analysis. Infection density rate (IDR), conditional maximum likelihood estimate (CMLE) of rate ratio (RR), 95% confidence intervals (CI), and $P$ values were calculated. The Fisher exact test was used to compare IDRs among years. $P < .05$ was considered statistically significant.

The IDR did not increase for ESBL-EC after cessation of contact precautions in our hospital. Also, no change was observed for IDR for ESBL-producing $K$. pneumoniae or for CR $K$. pneumoniae between 2015 and 2016. An increase in CR $E$. coli bacteremia at the Oncology Hospital was observed, but it was not statistically significant (Table 1).

A recent Swiss study showed the safety of cessation of contact precautions for ESBL-EC in a setting where compliance with standard infection control precautions and hand hygiene is high. Compliance with infection control precaution is highly variable in our hospital. The rate of compliance with hand hygiene before patient contact is nearly 90% in the oncology ICU and BMT units; however, it was 30%–60% in the surgical ICUs. Nevertheless, we did not observe an increase in the rate of ESBL-EC bacteremia.

This study has some limitations. First, we did not compare the types of ESBL-EC infection other than bacteremia between 2015 and 2016, but no clusters of ESBL-EC infections were detected in any of the wards during surveillance activities. Bacteremia surveillance is the only type of surveillance that is performed hospital-wide, so we decided to compare the bacteremia rates. Also, we did not have access the molecular epidemiology of ESBL-EC because it is very difficult to analyze the genetic relatedness of ESBL-EC in daily practice for infection control purposes.

Despite all limitations, our study showed that, in a middle outcome country where compliance to infection control precaution is highly variable, cessation of contact precautions for ESBL-EC did not result in a negative outcome. However, infection control teams practicing in crowded hospitals under high workload with insufficient staff should be cautious because ESBL-EC outbreaks are common.

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**ICD-9-CM Coding for Multidrug Resistant Infection Correlates Poorly With Microbiologically Confirmed Multidrug Resistant Infection**

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**References**

Table 1. Organism and Multidrug-Resistant Organism (MDRO) Discharge International Classification of Diseases, Ninth Revision, Clinical Modification (ICD-9-CM) Codes for Various Sterile Site MDRO Infections

<table>
<thead>
<tr>
<th>Drug-Resistant Organism (No.)</th>
<th>Coded for Correct Organism, No. (%)</th>
<th>Any MDRO Code, No. (%)</th>
<th>Any V09 Code, No. (%)</th>
<th>Any V098, V0981, V099, V0991 Code, No. (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRSA after 10/1/2008 (1,113)</td>
<td>835 (75.0)</td>
<td>843 (75.7)</td>
<td>39 (3.5)</td>
<td>10 (0.9)</td>
</tr>
<tr>
<td>MRSA before 10/1/2008 (504)</td>
<td>300 (59.5)</td>
<td>168 (33.3)</td>
<td>168 (33.3)</td>
<td>0</td>
</tr>
<tr>
<td>VRE (735)</td>
<td>209 (29.4)</td>
<td>169 (23.0)</td>
<td>162 (22.0)</td>
<td>24 (3.3)</td>
</tr>
<tr>
<td>Enterococcus (851)</td>
<td>242 (28.4)</td>
<td>172 (20.2)</td>
<td>164 (19.3)</td>
<td>24 (2.8)</td>
</tr>
<tr>
<td>Enterobacteriaceae (1226)</td>
<td>802 (65.4)</td>
<td>41 (3.3)</td>
<td>26 (2.1)</td>
<td>6 (0.5)</td>
</tr>
<tr>
<td>Acinetobacter spp. (107)</td>
<td>31 (29.0)</td>
<td>12 (11.2)</td>
<td>9 (8.4)</td>
<td>3 (2.8)</td>
</tr>
<tr>
<td>Pseudomonas aeruginosa (204)</td>
<td>152 (74.5)</td>
<td>17 (8.3)</td>
<td>10 (4.9)</td>
<td>6 (2.9)</td>
</tr>
</tbody>
</table>

**NOTE.** MRSA, methicillin-resistant Staphylococcus aureus; VRE, vancomycin-resistant Enterococcus.

*a* For MRSA after 10/1/2008: 038.12, 482.42, 041.12. For MRSA before 10/1/2008: 038.11, 482.41, 041.11. For VRE and Enterococcus: 041.04. For Enterobacteriaceae: 038.4, 038.40, 038.42, 038.44, 038.49, 041.3, 041.4, 041.49, 041.6, 041.85, 48.20, 48.282, 48.283. For Acinetobacter spp.: 038.40, 038.49, 482.83. For Pseudomonas aeruginosa: 038.43, 041.7, 48.21.

*b* Any of the following: 038.12, 482.42, 041.12 (MRSA codes); V09, V09.0, V09.1, V09.2, V09.3, V09.4, V09.5, V09.50, V09.51, V09.6, V09.7, V09.71, V09.70, V09.8, V09.80, V09.81, V09.9, V09.91, V09.90.

*c* A distinction was made for V098, V0981, V099, and V0991 because these code for multidrug resistance, rather than single drug or single class resistance of the other V09 codes.
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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References


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

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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

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