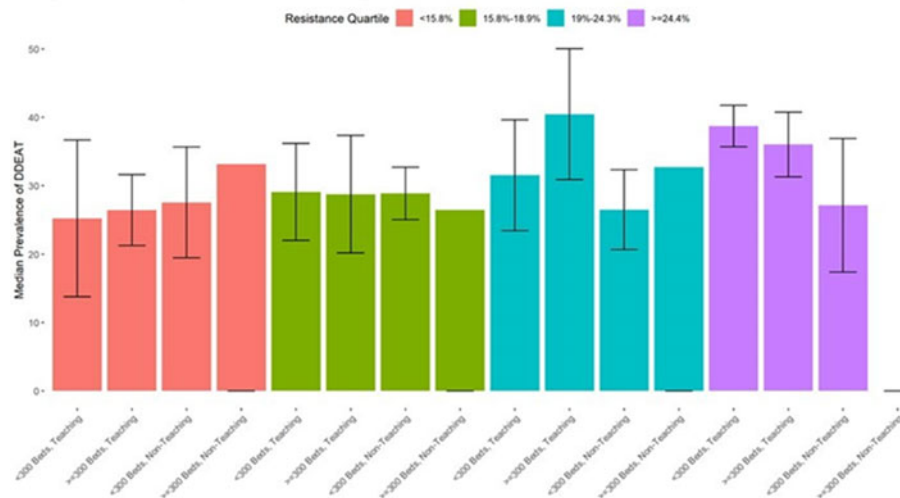


Figure 2: Median proportion of delayed or discordant empiric antibiotic therapy in BSI by hospital-type and baseline resistance quartile. Bars represent median proportions and vertical black lines represent 95% confidence intervals. Bars with stars represent categories with one hospital and are hence missing confidence intervals.



Funding Statement: This work was funded in part by the National Institutes of Health Clinical Center, National Institute of Allergy and Infectious Diseases, the National Cancer Institute (NCI Contract No. HHSN261200800001E) and the Agency for Healthcare Research and Quality.

Fig. 2.

Funding: This study was funded in part by the National Institutes of Health Clinical Center, National Institutes of Allergy and Infectious Diseases, National Cancer Institute (NCI contract no. HHSN261200800001E) and the Agency for Healthcare Research and Quality.

Disclosures: None

Doi:[10.1017/ice.2020.526](https://doi.org/10.1017/ice.2020.526)

Presentation Type:

Oral Presentation

Predicting Vancomycin-Resistant Enterococci (VRE) and Carbapenem-Resistant Organism (CRO) Colonization in the Intensive Care Unit

Çağlar Çağlayan, Clemson University; Scott Levin, Johns Hopkins School of Medicine; Aaron Michael Milstone, Johns Hopkins School of Medicine; Pranita Tamma, Johns Hopkins School of Medicine; Patricia Simner, Johns Hopkins School of Medicine; Katherine Goodman, University of Maryland School of Medicine; Joe Amoah, Johns Hopkins School of Medicine; Aria Smith, Johns Hopkins School of Medicine; Matt Toerper, Johns Hopkins School of Medicine; Sean Barnes, University of Maryland School of Business; Eili Klein, Johns Hopkins School of Medicine

Background: Rapidly identifying patients colonized with multidrug-resistant organisms (MDROs) upon ICU admission is critical to control and prevent the spread of these pathogens in healthcare facilities. Electronic health records (EHR) provide a rich source of data to predict the likelihood of MDRO colonization at admission, whereas surveillance methods are resource intensive and results are not immediately available. Our objectives were (1) to predict VRE and CRO colonization at ICU admission and (2) to identify patient subpopulations at higher risk for colonization with these MDROs. **Methods:** We conducted a retrospective analysis of patients aged ≥ 16 years admitted to any of 6 medical or surgical intensive care units (ICU) in the Johns Hopkins Hospital from July 1, 2016, through June 30, 2018. Perirectal swabs were collected at ICU unit admission and were tested for VRE and CRO. Patient demographic data, prior

