Risk Adjustment for Healthcare Facility-Onset *C. difficile* and MRSA Bacteremia Laboratory-identified Event Reporting in NHSN

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Background

The Centers for Disease Control and Prevention (CDC) introduced the Multidrug-Resistant Organism and *Clostridium difficile* Infection (MDRO/CDI) Module in the National Healthcare Safety Network (NHSN) in March 2009 to enable reporting of CDI, methicillin-resistant *Staphylococcus aureus* (MRSA), and other MDROs. State reporting mandates beginning in 2009, coupled with reporting incentives that the Centers for Medicare and Medicaid Services (CMS) initiated in 2013, account for rapid uptake of the MDRO/CDI Module by acute care hospitals. Use of data from this Module for prevention, public reporting, and payment purposes places a premium on adherence to methodologically sound surveillance practices, including risk adjustment of proxy infection measures. This report describes the risk modeling that CDC applied to laboratory-identified (LabID) event CDI and MRSA bacteremia data submitted to NHSN, the results of which have been incorporated into the analysis options in the NHSN application.

Methods

This analysis was limited to LabID event CDI and MRSA bacteremia surveillance data reported from facilities as in-plan, overall inpatient facility-wide (FacWideIn) during the 2010-2011 baseline time period. As of July 2, 2012, 893 and 759 facilities reported at least one month of CDI and MRSA bacteremia LabID event data, respectively. LabID events were categorized as community-onset (CO - collected ≤3 days after facility admission), healthcare facility-onset (HO - collected >3 days after facility admission), and for CDI, community-onset healthcare facility-associated (CO-HCFA- a CO event collected from a patient who was discharged from the facility ≤4 weeks earlier). Note that the categorization of onset excluded LabID events collected from patients not admitted to the hospital. Additional details regarding the surveillance protocols for these events have been described elsewhere.[1] Facilities were excluded from all analyses if they were defined as a long term acute care (LTAC) hospital or had reported incomplete data (Table 1).

HO CDI and HO MRSA bacteremia LabID incidence rates (per 10,000 and 1,000 patient days, respectively) were calculated to evaluate potential risk adjustment variables. Potential risk factors for this analysis included data from each facility's most recent annual survey, as well as summary-level factors (e.g., CO prevalence rate). Univariate analyses were performed on each potential risk factor prior to building the multivariate model. During the univariate analysis for both event types, various levels of facility bedsize and medical school affiliation were evaluated for significant association and best fit. For CDI events, the significance of CDI test type as reported on the annual facility survey was also assessed. The distribution of two-year cumulative CO prevalence rates and

the distribution for outliers were reviewed; an outlier was defined as a prevalence rate that was five times the interquartile range above the 75th percentile (IQR5). Facilities that reported outlier prevalence rates were excluded from further analyses. The CO CDI prevalence rates did not include those events that were defined as CO-HCFA.

Due to the observed variability of HO incidence in these data over time, risk modeling was performed at the facility, calendar year quarter level, using negative binomial regression. The likelihood ratio and Akaike information criterion (AIC) statistics were used to determine goodness of fit.

Results

After applying exclusion criteria, 846 and 705 facilities had sufficient data to be included in the baseline analysis for CDI and MRSA bacteremia LabID events, respectively. A large proportion (82%) of facilities reporting CDI LabID event data resided in states with mandate-related reporting of this event type at any time during the baseline period. Likewise, 83% of facilities reporting MRSA bacteremia LabID event data were in states that, by the end of 2011, promoted mandate-related reporting. Additional characteristics of contributing facilities can be found in Table 2.

There were 45,323 HO CDI LabID events reported from 62,262,776 patient days during 5,086 facility-quarters. Four factors were found to be significant in predicting HO CDI LabID event incidence: CDI test type, medical school affiliation, facility bedsize, and CO CDI prevalence rate (Table 3). CDI test type is a hierarchical variable that was split into three categories: nucleic acid amplification test (NAAT), enzyme immunoassay (EIA) for toxin, and all other tests. Medical school affiliation and facility bedsize were also categorized into three different categories. CO CDI prevalence rate was assessed at various levels, although provided the best fit as a continuous variable.

There were 2,885 HO MRSA bacteremia LabID events reported from 44,791,753 patient days during 3,849 facility-quarters. Three factors were found to be significant in predicting HO MRSA bacteremia LabID incidence: medical school affiliation, facility bedsize, and CO MRSA bacteremia prevalence rate (Table 4). Medical school affiliation and facility bedsize provided the best fit as dichotomous variables. CO MRSA bacteremia prevalence rate was significant as a continuous variable.

