

1**TITLE: “Variation in Empiric Coverage Versus Detection of MRSA and *Pseudomonas***
2***aeruginosa* in Hospitalizations for Community-Onset Pneumonia across 128 U.S. VA**
3**Medical Centers.”**

4**AUTHORS:**

5Corresponding Author:

6Barbara E Jones, MD, MSc

7 Division of Pulmonary & Critical Care Medicine. SLC VA Health System and University
8 of Utah

9 Barbara.jones@hsc.utah.edu

10 30N 1900 E 701 Wintrobe

11 Salt Lake City, UT 84132

12 406-581-1930

13Kevin Antoine Brown, PhD. SLC VA Health System.

14Makoto Jones, MD, MSc. Division of Epidemiology and Infectious Disease, Salt Lake City VA
15 Health System and University of Utah.

16Benedikt Huttner, MD, MS. Infection Control Program and Division of Infectious Diseases,
17 Geneva University Hospital, Geneva Switzerland.

18Tom Greene, PhD, Division of Epidemiology, University of Utah.

19Brian C Sauer, PhD. Division of Epidemiology, SLC VA Health System and University of Utah.

20Karl Madaras-Kelly, PharmD, MPH. Boise VA Medical Center and Idaho State University
21 College of Pharmacy, Meridian ID.

22Michael Rubin, MD, PhD. Division of Epidemiology, Salt Lake City VA Health System and
23 University of Utah.

24Matthew Bidwell Goetz, MD. Division of Infectious Disease, Veterans Affairs Greater Los
25 Angeles Healthcare System and David Geffen School of Medicine at UCLA.

26Matthew Samore, MD. Division of Epidemiology, Salt Lake City VA Health System and
27 University of Utah.

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30**ABBREVIATED TITLE:**

31MRSA and *Pseudomonas aeruginosa* in Community-onset Pneumonia.

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35

36ABSTRACT

37

38**Objective:** To examine variation in antibiotic coverage and detection of resistant pathogens in
39community-onset pneumonia.

40**Design:** Cross-sectional.

41**Setting:** 128 VA hospitals.

42**Participants:** Hospitalizations with a principal diagnosis of pneumonia from 2009 through 2010.

43**Methods:** We examined proportions of hospitalizations with empiric antibiotic coverage for
44methicillin-resistant *Staphylococcus aureus* (MRSA) and *Pseudomonas aeruginosa* (PAER) and
45those with initial detection in blood or respiratory cultures, compared lowest- versus highest-
46decile hospitals, and estimated adjusted probabilities (AP) for patient and hospital-level factors
47predicting coverage and detection using hierarchical regression modeling.

48**Results:** Among 38,473 hospitalizations, empiric coverage varied widely across hospitals
49(MRSA: 8.2% versus 42.0%, lowest vs highest; PAER: 13.9% versus 44.4%). Detection also
50varied (MRSA 0.5% versus 3.6%; PAER 0.6% versus 3.7%). While coverage was greatest in
51patients with recent hospitalizations (AP for anti-MRSA 54%, anti-PAER 59%) and long-term
52care (anti-MRSA 60%, anti-PAER 66%), detection was greatest in patients with a previous
53history of a positive culture (MRSA 7.9%, PAER 11.9%) and in hospitals with high prevalence
54of the organism in pneumonia (AP for MRSA 3.9%, PAER 3.2%). Low complexity and rurality
55were strong negative predictors of coverage but not detection.

56**Conclusions:** Hospitals demonstrated widespread variation in both coverage and detection of
57MRSA and PAER, but probability of coverage correlated poorly with probability of detection.
58Factors associated with empiric coverage (healthcare exposure) were different from those
59associated with detection (microbiology history). Providing microbiology data during empiric
60antibiotic decision-making could better align coverage to risk for resistant pathogens and
61promote more judicious use of broad-spectrum antibiotics.