hospitalizations, and preadmission clinical data, including prior medication administration, prior diagnoses, and prior procedures, were extracted to develop prediction models. We employed the machine-learning algorithms logistic regression (LR), random forest (RF), and XGBoost (XG). The sum of sensitivity and specificity (ie, Youden's index) was selected as the performance metric. **Results:** In total, 5,033 separate ICU visits from 3,385 patients were included, where 555 (11%) and 373 (7%) admissions tested positive for VRE and CRO, respectively. The sensitivity and specificity of our models for VRE were 78% and 80% with LR, 80% and 82% with RF, and 77% and 87% with XG. Predictions for CRO were not as precise, with LR at 73% and 53%, RF at 81% and 48%, and XG at 69% and 61%. The XG algorithm was the best-performing algorithm for both VRE and CRO. Prior VRE colonization, recent (<180 days) long-term care facility stay, and prior hospitalization >60 days were the key predictors for VRE, whereas the primary predictor for CRO colonization was prior carbapenem use. **Conclusions:** We demonstrated that EHR data can be used to predict >75% of VRE positive cases with a <15% false-positive rate and ~70% of CRO cases with a <40% false-positive rate. Future studies using larger sample sizes may improve the prediction accuracy and inform model generalizability across sites and thus reduce the risk of transmission of MDROs by rapidly identifying MDRO-colonized patients.

Funding: This work was funded by the Centers for Disease Control and Prevention (CDC) Epicenters Program (Grant Number 1U54CK000447) and the CDC MInD-Healthcare Program (Grant Number 1U01CK000536).

Disclosures: Aaron Milstone, BD (consulting)

Doi:[10.1017/ice.2020.527](https://doi.org/10.1017/ice.2020.527)

Presentation Type:

Oral Presentation

Prevalence and Epidemiology of Healthcare-Associated Infections (HAI) in US Nursing Homes (NH), 2017

Nicola Thompson, Centers for Disease Control and Prevention; Nimalie Stone, Centers for Disease Control and Prevention; Cedric Brown, Centers for Disease Control and Prevention; Taniece Eure,

Centers for Disease Control and Prevention; Austin Penna, Centers for Disease Control and Prevention; Grant Barney BS, New York Emerging Infections Program, Rochester, NY; Devra Barter MS, Colorado Department of Public Health and Environment, Denver, CO; Paula Clogher MPH, Connecticut Emerging Infections Program and the Yale School of Public Health, New Haven, CT; Ghinwa Dumyati, University of Rochester; Erin Epson, California Department of Public Health, Healthcare-Associated Infections Program; Christina B. Felsen, University of Rochester Medical Center; Linda Frank, California Emerging Infections Program; Deborah Godine, California Emerging Infections Program; Lourdes Irizarry MD, New Mexico Department of Health, Santa Fe, NM; Helen Johnston, Colorado Department of Public Health and Environment; Marion Kainer MBBS, MPH, Tennessee Department of Health, Nashville, TN; Linda Li MPH, Maryland Department of Health, Baltimore, MD; Ruth Lynfield MD, Minnesota Department of Health, St. Paul, MN; J.P. Mahoehney RN, MPH, Minnesota Department of Health, St. Paul, MN; Joelle Nadle, California Emerging Infections Program; Valerie Ocampo, Oregon Health Authority; Susan Ray, Emory Univ Sch of Med and Grady Health System; Monika Samper, Oregon Health Authority; Sarah Shrum, New Mexico Department of Health; Marla Sievers, New Mexico Department of Health; Srinivasan Krithika, Yale University; Lucy E. Wilson MD ScM, Maryland Department of Health, Baltimore, MD; Alexia Zhang, Oregon Health Authority; Shelley Magill, Centers for Disease Control and Prevention