Discussion

The large number of facilities participating in mandate-related reporting provided a sufficient amount of baseline data with which to risk adjust. The results of the regression modeling will allow CDC and external partners to calculate risk adjusted measurements of these data that are appropriate for public reporting purposes.

Few LTAC hospitals reported either CDI or MRSA bacteremia LabID data during the baseline period, yet the crude incidence rates in these facilities were found to be significantly higher than

all other facilities in this analysis. Therefore, LTAC hospitals were excluded from this risk adjustment and will be re-evaluated as participation increases, in order to determine appropriate risk adjustment for this facility type.

CO-HCFA CDI LabID events, identified upon readmission to the facility, are those in which the facility could have had an impact on prevention of that infection during the patient's previous admission (i.e. prevented the new transmission of *C. difficile* to the patient or avoided unnecessary antibiotic use in the patient). Therefore, it was determined that all CO-HCFA LabID events would be excluded from the CDI prevalence rates and ultimately, excluded from adjusting for a facility's risk of HO CDI LabID incidence.

Univariate analysis of both CDI and MRSA bacteremia CO prevalence rates included the review and determination of outliers. An exclusion criterion based on prevalence rates greater than the IQR5 was invoked in order to remove the potential impact of extreme prevalence rates on the prediction of HO incidence.

Additional factors were considered for inclusion into the model, but were ultimately removed due to limitations in the use of these factors. Specifically, the previous time period's prevalence rate (i.e., "lag prevalence") was factored into each model and assessed for goodness of fit. While this factor was statistically significant, the relevance of this factor was questionable due to lack of consistent, continuous reporting within the baseline data. Risk models that were developed based on seasonal, as opposed to calendar year quarter, were also considered. However, the significance of seasonality was inconclusive due to the variable onset of reporting from the majority of contributing facilities; as a result of mandate-related reporting, many facilities began reporting mid-year within the baseline time period, or within only 6 months of the end of the baseline time period. As reporting for these events increases, these factors will be reconsidered for future risk adjustment.

Facilities reporting FacWideIn CDI and MRSA bacteremia LabID event data to NHSN will be able to obtain standardized infection ratios (SIRs) for each LabID event type from the NHSN application's analysis features. The SIR compares the actual number of HO incident cases with the predicted (expected) number based on the baseline data, adjusting for the significant risk factors, as described. When calculating SIRs for facilities, a quarter will be excluded from the SIR (by way of not calculating the number of expected infections) if any of the exclusion criteria are met for that quarter (Table 1).

For those who do not report these data to NHSN but would like to use these data for comparison, the information must first be collected from your facility in accordance with the surveillance methods described for this module.[1] Refer to the Appendix for examples demonstrating the application of these models.

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Available at: http://www.cdc.gov/nhsn/pdfs/mrsa-cdi/RiskAdjustment-MRSA-CDI.pdf.

Table 1. Exclusion criteria applied prior to risk adjustment of CDI and MRSA bacteremia LabID event data.
Incomplete/missing information on survey regarding facility bedsize, medical school affiliation, and/or CDI test type*
Extreme outlier prevalence rate, defined as a prevalence rate greater than five times the interquartile range above the 75th percentile (IQR5) **
Incomplete/missing denominator data (i.e., patient days, admissions)
Long Term Acute Care Hospitals

**exclusion based on CDI Test Type applied for CDI risk adjustment only.*
***CO CDI prevalence rate IQR5 = 1.78; CO MRSA bacteremia prevalence rate IQR5 = 0.88*

Table 2. Characteristics of facilities contributing to the baseline data, by LabID event type.

CDI		MRSA bacteremia	
Characteristic	**N (%)**	**Characteristic**	**N (%)**
Medical School Affiliation		Medical School Affiliation	
Major teaching	103 (12.2)	Major teaching	81 (11.5)
Graduate teaching	82 (9.7)	All Others	624 (88.5)
Undergraduate/Non-teaching	661 (78.1)		
Facility Bedsize		Facility Bedsize	
>245 beds	273 (32.4)	>400 beds	93 (13.2)
101-245 beds	267 (31.7)	≤ 400 beds	612 (86.8)
≤ 100 beds	302 (35.9)		
CDI Test Type			
NAAT	388 (45.9)		
EIA	399 (47.2)		
All Others	59 (6.9)		
Facility Type		Facility Type	
General Acute Care	799 (94.4)	General Acute Care	667 (94.6)
All others	47 (5.6)	All Others	38 (5.4)
State		State	
California	361 (42.7)	California	360 (51.1)
New York	179 (21.2)	Tennessee	83 (11.8)
Tennessee	84 (9.9)	Illinois	66 (9.4)
Illinois	66 (7.8)	New Jersey	57 (8.1)
All others	156 (18.4)	All others	139 (19.6)

