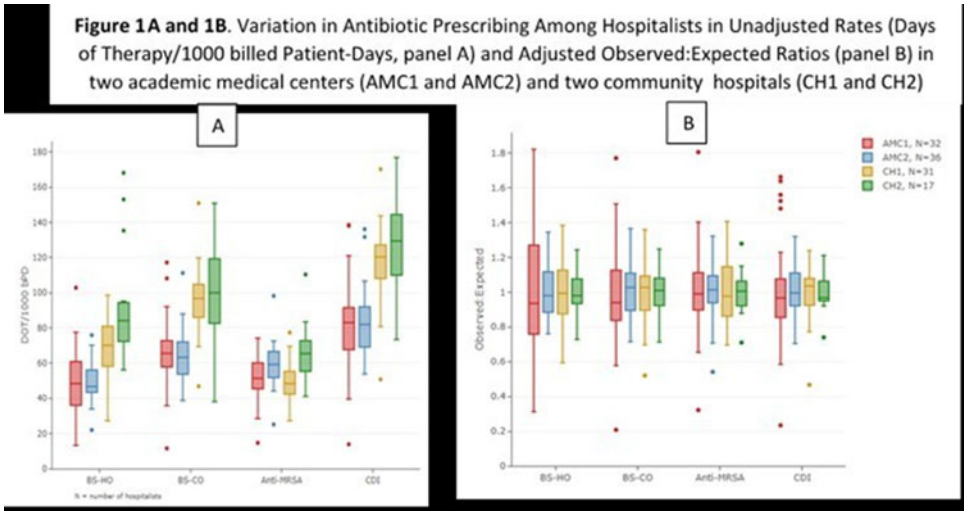

Fig. 1.

but we detected no significant differences in median O:E between hospitals (all antibiotic categories $P > .10$) (Fig. 1B). **Conclusions:** Adjusting for patient-level factors significantly reduced much of the variation in hospitalist-specific DOT per 1,000 bPD in some but not all hospitals, suggesting that unmeasured factors may drive antibiotic prescribing. This metric may represent a target for stewardship intervention, such as hospitalist-specific feedback of antibiotic prescribing practices.

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Oral Presentation

Whole-Genome Sequencing Reveals a Novel Subclade of Pansusceptible *Candida auris* in Ontario, Canada

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Background: *Candida auris* is an emerging pathogen that has recently disseminated globally and caused challenging outbreaks in healthcare facilities (HCFs), in part because it is commonly multidrug-resistant. *Candida auris* remains rare in Canada, with ~20 known cases to date. We describe the emergence of a novel subclade of *C. auris* in Ontario, Canada, using whole-genome sequencing (WGS). **Methods:** In Ontario, many HCFs submit yeast isolates from sterile sites requiring species-level characterization and antifungal susceptibility testing (AFST) to the provincial reference laboratory. Yeasts were identified using a combination of standard methods (morphology, API 20C, MALDI-ToF MS) including ITS2 sequencing. Sensititre YO9 panels were used for AFST. Genomic analysis of *C. auris* was performed using an Illumina HiSeq platform with at least 50× coverage; variants were called against the reference genome by using the previously published North Arizona SNP pipeline (NASP). Phylogenetic trees were produced by maximum parsimony method (MEGA7.0). **Results:** Between 2014 and 2018, yeast isolates from 5 different patients from 4 HCFs in the same region of Ontario were confirmed to be *C. auris* by ITS2 PCR and sequence analysis (Table 1). Based on interim CDC criteria for antifungal drug break points, all isolates were pansusceptible to common antifungals. WGS analysis demonstrated that the *C. auris* isolates were part of the South American clade (IV) and formed an isolated subclade that is well supported by bootstrap analysis, indicating clonal relationships among these isolates (Fig. 1). **Conclusions:** Although *C. auris* isolates are usually drug resistant, all 5 initial Ontario isolates were pansusceptible. WGS determined that these isolates clustered within clade IV and were clonal. This cluster of *C. auris* appears to represent a new subclade of the South American clade that has been transmitted among patients within a region of Ontario. *C. auris* may have been present in Ontario for some time, escaping earlier detection due to lack of screening programs in HCFs, historical challenges with microbiologic detection of *C. auris*, and the antifungal susceptibility of the circulating isolates. Investigations are underway to determine clinical features and epidemiologic relatedness among patients in this cluster.

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Table 1. Summary of *Candida auris* isolates in Ontario, Canada 2014–2018

Year	Patient	Specimen	HCF	AFST profile	Clade
2014	1	Blood	A	Pansusceptible	IV
2014	2	Blood	B	Pansusceptible	IV
2014	3	Blood	A	Pansusceptible	IV
2015	4	Wound	C	Pansusceptible	IV
2017	5	Peritoneal fluid	D	Pansusceptible	IV