Background: With an aging population, increasingly complex care, and frequent re-admissions, prevention of healthcare-associated infections (HAIs) in nursing homes (NHs) is a federal priority. However, few contemporary sources of HAI data exist to inform surveillance, prevention, and policy. Prevalence surveys (PSs) are an efficient approach to generating data to measure the burden and describe the types of HAI. In 2017, the Centers for Disease Control and Prevention (CDC) performed its first large-scale HAI PS through the Emerging Infections Program (EIP) to measure the prevalence and describe the epidemiology of HAI in NH residents. **Methods:** NHs from several states (CA, CO, CT, GA, MD, MN, NM, NY, OR, & TN) were randomly selected and asked to participate in a 1-day HAI PS between April and October 2017; participation was voluntary. EIP staff reviewed available medical records for NH residents present on the survey date to collect demographic and basic clinical information and infection signs and symptoms. HAIs with onset on or after NH day 3 were identified using revised McGeer infection definitions applied to data collected by EIP staff and were reported to the CDC through a web-based system. Data were reviewed by CDC staff for potential errors and to validate HAI classifications prior to analysis. HAI prevalence, number of residents with >1 HAI per number of surveyed residents $\times 100$, and 95% CIs were calculated overall (pooled mean) and for selected resident characteristics. Data were analyzed using SAS v9.4 software. **Results:** Among 15,296 residents in 161 NHs, 358 residents with 375 HAIs were identified. The most common HAI sites were skin (32%), respiratory tract (29%), and urinary tract (20%). Cellulitis, soft-tissue or wound infection, symptomatic UTI, and cold or pharyngitis were the most common individual HAIs (Fig. 1). Overall HAI prevalence was 2.3 per 100 residents (95% CI, 2.1–2.6); at the NH level, the median HAI prevalence was 1.8 and ranged from 0 to 14.3 (interquartile range, 0–3.1). At the resident level (Fig. 2), HAI prevalence was significantly higher in persons admitted for postacute care with diabetes,

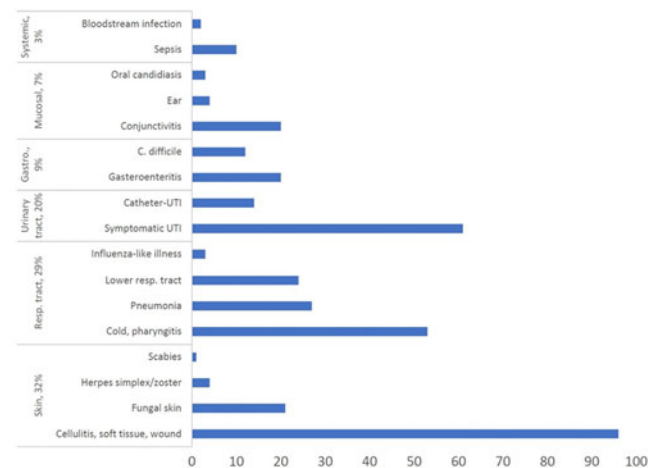


Figure 1: HAIs by site and individual infection type, defined using revised McGeer infection definitions for long-term care.

Fig. 1.

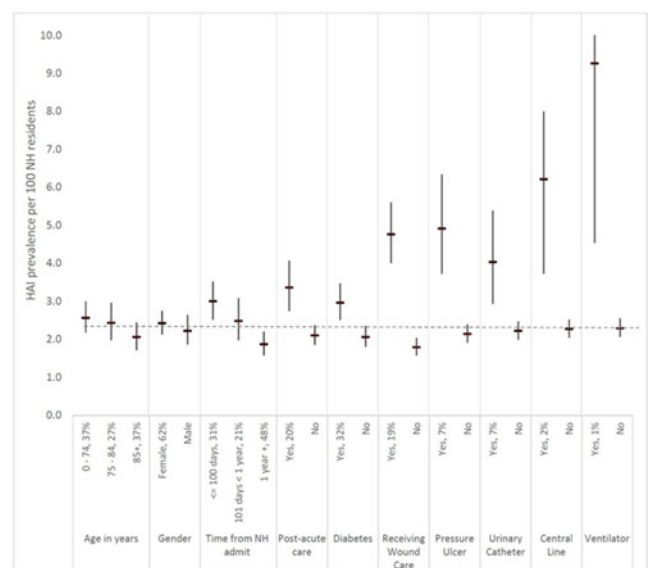


Figure 2: HAI prevalence rate per 100 nursing home residents and 95% confidence interval for selected resident characteristics. Pooled mean HAI prevalence rate (2.34) shown by dotted line. Upper limit for ventilator (16.37) is not shown.

Fig. 2.

with a pressure ulcer, receiving wound care, or with a device. **Conclusions:** In this large-scale survey, 1 in 43 NH residents had an HAI on a given day. Three HAI types comprised >80% of infections. In addition to identifying characteristics that place residents at higher risk for HAIs, these findings provide important data on HAI epidemiology in NHs that can be used to expand HAI surveillance and inform prevention policies and practices.

Funding: None

Disclosures: None

Doi:10.1017/ice.2020.528