NAAT, nucleic acid amplification test (e.g., PCR, LAMP); *EIA*, enzyme immunoassay for toxin.
Major teaching, facility has a program for medical students and post-graduate medical training; *Graduate teaching*, facility has a program for post-graduate medical training (i.e., residency and/or fellowships); *Undergraduate*, facility has a program for medical students only (formerly referred to as *Limited*).

Table 3. Model to predict healthcare facility-onset (HO) CDI LabID events, NHSN, 2010-2011.

Effect	Parameter Estimate	p-value
Intercept	*-7.8983*	*<0.0001*
CDI Test Type (NAAT vs. non-NAAT/EIA others)	0.3850	<0.0001
CDI Test Type (EIA vs. non-NAAT/EIA others)	0.1606	0.0013
CO Admission prevalence rate (continuous)*	0.3338	<0.0001
Facility Bedsize (>245 vs. ≤100)	0.2164	<0.0001
Facility Bedsize (101-245 vs. ≤ 100)	0.0935	0.0022
Medical School Affiliation (Major teaching vs. Undergraduate/Non-Teaching)	0.1870	<0.0001
Medical School Affiliation (Graduate vs. Undergraduate/Non-Teaching)	0.0918	0.0038

* $\frac{\text{Number of community-onset CDI LabID events}}{\text{Number of admissions to the facility}}$ X 100

Table 4. Model to predict healthcare facility-onset (HO) MRSA bacteremia LabID events, NHSN, 2010-2011.

Effect	Parameter Estimate	p-value
Intercept	*-10.2368*	*<0.0001*
Admission prevalence rate (continuous)*	2.2760	<0.0001
Facility Bedsize (>400 vs. ≤400)	0.3672	<0.0001
Medical School Affiliation (Major teaching vs. all others)	0.3248	<0.0001

* $\frac{\text{Number of community-onset MRSA bacteremia LabID events}}{\text{Number of admissions to the facility}}$ X 100

[1] Centers for Disease Control and Prevention. Multidrug-resistant organism & *Clostridium difficile* Infection (MDRO/CDI) Module. Available from: http://www.cdc.gov/nhsn/PDFs/pscManual/12pscMDRO_CDADcurrent.pdf. Accessed January 24, 2013.

Appendix. Applying the Risk Models for MRSA bacteremia and CDI LabID events

If you would like to calculate a CDI or MRSA bacteremia LabID SIR on your own, here are a couple of examples on how to apply the risk model to calculate the expected number of LabID events. In order to apply each risk model, you must first collect data according to the NHSN protocols and then gather additional information on your facility's risk based on the specific risk factor variables used in the model. The examples shown below use fictitious data.

Example 1: SIR calculation for MRSA bacteremia LabID event

Suppose you are at an acute-care hospital with **450 beds** and a **major medical school affiliation**. You would like to calculate your MRSA bacteremia LabID SIR for the 1st quarter of 2012.

You found that your facility had **23,500 patient days** and **3 healthcare facility-onset (HO) MRSA bacteremia LabID events** in the 1st quarter of 2012.

Next, you must calculate your facility's community-onset (CO) MRSA bacteremia prevalence rate for the time period of interest (1st quarter 2012). The formula used to calculate prevalence rate is shown below:

(# CO MRSA bacteremia LabID events / # facility admissions) x 100

In our example, the facility reported **22 CO MRSA bacteremia LabID events** and had a total of **11,000 admissions** in the 1st quarter of 2012. This resulted in a CO MRSA prevalence rate of **0.20**.
Note: Total number of admissions and CO MRSA bacteremia LabID events (as well as your CO MRSA prevalence rate) can be found by running the MRSA LabID event rate table in NHSN.

Once you know your facility's total number of patient days and CO MRSA prevalence rate (and given that you know your facility's medical school affiliation and bedsize), you are ready to calculate the number of expected HO MRSA bacteremia LabID events using the risk model.