62BACKGROUND

63

64Pneumonia is the leading infectious cause of death in the United States^{1 2} and is the target of
65numerous quality improvement efforts, including the dissemination and implementation of
66practice guidelines^{3 4} and performance measures.⁵ Starting in 2005, the Infectious Disease
67Society of America (IDSA) and American Thoracic Society (ATS) recommended empiric
68coverage for organisms resistant to standard antibiotics, predominantly methicillin-resistant
69*Staphylococcus aureus* (MRSA) and *Pseudomonas aeruginosa* (PAER), for patients with
70community-onset pneumonia but recent healthcare exposure (such as previous hospitalizations,
71residence at nursing facilities, parenteral therapy, wound care, and hemodialysis).^{3 4} The
72substantial increase in the use of broad-spectrum antibiotics for pneumonia that followed^{6 7} has
73raised concerns that this recommendation may have encouraged overuse.⁸ Widespread variation
74in antibiotic prescribing for pneumonia has been reported,^{7 9} as has a wide range in prevalence of
75resistant organisms.^{10 11 12} It is unclear whether variation in antimicrobial coverage is related to
76variation in pathogen detection. The aims of our study were to examine variation in 1) detection
77of MRSA and PAER in initial cultures and 2) empiric antibiotic coverage for MRSA and PAER
78among patients hospitalized for community-onset pneumonia, and to identify patient and hospital
79factors driving variation.

80

81METHODS

82

83Study Population

84The study used data from all VA Medical Centers (VAMCs) with ≥ 10 acute care beds and
85complete electronic medication records. We included hospitalizations between January 1, 2006
86through December 31, 2010, of patients ≥ 18 years old at acute medical, surgical, or neurological
87wards and intensive care units with a principal *International Classification of Disease, 9th*

88Revision (ICD-9) code consistent with pneumonia (481-486), similar to other studies.^{13 14} Data

89were accessed using Veterans Informatics, and Computing Infrastructure (VINCI).¹⁵

90

91*Patient and hospital factors*

92We assessed 4 patient-level risk factors: age, history of a positive culture from any body site for

93MRSA or PAER in the past 2 years, the number of days a patient spent in a VA hospital in the

94previous 90 days according to previous definitions of hospital exposure and rounded to whole

95weeks (<2, 2-14, or ≥ 15 days), and the number of days a patient spent in a long-term care

96facility in the previous 90 days rounded to months (zero, 1-28, or ≥29 days). We assessed 4

97hospital-level risk factors: historical prevalence of MRSA and PAER-positive respiratory or

98blood cultures in previous pneumonia cases (based on a 3-year retrospective window using data

99from 2006-2008), rural or urban status, region (Northeast, South, Midwest, or West), and hospital

100complexity score (a 5-point ordinal scale that incorporates levels of hospital services, patient

101volume, intensive care and surgical services, patient risk, and resident or research involvement).¹⁶

102To adjust for regression to the mean, the observed prevalence was shrunken towards the grand-

103mean of MRSA and PAER using a hierarchical logistic model with random intercepts

104corresponding to each facility.¹⁷

105

106*Detection and coverage*

107We accessed microbiology data on cultures drawn during each hospitalization, standardized into

108Systemized Nomenclature of Medicine format.¹⁸ Since we were interested in identifying cultures

109that were clinically relevant to pneumonia and were present upon hospital admission rather than

110acquired during a hospitalization, we defined a positive culture as the detection of MRSA and

111PAER from blood or respiratory sources (sputum, endotracheal aspirate, bronchiolar lavage,

112wash, biopsy, or pleural fluid) obtained during the first 2 calendar days of the hospitalization.

113Antibiotic coverage was measured using bar code medication administration, which records all
114medications administered to patients hospitalized on acute care wards.¹⁹ To identify antibiotic use
115prior to culture results, we identified the systemic administration of at least one dose within the
116first 2 calendar days of hospitalization. We identified antibiotics with activity against MRSA
117pneumonia (vancomycin and linezolid) and specific activity against PAER (piperacillin-
118tazobactam, ticarcillin-clavulanate, ceftazidime, cefepime, meropenem, doripenem, imipenem,
119aztreonam and aminoglycosides).

