3.3% (*Enterobacteriaceae*) to 23.0% (vancomycin-resistant *Enterococcus*) (Table 1).

The correlation between microbiologically confirmed non-MRSA MDRO infection and V09 diagnosis codes for drug resistance was poor. Previous research showed poor correlation between V09 codes and confirmed MRSA infection prior to the introduction of MRSA-specific ICD-9-CM codes.[3] Our MRSA coding rates after the introduction of MRSA-specific ICD-9-CM codes were higher than previously reported.[7] We also found that ID consultation increased rates of MRSA coding, likely due to increased recognition and documentation of the presence and importance of MRSA by ID physicians.

In addition, coding rates for MRSA were significantly higher than coding rates of drug resistance for other organisms, suggesting a need for unique codes for other MDROs. This conclusion is reinforced by the fact that for patients with MRSA, introduction of MRSA-specific codes resulted in a dramatic increase in coding for resistant *S. aureus*. As ICD-9-CM codes are assigned by nonmedical personnel, universal drug resistance definitions and organism-specific drug resistance codes will likely assist in the proper coding of MDROs. Our findings are likely applicable to ICD-10-CM codes because the structure of ICD-10-CM drug resistance codes mimics those from ICD-9-CM.

Our results demonstrate that ICD-9-CM diagnosis codes cannot be used to estimate the burden of MDRO infections in hospitals. Additionally, researchers should be aware of the limitations of ICD-9-CM codes for studying MDRO infections from large retrospective medical databases. More specific MDRO codes are needed to facilitate future research using administrative data, a problem not addressed by ICD-10-CM.

To our knowledge, this study is the first to examine drug resistance coding rates for a variety of MDRO pathogens. The study is limited to a single tertiary-care referral center, and these results may not be generalizable. However, the study draws strength from its large sample size and has implications for hospital rankings, reimbursements, and future MDRO research utilizing large administrative databases.

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Clostridium difficile RT 078/ST11: A Threat to Community Population and Pigs Identified in Elder Hospitalized Patients in Beijing, China

To the Editor—Clostridium difficile ribotype (RT) 078 has been known as the predominant strain in animals (swine and cattle), and it has been increasingly identified in human *C. difficile* infection causing severe disease and increased

mortality, especially in the community setting[1,2]. Recently, *C. difficile* RT 078 has been reported from both hospitalized patients (ages unknown) and environmental surfaces in eastern China.[3] In our study, we identified 6 *C. difficile* isolates of RT 078 from elderly patients (average age, 85 years) in a tertiary hospital in Beijing, China, from April 2015 to December 2015. A total of 50 *C. difficile* isolates, including RT 078, were obtained from 642 feces samples. Toxin genes *tcdA*, *tcdB*, *cdtA*, and *cdtB*, were identified using polymerase chain reaction (PCR) ribotyping, sequencing of *tcdC*, and multilocus sequence typing (MLST) for all isolates. In addition, *C. difficile* isolates of 6 RT 078 were tested for susceptibility to rifampin, moxifloxacin, vancomycin, clindamycin, levofloxacin, tetracycline, and erythromycin using Etest strips (bioMèrieux, Marcy-l'Étoile, France). The interpretation of minimal inhibitory concentration (MIC) results followed the Clinical and Laboratory Standards Institute (CLSI) M100-S23 guideline recommendations published in 2013[4] and other previous studies.[5–7]

In total, 12 nontoxingenic isolates were identified; the rest were positive for *tcdA*/*tcdB*. A total of 20 strain types (STs), distributed in clades 1 (38 isolates), 3 (1 isolate), 4 (3 isolates), and 5 (8 isolates) were identified (Figure 1A). The most frequent STs were ST2 (9 isolates), ST3 (8 isolates), and ST11 (8 isolates). Overall, 19 PCR RTs were found after comparing with the reference strains from European Centers for Disease Control (ECDC)-Brazier Collection and the American Tissue Culture Collection (ATCC) by capillary electrophoresis (Figure 1B). Of 8 ST11 isolates, 6 displayed the same band with ECDC 078 and ATCC 1875 (Figure 1C). In addition, all 6 isolates were also confirmed as RT078, with a mutation point at position 184 and Δ39-bp deletion. Our results resemble previous findings: a single ST11 was associated with several PCR RTs, including RTs 033, 045, 066, 078, 126, and 193,[8] suggesting that PCR ribotyping is essential for the subtyping of ST11 and ST1 (including RTs 016, 027, 036, and 176). The 6 RT 078 isolates were all sensitive to rifampin and vancomycin; only 1 of the 6 isolates (ie, 25053-2) was resistant to moxifloxacin and levofloxacin. Almost all RT 078 isolates were intermediately resistant or resistant to clindamycin, except for 25053-2. Antibiotic misuse in a large aging population is an area of concern in China; increased reports of *C. difficile* infection and the emergence of hypervirulent RT 027 and RT 078 CDI strains might represent a threat to the public health in the near future. Thus, we are seeking to develop standardized methods to diagnosis, treat, and prevent CDI and to identify and characterize the isolates by molecular typing through a nationwide surveillance network in China.

