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.

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

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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.

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

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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.

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and (3) *C. difficile* negative. **Results:** A diagnosis of *C. difficile* adds significantly (>$3,000) to unadjusted hospital cost compared to a negative result. Propensity-adjusted analyses demonstrated that *C. difficile* colonization was associated with significantly increased (median, $5,000) hospital cost whereas any positive or true diagnoses of *C. difficile* were not associated with increased cost. Colonized patients also had significantly higher lengths of stay (1 day) and cost per length of stay ($218 per day). **Conclusions:** This is the first *C. difficile* cost analysis to utilize PCR CT data to differentiate colonization. Surprisingly, patients with a high CT had disproportionately higher hospital costs compared to matched *C. difficile*–negative patients, which was not seen among patients with a low CT or with any positive result. We hypothesize that this unexpected finding may be due to misdiagnosis and mistreatment of diarrhea not caused by *C. difficile* or unadjusted factors associated with high cost and non–*C. difficile* diarrhea. In addition, the discrepantly high cost attributed to *C. difficile* diagnosis cited in the literature ($3,000–11,000 per hospitalized case) could be explained by the common use of administrative data to identify *C. difficile* cases and controls as opposed to our study, which directly linked cost data to *C. difficile*–positive and –negative test results.

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Meta-analysis of Outcomes Using Ceftolozane-Tazobactam and Ceftazidime-Avibactam for Multidrug-Resistant Organism Infections

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Background: Ceftolozane-tazobactam (C/T) and ceftazidime-avibactam (C/A) are new β-lactam/β-lactamase combination antibiotics that were approved by the FDA in 2014 and 2015, respectively, to treat complicated intra-abdominal and urinary tract infections. They are commonly used to treat multidrug-resistant *Pseudomonas aeruginosa* (MDRPA) and carbapenem-resistant *Enterobacteriaceae* (CRE) infections at any site. Both medications are also often used as salvage therapy when empiric therapy has failed or when the infectious organism tests resistant to all other available antibiotics. The purpose of this review is to present the clinical experience and reported clinical success rates of C/T and C/A. **Methods:** PubMed, EMBASE, and Google Scholar were searched from January 1, 2013, through October 1, 2019, for publications detailing clinical experience with C/T and C/A in patients with CRE and MDRPA infections. Included study designs were extended cases series and clinical observational studies. Information on infection type, bacterial agent, salvage therapy uses, clinical success, and resistance development during treatment were abstracted. Meta-regression analysis was used to determine the pooled effectiveness of C/T and C/A among included studies. **Results:** The literature search returned 1,645 publications. After exclusion criteria were applied, 16 publications representing 769 patients were retained. The study population was mostly male (pooled average, 62%). The major comorbidities represented in the pooled population were solid organ transplantation (20.0%), kidney disease (19.5%), cardiovascular disease (15.3%), and diabetes (15.3%). Pneumonia was the predominant infection type (41.4%) and MDRPA was the pathogen most frequently evaluated (57.7%). The pooled clinical success rate was 70.2% (95% CI, 64.5%–75.3%). Also, 10 studies explicitly evaluated C/A or C/T as salvage therapy. The pooled clinical success rate for salvage therapy studies was 75.2% (95% CI, 69.7%–80.0%). Development of resistance to C/T or C/A during or after treatment was reported for 2.0% of the population. **Conclusion:** Overall, these medications have a high clinical success rate in patients with severe and complicated infections and limited treatment options. Pooled clinical success rates were high (70.2%) and the medications were particularly effective as salvage therapy. Resistance rates were low, although this could have been biased by the small percentage of studies that reported on this outcome. More longitudinal studies comparing the effectiveness of C/T and C/A against other antibiotic regimens are needed.

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Methicillin-Resistant *Staphylococcus aureus* Prevalence Among Healthcare Workers in Contact Tracings in a Dutch Hospital

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Background: In The Netherlands, the national guidelines on Methicillin-Resistant *Staphylococcus aureus* (MRSA) prevention and control advocate screening of healthcare workers (HCWs) after unprotected exposure to MRSA carriers. Although this strategy is largely successful, contact tracing of staff is a time-consuming and costly component. We evaluated our contact tracing policy for HCWs over the years 2010–2018. **Methods:** A retrospective, observational study was performed in a Dutch teaching hospital. All HCWs who had unprotected contact with an MRSA carrier were included in contact tracing. When there had been a long period of unprotected admission prior to an MRSA finding, or when the index case was an HCW, the entire (nursing) team was tested. All samples of HCWs who were tested for MRSA carriage as part of contact tracing from 2010 until 2018 were included. A pooled nose, throat, and perineum swab was collected using the eSwab medium (Copan) and inoculated on chromID MRSA agar plates (bioMérieux) after enrichment in a broth. Molecular typing was performed using multiple-locus variable number of tandem repeat analysis (MLVA). **Results:** In total, we included 8,849 samples (range, 677–1,448 samples per year) from 287 contact tracings (range, 26–55 contact tracings per year). Overall, 32 HCWs were colonized with MRSA (0.36%; 95% CI, 0.26%–0.51%). None of them developed a clinical infection. Moreover, 8 HCWs (0.10%; 95% CI, 0.05%–0.19%) were colonized with the same MLVA type as the index case and were detected in 6 of 287 contact tracings (2%). In 4 of 8 of these cases, a positive HCW was the index for undertaking contact tracing. In 3 of 8 cases, it was clear that the HCW who was identified in the contact tracing was the source of the outbreak and was the cause of invasive MRSA infections in patients. Notably, a different MLVA type as the index case was found in 24 HCWs (0.27%; 95% CI, 0.18%–0.40%) of whom 7 of 24 HCWs (29.2%) were intermittent carriers. **Conclusions:** This study revealed a sustained low MRSA prevalence among