120To examine variation in thresholds of treatment with broad-spectrum agents, we measured
121coverage-to-culture ratios for MRSA and PAER, defined as the ratio of the proportion of patients
122administered anti-MRSA or anti-PAER coverage to the proportion of patients with MRSA or
123PAER. We calculated coverage-to-culture ratios for the entire 2009-2010 population, each
124hospital, and for quantiles of each patient-and facility-level risk factor.

125

126*Statistical Analysis*

127Because the facility-level prevalence variable required 3 years of prior data, we conducted all
128analyses on hospitalizations from 2009 and 2010 only. We compared rates of detection and
129coverage for the lowest (p10) versus the highest (p90) deciles by calculating inter-decile relative
130ratios (IDRs). We examined relationships between all factors and each of the 4 outcomes
131(detection and coverage, for MRSA and PAER) using bivariate and multivariable hierarchical
132logistic regression models with facility-level random intercepts. Individual and facility-level
133MRSA culture histories were used in models of MRSA detection and coverage, while PAER
134histories were used in models of PAER detection and coverage. For bivariate models, each
135patient-level and facility-level predictor was entered separately. For multivariable models,
136adjusted probabilities (APs) were estimated using logistic regression models by calculating
137marginal probabilities.²⁰ Inverse variance weighted linear regression on proportions was used to
138plot the graphs in Figure 1. Hospital-level cluster bootstrapping was used to calculate

139confidence intervals.²¹ All statistical analyses were performed using R (<http://cran.r-project.org>).
140The study was approved by the University of Utah Institutional Review Board and Salt Lake
141City VA Human Research Protection Program.

142

143RESULTS

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145We identified 95,511 hospitalizations for pneumonia at 128 facilities, of which 38,473 occurred
146during 2009-2010. Among those hospitalizations, 2.1% had positive cultures for MRSA and
1472.1% had positive cultures for PAER. Detection of positive cultures for MRSA varied across
148hospitals (Figure 1), ranging from 0.5% among the lowest decile (p10) to 3.6% among the
149highest decile (p90), for an IDR 95% confidence interval (IDRCI) of 6.1-16.1-fold. Detection of
150PAER also varied (Figure 1), ranging from 0.6% (p10) to 3.7% (p90) with an IDRCI of 4.1-10.0-
151fold.

152Anti-MRSA coverage was included in the initial treatment regimen for 30.2% hospitalizations
153while anti-pseudomonal coverage was used for 34.3%. Coverage varied significantly across
154hospitals (Figure 1) for both anti-MRSA (p10=8.2%, p90=42.0%, IDRCI=5.1 3.9-6.4) and anti-
155pseudomonal coverage (p10=13.9%, p90=44.4%, IDRCI=2.5-4.0).

156The overall coverage:culture ratio, or the number of hospitalizations receiving coverage per
157hospitalization with a positive culture, was 14.4 for MRSA and 16.3 for PAER. We found
158substantial hospital-level variation in coverage:culture ratios, which was greater for MRSA
159(p10=4.7, p90=51.4, IDRCI=7.0-21.8) than for PAER (p10=7.5, p90=39.5, IDRCI=4.1-8.7).

160Patient-level factors were predictive of detection (Tables 1, 2 and Figures 1 & 2; bivariate
161models in Appendix). The strongest predictor of MRSA and PAER was a history of a positive
162culture (AP=7.9% versus 1.6% for MRSA; 11.9% versus 1.4% for PAER). This factor was
163substantially more predictive than acute care stay of >14 days in the past 90 days and long-term
164care exposure of greater than 28 days (Tables 1 & 2).

