2017

ICD-9-CM coding for multidrug resistant infection correlates poorly with microbiologically confirmed multidrug resistant infection

Jason P. Burnham
Washington University School of Medicine in St. Louis

Jennie H. Kwon
Washington University School of Medicine in St. Louis

Hilary M. Babcock
Washington University School of Medicine in St. Louis

Margaret A. Olsen
Washington University School of Medicine in St. Louis

Marin H. Kollef
Washington University School of Medicine in St. Louis

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.[5] 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.

ACKNOWLEDGMENTS

Financial support: No financial support was provided relevant to this article.

Potential conflicts of interest: Gökhan Metan has received honoraria for speaking at symposia and lectures organized by Gilead; Merck, Sharp, and Dohme (MSD); and Pfizer. He received financial compensation from Pfizer for a meeting organized to discuss the content of a review paper, and he is a member of the advisory board of Pfizer and Astellas. He has received travel grants from MSD, Pfizer, and Gilead to participate in conferences. Serhat Üna has received honoraria for lectures from Pfizer, MSD, and Gilead, as well as travel grants from MSD, Pfizer, and Gilead to participate in conferences. All other authors report no conflicts of interest relevant to this article.

Gökhan Metan, MD;[1,2]
Baki Can Metin, MD;[3]
Zeynep Baştuğ;[2]
İlknur Tekin;[2]
Hanife Aytaç;[2]
Burcu Çınar, MSc;[2]
Hümeyra Zengin, MSc;[2]
Serhat Ünal, MD[1,2]

Affiliations: 1. Department of Infectious Diseases and Clinical Microbiology, Hacettepe University, Faculty of Medicine, Ankara, Turkey; 2. Infection Control Committee, Hacettepe University Hospital, Ankara, Turkey; 3. Department of Public Health, Hacettepe University, Faculty of Medicine, Ankara, Turkey.

Address correspondence to Gokhan Metan, MD, Hacettepe Üniversitesi Tıp Fakültesi Hastanesi, İç Hastalıkları Binası, Enfeksiyon Hastalıkları ve Klinik Mikrobiyoloji Anabilim Dalı, Sıhhıye, Ankara, Turkey (gokhanmetan@gmail.com, gokhanmetan@hacettepe.edu.tr).

Infect Control Hosp Epidemiol 2017;38:1379–1381
 0899-823X/2017/3811-0022. DOI: 10.1017/ice.2017.198

REFERENCES

1. Dhar S, Marchaim D, Tansek R, et al. Contact precautions: more is not necessarily better. *Infect Control Hosp Epidemiol* 2014;35:213–221.
2. Tacconelli E, Cataldo MA, Dancer SJ, et al; European Society of Clinical Microbiology. ESCMID guidelines for the management of the infection control measures to reduce transmission of multidrug-resistant gram-negative bacteria in hospitalized patients. *Clin Microbiol Infect* 2014;20(Suppl 1):1–55.
3. Metan G, Zarakolu P, Cakir B, Hascelik G, Uzun O. Clinical outcomes and therapeutic options of bloodstream infections caused by extended-spectrum beta-lactamase-producing *Escherichia coli*. *Int J Antimicrob Agents* 2005;26:254–257.
4. Gulmez D, Woodford N, Palepou MF, et al. Carbapenem-resistant *Escherichia coli* and *Klebsiella pneumoniae* isolates from Turkey with OXA-48-like carbapenemases and outer membrane protein loss. *Int J Antimicrob Agents* 2008;31:523–526.
5. Tschudin-Sutter S, Frei R, Schwahn F, et al. Prospective validation of cessation of contact precautions for extended-spectrum β-lactamase-producing *Escherichia coli*. *Emerg Infect Dis* 2016;22:1094–1097.

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

To the Editor—The *International Classification of Diseases, Ninth revision, Clinical Modification* (ICD-9-CM) coding system is often used to conduct surveillance for various infections.[1] Unfortunately, ICD-9-CM coding is subject to error and does not always reflect the true level of comorbid and acute illnesses.[2] Little research has been done to determine the accuracy of ICD-9-CM codes to identify multidrug-resistant organism (MDRO) infections.[3] Inaccurate coding of MDROs has implications for monitoring of MDRO transmission

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

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

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.

dynamics, assessments of MDRO epidemiology, calculations of hospital ratings and rankings, and hospital reimbursements. At present, no globally utilized MDRO reporting system exists. Therefore, understanding the sensitivity of ICD-9-CM codes for various MDROs will inform policy decisions regarding hospital rankings and reimbursements and determine the limitations of ICD-9-CM codes for studying MDRO infections from large retrospective administrative databases. Our goal was to determine the correlation between microbiologically confirmed MDRO infection in sterile sites or bronchial wash/bronchoalveolar lavage (BAL) cultures and ICD-9-CM coding for various MDROs.

This study was conducted at Barnes-Jewish Hospital, a 1,250-bed academic medical center in St Louis, Missouri. The study period was January 1, 2006, to October 1, 2015. Hospitalized patients with a positive sterile site or BAL/bronchial wash culture for any of the following MDROs were identified from the hospital clinical data repository and assessed for eligibility: *Enterobacteriaceae*, *Enterococcus* spp., *Staphylococcus aureus*, *Pseudomonas aeruginosa*, or *Acinetobacter* spp. Antimicrobial susceptibilities were determined in the clinical microbiology laboratory using disc diffusion methodology, and drug resistance was defined according to accepted definitions.[4–6] Sterile sites were defined as bloodstream; pleural, intra-abdominal, pericardial, cerebrospinal, and synovial fluids; bone marrow; and surgical specimens collected from lymph nodes, central nervous system, liver, spleen, kidney, pancreas, ovary, or vascular tissue. This study was approved with a waiver of informed consent by the Washington University School of Medicine Institutional Review Board.

