Intraoperative transfusion was a risk factor for SSI (OR, 4.7) (Fig. 1). Among the 205 patients with no indication for transfusion, 98 received blood even without the indication: there was no difference in hemoglobin outcome when discharge and admission were compared, and the 98 patients were exposed to unnecessary risk. Regarding restrictive versus liberal transfusion strategies, there were differences in the variables, age ($P = .000$), duration of surgery ($P = .003$), number of comorbidities ($P = .000$), body mass index (BMI) ($P = .027$), previous hemoglobin ($P = .000$), and high hemoglobin ($P = .000$), considering the transfusion practice employed (Fig. 2). **Conclusions:** The indications for and definition of protocols and careful evaluation of blood transfusion are critical to avoid infectious complications in orthopedic patients with lower-limb fractures.
Funding: None
Disclosures: None
Doi:10.1017/ice.2020.904

Presentation Type:
Poster Presentation

Like a Bat Out of.... the Hospital? Development of a Bat Capture and Testing Protocol Prompted by Two Nosocomial Encounters

Michael Kessler, Fellowship; Daniel Shirley, University of Wisconsin School of Medicine and Public Health; Laura Anderson, UW Health; Nasia Safdar, University of Wisconsin, Madison

Background: In the state of Wisconsin, 3%–4% of bats submitted for rabies testing are positive. Inpatient bat encounters at 2 affiliated healthcare facilities at nearly the same time were brought to the attention of the infection prevention and control (IPC) team. The first bat was captured in a patient room and was submitted for testing. Postexposure prophylaxis (PEP) was initiated for 1 patient before the bat testing results came back negative. The second bat was found in a transplant unit hallway and was released before we could request testing. We observed significant variations in responses, including decision to administer PEP and submission of bats for rabies testing. The IPC team developed a protocol to minimize unnecessary PEP, to prevent nosocomial rabies infection from bat exposure, and to limit associated panic. **Methods:** A systematic literature review of multiple databases was performed. A search of nonscientific articles using Google was also performed to assess unpublished inpatient bat encounters. A workgroup was established including IPC staff, physicians, and facilities management. The county animal services department and the state public health department veterinarian were consulted to aid in development of a protocol. **Results:** Literature review yielded a single report of a bat discovered in a neonatal intensive care unit (NICU). A lack of protocol resulted in PEP administration to 7 neonates without observed exposure after the bat was released instead of being submitted for testing. Of the first 100 articles retrieved via Google search of "bat in hospital," 9 pertained to nosocomial discovery of bats in 5 different states over the past 7 years. Encounters included infestations requiring unit shutdowns and PEP administration. One tertiary-care referral center reported 10 encounters per year but did not elaborate on associated procedures. The county animal services staff assisted in training maintenance and engineering services (MES) personnel on how to secure bats for testing and helped develop a "bat kit" with protective gear and equipment to do so safely. In the new protocol, an inpatient bat encounter prompts personnel to capture the bat and begin an investigation into known or potential occult exposure. Known or potential exposures merit submission of the bat for rabies testing, the results of which guide PEP recommendations. All encounters are investigated for point of entry or roost. **Conclusions:** Inpatient bat encounters are not uncommon. Encounters should prompt systematic assessment for exposures and an investigation of the root cause. Following a protocol may limit unnecessary PEP administration, prevent nosocomial transmission of rabies from bat to patient, and attenuate associated anxiety.
Funding: None
Disclosures: None
Doi:10.1017/ice.2020.905

Presentation Type:
Poster Presentation

Linezolid-Resistant *Staphylococcus haemolyticus*: Emergence of G2447U and C2534U Mutations at the Domain V of 23Sr RNA Gene

Sanjana Kumari, Senior Resident*; Jyoti Rawre, All India Institute of Medical Sciences; Anjan Trikha, All India Institute of Medical Sciences; Vishnubhatla Sireenivas, All India Institute of Medical Sciences; Seema Sood, All India Institute of Medical Sciences; Arti Kapil, All India Institute of Medical Sciences; Benu Dhawan, All India Institute of Medical Sciences