165 Patient-level factors were also predictive of coverage, but in different ways (Tables 1, 2, Figures
166 1 & 2). In contrast to detection, the individual factors that were predictive of coverage were long-
167 term care exposure in the past 90 days for both MRSA (59.4% versus 28.8%) and PAER (65.8%
168 versus 31.7%), recent history of hospitalization in the past 90 days, and to a lesser degree,
169 individual positive culture history (Tables 1 and 2). As individual risk of detection increased,
170 actual detection increased proportionately (Figure 2, A & B); however coverage increased to a
171 disproportionately high degree for the lower deciles of risk, and not to the same degree for the
172 highest decile of risk. (Figure 2, C and D)

173 Hospital factors were also predictive of both detection and coverage in different ways (Tables 1,
174 2). Prevalence of MRSA and PAER was associated with detection, but not treatment decisions.
175 Hospitals with the highest group of prevalence demonstrated higher detection for MRSA (Tables
176 1: 4.7% versus 1.6%) and to a smaller degree PAER (Table 2: 2.7% versus 1.7%), but they
177 demonstrated no significant increase in coverage. Similarly, hospital-level predicted risk of
178 detection was associated with detection but not coverage (Figure 1). Hospitalizations at rural and
179 low complexity facilities had low probability of coverage for both MRSA and PAER, despite
180 detection rates that were similar to urban or high-complexity hospitals. As a result of this
181 mismatch between prevalence of resistance and prescribing, facilities with the highest MRSA
182 and PAER prevalence had lower coverage-to-culture ratios than facilities with low prevalence
183 (Table 1 and 2).

184

185 DISCUSSION

186

187 We compared variation in antibiotic coverage to variation in MRSA and *P. aeruginosa* detection
188 among patients admitted to VA hospitals with a principal diagnosis of pneumonia. The factors
189 most predictive of detection were the patient's microbiological history and the hospital's past
190 prevalence of these organisms among pneumonia cases. In their choice of antibiotics, we found

191that clinicians overestimated the importance of prior nursing home or hospital exposure,
192underestimated the significance of individual microbiologic history, and neglected population
193prevalence of MRSA and *Pseudomonas*. Our analysis, which included detailed electronic health
194record data from 128 acute inpatient facilities, significantly extends the findings of previously
195published studies and points the way toward using tailored patient and population data to
196improve clinical decision-making.

197Our findings suggest that incorporating microbiology data into the empiric antibiotic selection
198decision could improve patient care and curb inappropriate use of broad-spectrum antibiotics.
199The two most common risk factors from the previous “healthcare-associated pneumonia”
200(HCAP) criteria – previous exposure to acute care and long-term care facilities – were only
201weakly associated with MRSA and PAER detection, a finding that is consistent with other
202studies,^{22 23} some of which also found patient history of colonization or infection to be a more
203important factor.^{24 25} We found data tailored to a specific organism to be far more informative
204than generic exposure to nosocomial pathogens through healthcare exposure. We found
205differences between MRSA and PAER: population prevalence demonstrated a stronger
206correlation with risk of MRSA infection than risk of PAER infection, while individual
207microbiological history was a comparatively stronger predictor of PAER infection than of MRSA
208infection. These findings are consistent with the hypothesis that exposure to organisms due to
209person-to-person transmission is a more important risk factor for MRSA infection,²⁶ while *P.*
210*aeruginosa* may depend more upon host susceptibility.^{27 28}

211Incorporating microbiology information into decision-making for pneumonia will require greater
212recognition and availability of this data as well as guidance in its interpretation. Some – but not
213all – of the newly proposed predictive models intended to replace HCAP incorporate MRSA
214colonization or infection histories;^{29 30} only one includes history of gram-negative organism
215infection as an important factor.³¹ Although the use of local prevalence and susceptibility data
216was recommended to enhance antibiotic decision-making for community-acquired pneumonia³

217and has been recently emphasized by the IDSA updated guidelines for hospital-acquired
218pneumonia,³² no clear guidance has been provided on how to access or interpret this information,
219and few clinicians are aware of local prevalence. Because of the varied performance of the newer
220prediction models, experts have called for healthcare systems to examine the microbiology of
221their own populations rather than rely upon data from other sites to determine appropriate
222treatment thresholds.^{33 34} However, none of the currently proposed risk prediction models uses
223local prevalence, and most clinicians lack this information about their settings. Standardized,³⁵
224setting-³⁶ and population-specific³⁷ antibiograms may improve use. Providing clinicians with
225patient- and setting-specific microbiology information at the point of care is well within the
226capabilities of an electronic health record and is an important step to helping clinicians better
227align their antimicrobial coverage decisions with actual risk.