All discharge ICD-9-CM diagnosis codes from the index MDRO hospitalization were utilized. Medical coders can assign an ICD-9-CM code for an organism and add a V09 code if drug resistance is present. V09 codes were used to identify drug resistance for all organisms except methicillin-resistant *S. aureus* (MRSA) after October 1, 2008, when unique MRSA codes were introduced.

The primary end points were the proportion of patients with clinically identified MDROs who had a discharge ICD-9-CM code for the correct organism and the proportion of patients with a discharge ICD-9-CM code for drug resistance. We also examined whether infectious disease (ID) consultation was associated with higher rates of coding for drug resistance.

In total, 4,429 patients met the eligibility criteria. Patients with MDR *S. aureus* that were not MRSA and with polymicrobial MDRO infections were excluded, leaving 4,005 patients for analysis. MRSA patients were analyzed in 2 groups: (1) patients discharged prior to October 1, 2008, and (2) patients discharged after introduction of MRSA-specific ICD-9-CM codes on October 1, 2008. Rates of organism and drug resistance ICD-9-CM coding are shown in Table 1.

Patients with MRSA infections after introduction of the MRSA-specific ICD-9-CM codes had high rates of appropriately coded organism (75.0%) and MDRO status (75.7%). The proportion of MRSA patients with any drug resistance code increased from 33.3% to 75.7% after the introduction of MRSA-specific codes. Among patients surviving ≥48 hours after cultures were drawn, ID consultation was associated with a higher rate of coding for MRSA (519 of 587, 88.4%) than for patients without ID consultation (306 of 474, 64.6%; $P < .001$).

Patients with drug-resistant *P. aeruginosa* had the next highest rate of appropriately coded organism (74.5%) but low rates of drug resistance codes (8.3%). Drug-resistance coding was poor for all non-MRSA pathogens, ranging from

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.

ACKNOWLEDGMENTS

The content is solely the responsibility of the authors and does not necessarily represent the official view of the National Institutes of Health (NIH).

Financial support: This work was supported by the Washington University Institute of Clinical and Translational Sciences (grant no. UL1TR000448) from the National Center for Advancing Translational Sciences (NCATS) of the NIH. Dr Marin Kollef is supported by the Barnes-Jewish Hospital Foundation. Dr. Kwon reports that the research reported in this publication was supported by the Washington University Institute of Clinical and Translational Sciences (grant no. UL1TR000448, sub-award KL2TR000450) from the National Center for Advancing Translational Sciences (NCATS) of the National Institutes of Health (NIH).

Potential conflicts of interest: All authors report no conflicts of interest relevant to this article.

Jason P. Burnham, MD;[1]
Jennie H. Kwon, DO, MSCI;[1]
Hilary M. Babcock, MD, MPH;[1]
Margaret A. Olsen, PhD, MPH;[1]
Marin H. Kollef, MD[2]

Affiliations: 1. Division of Infectious Diseases Washington University School of Medicine, St. Louis, Missouri; 2. Division of Pulmonary and Critical Care Medicine, Washington University School of Medicine, St. Louis, Missouri.

Address correspondence to Jason P. Burnham, MD, Division of Infectious Diseases, Washington University School of Medicine, 4523 Clayton Avenue, Campus Box 8051, St. Louis, MO 63110 (burnham@wustl.edu).

Infect Control Hosp Epidemiol 2017;38:1381–1383
 0899-823X/2017/3811-0023. DOI: 10.1017/ice.2017.192

REFERENCES

1. Olsen MA, Ball KE, Nickel KB, Wallace AE, Fraser VJ. Validation of ICD-9-CM diagnosis codes for surgical site infection and noninfectious wound complications after mastectomy. *Infect Control Hosp Epidemiol* 2017;38:334–339.
2. Bouza C, Lopez-Cuadrado T, Amate-Blanco JM. Use of explicit ICD9-CM codes to identify adult severe sepsis: impacts on epidemiological estimates. *Crit Care (London)* 2016;20:313.
3. Schweizer ML, Eber MR, Laxminarayan R, et al. Validity of ICD-9-CM coding for identifying incident methicillin-resistant *Staphylococcus aureus* (MRSA) infections: Is MRSA infection coded as a chronic disease? *Infect Control Hosp Epidemiol* 2011;32:148–154.
4. Magiorakos AP, Srinivasan A, Carey RB, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect* 2012;18:268–281.
5. Multidrug-resistant organism & *Clostridium difficile* infection (MDRO/CDI) module. 2016. Centers for Disease Control and Prevention website. http://www.cdc.gov/nhsn/PDFs/pscManual/12pscMDRO_CDADcurrent.pdf. Accessed July 19, 2016.
6. Unusual susceptibility profiles alert. Centers for Disease Control and Prevention website. http://www.cdc.gov/nhsn/pdfs/gen-support/usp-alert-current.pdf. Accessed July 19, 2016.
7. Schaefer MK, Ellingson K, Conover C, et al. Evaluation of *International Classification of Diseases, Ninth Revision, Clinical Modification* codes for reporting methicillin-resistant *Staphylococcus aureus* infections at a hospital in Illinois. *Infect Control Hosp Epidemiol* 2010;31:463–468.

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