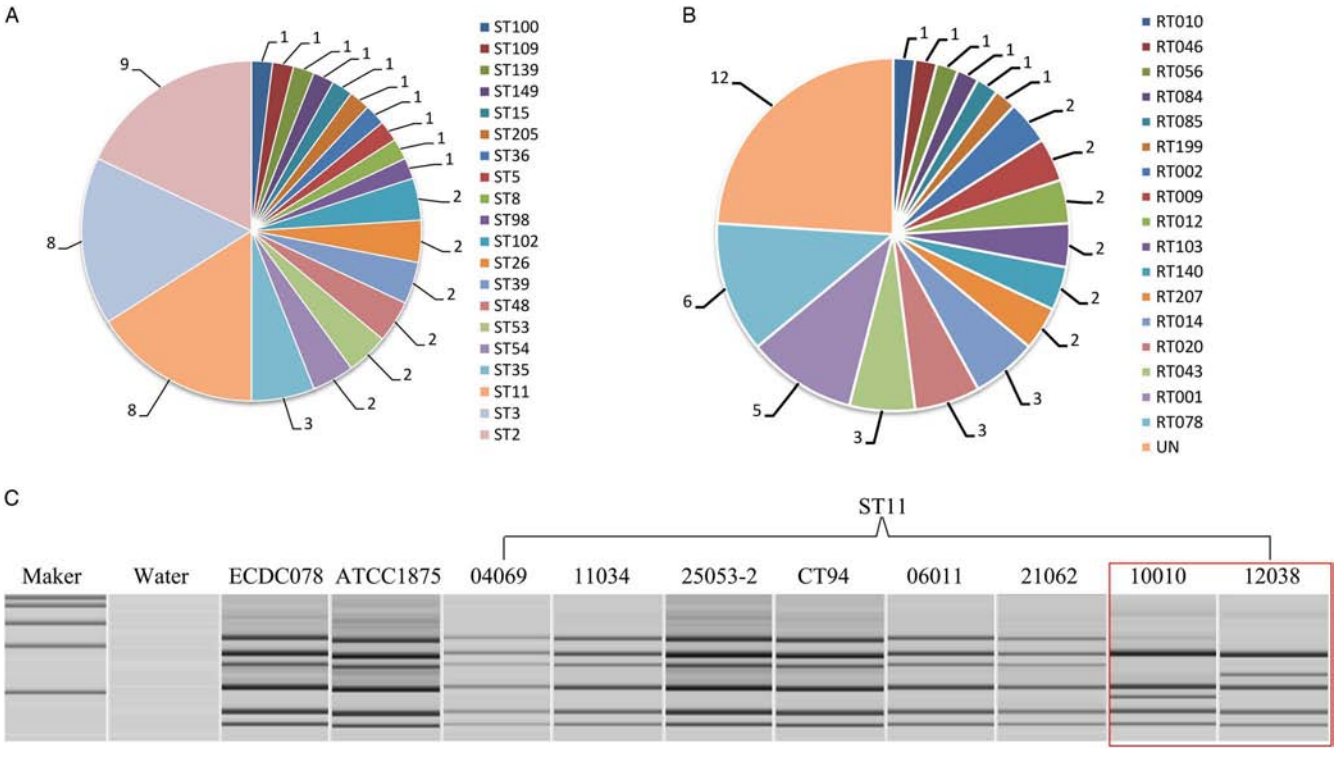

FIGURE 1. Strain types (STs) and PCR riboypes (RTs) identified in this study, and the capillary electrophoresis bands of 8 isolates with ST 11. **A**. Proportion of STs in this study. **B**. Proportion of RTs in this study. **C**. The capillary electrophoresis bands of 8 ST 11 isolates, of which 6 strains are RT 078 after comparing with references from the European Centre for Disease Prevention and Control and the American Type Culture Collection. The isolates in the red square are not RT 078, although they are ST11.

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Mucosal Barrier Injury Central-Line–Associated Bloodstream Infections: What is the Impact of Standard Prevention Bundles?

To the Editor—Central-line–associated bloodstream infections (CLABSIs) remain a significant problem for hospitalized children, particularly among hematology-oncology populations. Recognizing the unique challenges posed by neutropenia and impaired gut integrity, the Centers for Disease Control and Prevention's National Healthcare Safety Network introduced a revised surveillance protocol for CLABSIs in January 2013 that included a new classification for mucosal-barrier injury (MBI) laboratory-confirmed bloodstream infection.[1–4] Many hypothesize that MBI CLABSIs are related to translocation of enteric microorganisms across a disrupted intestinal epithelium, suggesting that bundles focused on catheter insertion and maintenance would not impact infection rates.[3,5] Through a retrospective, stratified analysis of in-house data, we describe changes in MBI and non-MBI CLABSIs in oncology patients at our institution.

METHODS

Study Design

A retrospective observational study was performed, comparing the monthly rate of MBI and non-MBI CLABSIs (per 1,000 central-line days) among oncology inpatients at the Children's Hospital of Philadelphia from January 2013 to March 2016. This study utilized existing data reviewed for quality improvement purposes; therefore, it was deemed exempt from the Children's Hospital of Philadelphia Institutional Review Board oversight.

Study Setting

The Children's Hospital of Philadelphia is a 546-bed quaternary-care pediatric hospital, which has 50 oncology and bone marrow transplant (BMT) beds and an average of 1,557 oncology admissions per year. The Department of Infection Prevention and Control includes 8 certified infection preventionists and a full-time medical director.