228Our metric, the coverage-to-culture ratio, helped us to identify differences in antibiotic decision-
229making across hospitals and patient groups, and could be useful for both research and policy to
230examine variation or track the impact of interventions. Differences in coverage-to-culture ratio
231reflect differences in either estimated risk of organisms or the threshold of risk at which
232providers decide to cover those organisms. We found substantially lower coverage-to-culture
233ratios in lower-complexity, rural hospitals compared to higher-complexity, urban hospitals.
234Whether this reflects differences in uptake of guidelines, concern for resistant organisms, or
235patient illness severity or complexity, and whether it represents overtreatment by urban providers
236or under-treatment by rural providers, requires further study. We did not examine the relationship
237between coverage and clinical outcomes, so the question remains: at which threshold of risk for
238resistant pneumonia *should* clinicians administer broad-spectrum antibiotics, and which factors
239should change this threshold? Future study is warranted to address this question.

240Our study has limitations. We identified our population retrospectively using principal diagnosis
241codes that did not include clinical data such as radiographic findings or symptoms. Incomplete
242culturing practices and imperfect performance of microbiologic tests may have underestimated

243the true prevalence of MRSA and PAER or contributed to some of the variation observed;
244additionally, since no gold standard exists for the diagnosis of pneumonia, misdiagnosed patients
245with positive cultures could represent colonization rather than infection. We did not examine
246MRSA surveillance swab data, a potentially useful factor for decision-making in MRSA
247pneumonia,³⁸ as the data were incomplete during the study period. As the intent of our study was
248to compare coverage to detection rather than to provide a comprehensive model for clinical use,
249we did not examine all of the previously proposed predictors of resistant organisms or empiric
250coverage, including antibiotic use, non-VA care history of hemodialysis, outpatient parenteral
251therapy, or antibiotic use.^{11 10 30} Our study also did not address the reasons why MRSA and
252Pseudomonas prevalence were heterogeneous across facilities. Further investigation is needed to
253identify the drivers of inter-hospital differences in prevalence, which may include variation in
254antibiotic selection pressure or environmental factors. Evaluating models that incorporate all
255relevant factors is the subject of future work. However, our examination of accurate, granular
256clinical microbiology and coverage data from a national system revealed a larger number of
257positive cases across more settings than other studies, which increased our ability to measure
258variation and relationships between factors and independent pathogens.

259The discordance between the factors associated with detection and those associated with
260coverage represents an important opportunity to improve practice. The substantial variation in
261antibiotic decision-making that we observed has implications for guideline recommendations,
262clinical prediction models, and antibiotic stewardship efforts. As we continue to develop ways to
263improve pneumonia care in the future, exploring the mechanisms of this variation and
264determining optimal risk thresholds at which to treat with broad-spectrum antibiotics will be
265crucial.

266

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277Table 1. Predictors of MRSA detection and coverage.

278Multivariable model is shown using 38,473 hospitalizations at 128 hospitals during the years
2792009-2010. Bivariate models are available in the Appendix.