Background: Linezolid an oxazolidinone drug available in both parenteral and oral formulations has emerged as a novel alternative to vancomycin and other second-generation drugs for the treatment of infections from gram-positive cocci. Clinical isolates of linezolid-resistant staphylococci and enterococci were reported. Since then, linezolid-resistant strains have become an increasing problem worldwide. The most frequently reported mechanisms of linezolid resistance include the mutation in 23S ribosomal nucleic acid and presence of *cfr* gene. Methicillin-resistant coagulase-negative staphylococci (MR-CoNS) and vancomycin-resistant *Enterococcus (V*RE) have become a worrisome clinical problem. **Objective:** Therefore, we aimed to determine the distribution of linezolid-resistant strains in an inpatient setting of a tertiary-care hospital in India and to evaluate the resistance mechanisms among these isolates. In addition, the clonal diversity of the isolates was determined by pulsed-field gel electrophoresis (PFGE). **Methods:** The distribution, clonal diversity, and resistance mechanism of linezolid resistant-*Staphylococcus haemolyticus* (LRSH) strains were determined. The isolates were identified by MALDI-TOF. The mechanism of resistance was determined by sequence analysis of the domain V of 23SrRNA and screening for *cfr* gene. Clonal relatedness was defined by PFGE. **Results:**

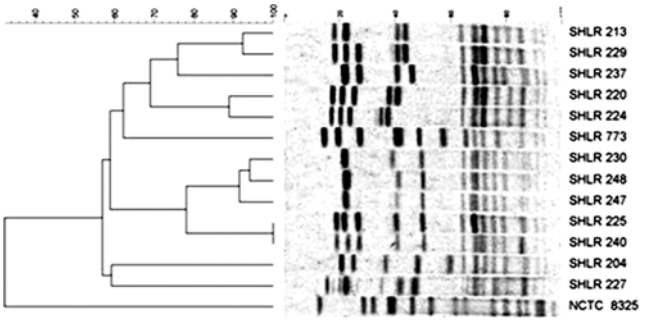

Fig. 1.

In total, 13 LRSH isolates were recovered from pus specimens. The 13 LRSH strains isolated had an linezolid MIC of ≥256 μg/mL. Sequencing results revealed G2576T mutations in 7 (53.8%), G2447U in 4 (30.7%) and C2534U in 1 (7.6%) isolate of *S. haemolyticus*. One isolate of *S. haemolyticus* showed 2 simultaneous mutations (G2576T and G2447U) in the domain V region of 23Sr RNA gene. PFGE of the LR-SH isolates revealed the presence of 11 clones. Of the 11 clones, clones I and II had 2 isolates each. Isolates of clone I exhibited a band pattern identical with the previous isolates of LRSH isolated from the orthopedic unit. Similarly, isolates of clone II also shared the same band pattern with the previous LRSH isolates from the dermatology unit of our center. **Conclusions:** This study highlights the importance of continuous monitoring of vigilance of linezolid resistance in staphylococci. Rationalizing the use of linezolid and implementing methods to control the spread of hospital clones is of paramount importance to prevent further dissemination of these strains.

Funding: None
Disclosures: None
Doi:10.1017/ice.2020.906

Presentation Type:
Poster Presentation

Machine-Learning Accurately Predicts Adverse Outcomes Following *Clostridioides difficile* Infection in Colorectal Surgery

Brett Tracy, Emory University School of Medicine; Rondi Gelbard, University of Alabama; Joel Zivot, Emory University School of Medicine; Andrew Morris, Emory University School of Medicine; Jason Sciarretta, Emory University School of Medicine; Benjamin Hazen, Emory University

Background: *Clostridioides difficile* infection (CDI) following colorectal surgery can lead to significant adverse outcomes. Although previous studies have identified risk factors for CDI, their relative importance for predicting complications remains unclear. **Objective:** We sought to use machine-learning algorithms to accurately determine which perioperative risk factors are most predictive of adverse outcomes after CDI. **Methods:** The National Surgical Quality Improvement Project (NSQIP) database was used to identify all patients who developed CDI after a colorectal operation in 2016 (N = 14,392). We excluded patients without CDI and patients <18 years of age. Any missing data were replaced with multivariate singular value decomposition imputation. We collected data on patient demographics, comorbidities, preoperative laboratory values, operative details, and outcomes, including infectious, cardiovascular, hematologic, renal, and pulmonary complications, unplanned returns to the operating room (RTOR), non–home discharge, readmission, and mortality. Data were univariably assessed for significant association with outcomes. If an input variable significantly correlated with ≥5 outcomes, it was included in our machine-learning models. We utilized bootstrap aggregation with random forests to improve prediction accuracy. We then calculated each input variable's importance to the model outcome (VIP). The VIPs of each variable were averaged to yield an overall impact. Each model's accuracy was determined by the area under the receiver operator curve (AUROC). **Results:** There were 841 patients in our cohort (median age 66 years (IQR, 55–75.8), 482 (57%) were women, and the mean American Society of Anesthesiologists [ASA] class score was 2.9 (SD, ±0.7). Of all colorectal surgeries, 172 (20.5%) were emergent. Overall mortality was 3.8% (n=32), and 371 patients (44.1%) experienced at least 1 postoperative complication, of which infectious complications (eg, septic shock, sepsis, wound infection, urinary tract infection) were most common (n=255, 30.3%). The RTOR rate was 10.3% (n = 87), the non–home discharge rate was 23.8% (n = 200), and the readmission rate was 30.9% (n = 260). The input variables most predictive of any adverse outcome were hematocrit (VIP, 24.9%), ASA class (VIP, 24.4%), creatinine (VIP, 17.4%), and prealbumin (VIP, 11.6%). The probability of any adverse outcome was 90.6% in the setting of hematocrit ≤27%, ASA class ≥3, creatinine ≥1.6 mg/dL, and prealbumin ≤3.1 mg/dL. All machine-learning models had an AUROC ≥0.99. **Conclusions:** Although nonpatient factors can contribute to unfavorable outcomes in patients with CDI following colorectal surgery, we identified 4 patient-specific variables that account for almost 80% of any adverse outcomes. Although further prospective study is needed, individuals with these preoperative risk factors could consider delaying their elective colorectal operations until they are medically optimized.

