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

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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.

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

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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 x100, 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, 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.

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