	Adjusted Probability of Detection (%)	Adjusted Probability of Coverage(%)	Coverage:Culture Ratio
Patient-level factors			
Age			
Less than 60	2.16 (1.84-2.51)	31.02 (30.05-32.08)	14.37 (12.35-16.92)
60 to 69	1.97 (1.71, 2.22)	31.44 (30.63-32.23)	15.93 (14.12-18.34)
70 to 79	1.84 (1.55-2.12)	29.35 (28.43-30.32)	15.95 (13.88-18.96)
80 or more	2.22 (1.95-2.51)	29.01 (28.28-29.79)	13.05 (11.61-14.88)
History of MRSA-positive Cultures			
No	1.56 (1.44-1.69)	29.39 (28.92-29.86)	18.25 (16.17-20.79)
Yes	7.91 (6.87-9.12)	42.17 (40.13-44.08)	5.33 (4.65-6.17)
Acute Care Exposures in last 90 days			
0-1 days	1.62 (1.46-1.78)	22.53 (22.01-23.01)	13.93 (12.66-15.47)
2 to 14 days	2.59 (2.28-2.94)	47.33 (46.37-48.40)	18.25 (16.17-20.79)
15 or more days	3.78 (3.05-4.49)	54.09 (52.07-55.94)	14.32 (12.06-17.78)
Long-term care Exposures in last 90 days			
None	2.00 (1.55-2.96)	28.80 (28.35-29.28)	14.44 (13.41-15.70)
1 to 28 days	2.20 (1.55-2.96)	43.49 (40.37-48.40)	19.74 (14.60-28.65)
29 or more days	2.85 (2.13-3.62)	59.40 (56.74-61.90)	20.83 (16.43-27.75)
Facility-level factors			
Rural			
No (105 facilities)	2.10 (1.94-2.27)	30.87 (30.38-31.36)	14.69 (13.60-15.90)
Yes (23 facilities)	1.68 (1.26-2.05)	23.40 (21.58-25.18)	13.91 (11.37-18.65)
Census Regions			
Northeast (25 facilities)	2.05 (1.72-2.45)	30.43 (29.26-31.68)	14.69 (13.60-15.90)
Midwest (36 facilities)	2.00 (1.68-2.20)	30.24 (29.26-31.68)	13.91 (11.37-18.65)
South (40 facilities)	1.98 (1.74-2.24)	30.17 (29.30-31.04)	15.08 (13.66-18.07)
West (27 facilities)	2.27 (1.90-2.75)	29.91 (28.51-31.30)	13.17 (10.92-15.59)
Complexity Score			
1a (38 facilities)	2.06 (1.88-2.35)	34.66 (33.93-35.55)	16.83 (14.74-18.49)
1b (16 facilities)	2.15 (1.80-2.66)	34.57 (33.31-36.04)	16.09 (13.03-19.25)
1c (17 facilities)	2.06 (1.63-2.41)	32.04 (30.78-33.16)	15.58 (13.38-19.71)
2 (34 facilities)	1.94 (1.54-2.13)	25.14 (23.97-26.19)	12.92 (11.72-16.36)
3 (23 facilities)	2.08 (1.55-2.76)	10.62 (9.28-11.68)	5.11 (3.78-6.94)
Hospital prevalence of MRSA-positive cultures in pneumonia cases (%)			
0 to 1.4	1.57 (1.49-2.36)	31.35 (29.86-32.98)	19.96 (13.27-21.21)
1.5 to 2.4	1.72 (1.51-1.89)	30.30 (29.43-31.34)	17.62 (16.14-20.13)
2.5 to 3.4	2.29 (1.74-2.47)	30.33 (28.47-31.86)	13.27 (12.16-17.40)
3.5 to 4.4	3.50 (2.71-4.32)	28.37 (25.69-30.96)	8.10 (6.44-10.68)
4.5 or more	4.68 (3.11-5.65)	26.10 (21.71-29.81)	5.57 (4.40-8.29)

280

281Table 2. Predictors of *P. aeruginosa* detection and coverage.

282Multivariable model is shown using 38,473 hospitalizations at 128 hospitals during the years
2832009-2010. Bivariate models are available in the Appendix.