Funding: None
Disclosures: None
Doi:10.1017/ice.2020.907

Presentation Type:
Poster Presentation

Measuring the Cost of Overtesting and Overdiagnosis of *Clostridioides difficile* Infection

Gregory Madden, Infectious Diseases Fellowship Program; David Smith, UVA McIntire School of Commerce; Costi Sifri, University of Virginia Medical Center

Background: *C. difficile* is the leading healthcare-associated pathogen. The *C. difficile* real-time polymerase chain reaction (PCR) stool test, used by >70% of hospitals, is highly sensitive but cannot differentiate colonization from infection. Inappropriate *C. difficile* testing may result in overdiagnosis and unnecessary treatment. Healthcare costs attributed to *C. difficile* are substantial, but the economic burden associated with *C. difficile* false positives in colonized patients is poorly understood. *C. difficile* PCR cycle threshold (CT) is as an inverse proxy for organism burden; high CT (≥30.9) has a high (>98%) negative predictive value compared to the reference gold standard, thus is a marker of colonization. Conversely, a low CT (≤28.0) suggests high organism burden and high specificity for true infection. **Methods:** A propensity score matching model for cost per hospitalization was developed to determine the costs of a hospital stay associated with *C. difficile* and to isolate the financial impacts of both true *C. difficile* infection and false positives. Relevant predictors of *C. difficile* positivity used in the model were age, Charlson comorbidity index, white blood cell count, and creatinine. We used CT data to identify and compare 3 inpatient groups: (1) true CDI, (2) *C. difficile* colonization,

Propensity-Adjusted Hospital Costs According to *C. difficile* Diagnosis.

	Negative (n=4,410)	vs	Positive (n=*1,470*)	*P*	Negative (n=2,733)	vs	True (n=911)	*P*	Negative (n=1,077)	vs	Colonized (n=359)	*P*
Total Cost	$17,348		$17,465	.7929	$18,264		$16,148	.1220	$16,950		$21,950	.0061
Direct	$8,863		$8,682	.9917	$9,375		$8,101	.1065	$8,517		$11,435	.0134
Fixed	$9,762		$10,364	.3291	$10,311		$9,096	.3629	$9,463		$12,437	.0029
Length of Stay (IQR)	7 (2 - 16)		7 (3 - 17)	.0720	7 (2 - 16)		7 (2 - 16)	.7365	7 (2 - 15)		8 (3 - 18)	.0144
Total Cost Per Day	$2,144		$2,009	.0208	$2,150		$1,930	.0001	$2,077		$2,295	.0294
Inpatient Mortality	309 (7.0%)		87 (5.9%)	.1493	213 (7.8%)		56 (6.1%)	.0998	65 (6.0%)		22 (6.1%)	.9491
ICU Transfer	555 (12.6%)		190 (12.9%)	.7342	342 (12.5%)		119 (13.1%)	.6661	123 (11.4%)		50 (13.9%)	.2063

Data presented as US dollars ($) or n (%) unless unless otherwise specified. n values indicate the number of propensity-matched pairs with a 3:1 (Negative:Positive) ratio. *P* values for cost differences calculated using Mann-Whitney *U* test; *P* values for categorical variables using the Chi-squared test. True positive indicates *C. difficile* PCR cycle threshold ≤ 28.0; Colonized indicates cycle threshold ≥ 30.9. Abbreviations: ICU (Intensive Care Unit)

Table 1.