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

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

[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.

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 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,

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).

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.

ACKNOWLEDGEMENTS

REFERENCE

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. [PubMed: 27974057]

2. Bouza C, Lopez-Cuadrado T, Amate-Blanco JM. Use of explicit ICD9CM 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. [PubMed: 21460469]

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. [PubMed: 21793988]

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. [PubMed: 20353360]

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, V09.70, V09.71, 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.