	Adjusted Probability of Detection, % (CI)	Adjusted Probability of Coverage, %(CI)	Coverage:Culture Ratio (CI)
Patient-level factors			
Age			
Less than 60	1.98 (1.65-2.27)	33.01 (32.01-34.09)	16.71 (14.48-19.98)
60 to 69	2.27 (1.99-2.53)	34.21 (33.35-34.99)	15.02 (13.47-17.11)
70 to 79	2.57 (2.25-2.92)	32.66 (31.69-33.66)	12.71 (11.04-14.53)
80 or more	1.60 (1.39-1.85)	32.65 (31.90-33.44)	20.45 (17.71-23.53)
History of <i>PAER</i> -positive Cultures in past 2 years			
No	1.38 (1.26-1.51)	32.27 (31.79-32.76)	23.31 (21.30-25.62)
Yes	11.85 (10.46-13.30)	47.29 (45.29-49.32)	3.99 (3.57-4.53)
Acute Care Exposures in last 90 days			
0-1 days	1.83 (1.64-1.99)	24.88 (24.35-25.39)	13.62 (12.45-15.14)
2 to 14 days	2.48 (2.17-2.78)	52.14 (51.18-53.29)	21.04 (18.79-24.01)
15 or more days	2.72 (2.28-3.35)	59.17 (57.22-61.14)	21.72 (17.63-26.09)
Long-term care Exposures in last 90 days			
None	2.13 (1.99-2.29)	31.69 (31.22-32.17)	14.86 (13.81-15.97)
1 to 28 days	2.17 (1.49-2.93)	47.65 (44.35-50.84)	22.00 (16.14-31.98)
29 or more days	1.40 (0.95-1.94)	65.74 (62.81-68.49)	46.83 (33.89-69.17)
Facility-level factors			
Rural			
No (105 facilities)	2.12 (1.96-2.28)	33.62 (33.13-34.15)	15.87 (14.71-17.14)
Yes (23 facilities)	1.89 (1.46-2.35)	29.55 (27.73-31.49)	15.60 (12.48-20.51)
Census Regions			
Northeast (25 facilities)	2.36 (1.90-2.59)	30.87 (29.62-32.03)	13.10 (11.86-16.05)
Midwest (36 facilities)	1.96 (1.75-2.26)	34.74 (33.76-35.78)	17.73 (15.44-19.94)
South (40 facilities)	1.99 (1.76-2.28)	33.06 (32.12-33.99)	16.63 (14.51-18.71)
West (27 facilities)	2.27 (1.88-2.63)	33.25 (32.01-34.48)	14.62 (12.63-17.74)
Complexity Score			
1a (38 facilities)	2.12 (1.94-2.40)	36.05 (35.29-36.86)	16.98 (15.10-18.67)
1b (16 facilities)	2.03 (1.63-2.42)	37.61 (36.28-39.07)	18.57 (15.53-23.01)
1c (17 facilities)	2.12 (1.94-2.40)	33.79 (32.48-35.04)	15.97 (13.37-19.13)
2 (34 facilities)	2.07 (1.65-2.33)	30.84 (29.71-31.90)	14.93 (13.16-18.48)
3 (23 facilities)	2.04 (1.57-2.57)	18.39 (16.87-19.74)	9.04 (6.98-11.71)
Hospital prevalence of <i>PAER</i> - positive cultures in pneumonia cases (%)			
0 to 1.4	1.71 (1.60-2.32)	33.79 (32.49-35.46)	19.78 (14.52-21.21)
1.5 to 2.4	1.95 (1.57-2.57)	32.95 (32.07-33.77)	16.86 (15.21-18.70)
2.5 to 3.4	2.92 (2.19-3.05)	32.79 (30.88-34.49)	11.24 (10.65-15.07)
3.5 or more	2.70 (0.78-2.88)	36.25 (30.18-41.73)	13.45 (12.06-46.60)

285FIGURE LEGENDS.

286

287Figure 1. Hospital variation in detection and coverage of MRSA and PAER.

288Data are presented using 38,473 hospitalizations that occurred during 2009-2010.

289Predicted risks of MRSA (A, B) and PAER (C, D) were estimated for each hospital from
290the model represented in Table 1. Lines represent best-fit regression lines.

291

292Figure 2. Relationship between individual predicted risk, detection, and coverage. Data are
293presented using 38,473 hospitalizations that occurred during 2009-2010. X-axis represents
294patients categorized by decile of predicted risk of positive cultures for MRSA (A, C) and
295PAER (B, D) estimated from the model represented in Tables 1 & 2. Confidence intervals are
296shown. Y-axis represents percent of those hospitalizations with detection of positive cultures
297(A, B) and antibiotic coverage (C, D).

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