The general negative binomial regression model used in this analysis is presented below:

$$\text{Number of predicted LabID events} = e^{(\beta_0 + \beta_1 X_1 + \beta_2 X_2 + \ldots)} * \text{patient days}$$

After applying parameter estimates and significant variables to the general negative binomial regression model, the MRSA bacteremia risk model is used to calculate the number of expected HO MRSA bacteremia LabID events.

The risk model for MRSA bacteremia is as follows:

Number of predicted (expected) HO MRSA bacteremia LabID events =

exp [-10.2368
+ 0.3672(**bedsize > 400***)
+ 0.3248(**medical school affiliation = major***)
+ 2.2760(**CO MRSA prevalence rate**)**]** x **patient days**

*For these risk factors, if present = 1; if not = 0

Your facility's CO prevalence rate and patient days can be entered directly into the formula shown above. If your facility meets the description for bedsize and medical school affiliation listed in the formula, you essentially would replace these two variable names in parenthesis with a 1. For example, because your facility has 450 beds (bedsize is > 400), we would place a 1 in the parenthesis next to 0.3672, which would multiply this term by 1. If your facility had 400 beds or less, a 0 would be placed in the parenthesis and this term (0.3672) would drop out of the equation. The same logic applies to major medical school affiliation. Our facility in this example would calculate their number of expected infections as follows:

exp [-10.2368
+ 0.3672(**1**)
+ 0.3248(**1**)
+ 2.2760(**0.20**)**]** x **23,500** **= 2.65 expected HO MRSA bacteremia LabID events**

Note: The above formula can be entered into an Excel spreadsheet, shown here:
=(EXP(-10.2368+0.3672(1)+0.3248*(1)+2.276*(0.2)))*23500*

To calculate the MRSA bacteremia LabID SIR, divide the number of observed HO MRSA bacteremia LabID events in the 1st quarter of 2012 by the number expected (2.65). For example, 3 observed HO MRSA bacteremia LabID events/2.65 expected HO MRSA bacteremia LabID events = 1.13.

Example 2: SIR calculation for CDI LabID event

In this example, suppose your facility has **90 beds** and is considered to have an **undergraduate (limited) medical school affiliation**. Your facility has a CO CDI **prevalence rate of 0.19,** had **6,500 CDI patient days** for the time period of interest, and your laboratory uses **NAAT** to detect CDI infections (based on the answer provided on your most recent annual facility survey). Your facility observed 3 HO CDI LabID events during this time period.

The general negative binomial regression model used in this analysis is presented below:

Number of predicted LabID events = $e^{(\beta_0 + \beta_1 X_1 + \beta_2 X_2 + \ldots)}$ * **patient days**

After applying parameter estimates and significant variables to the general negative binomial regression model, the CDI risk model is used to calculate the number of expected HO CDI LabID events.

The risk model for CDI is as follows:

Number of predicted (expected) HO CDI LabID events =

exp [-7.8983
+ 0.3850(**CDI test type = NAAT***)
+ 0.1606(**CDI test type = EIA***)
+ 0.3338(**CO CDI prevalence rate**)
+ 0.2164(**bedsize > 245***)
+ 0.0935(**bedsize = 101-245 beds***)
+ 0.1870(**medical school affiliation = major***)
+ 0.0918(**medical school affiliation = graduate***)**]** x **CDI patient days**

*For these risk factors, if present = 1; if not = 0

Our example facility would calculate the number of expected infections as shown below:

exp [-7.8983
+ 0.3850(**1**)
+ 0.1606(**0**)
+ 0.3338(**0.19**)
+ 0.2164(**0**)
+ 0.0935(**0**)
+ 0.1870(**0**)
+ 0.0918(**0**)**]** x **6,500** **= 3.78 expected HO CDI LabID events**

Note: The above formula can be entered into an Excel spreadsheet, shown here:
=(EXP(-7.8983+0.385*(1)+0.1606*(0)+0.3338*(0.19)+0.2164*(0)+0.0935*(0)+0.187*(0)+0.0918*(0)))*6500

Because the facility had less than 100 beds, both parameters for bedsize in the model were not met, and therefore both parameters were multiplied by 0 and fell out of the equation. This same rule applied for medical school affiliation in this example.

To calculate the CDI LabID SIR, divide the number of observed HO CDI LabID events by the number expected. For example, 3 observed HO CDI LabID events/3.78 expected HO CDI LabID events = 0.79.