Social and healthcare factors of methicillin-resistant *Staphylococcus aureus* resistance to targeted antibiotics

THESIS

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By

Rachel Ann Tumin

Graduate Program in Public Health

The Ohio State University

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Master's Examination Committee:

Dr. Kurt Stevenson, Advisor

Dr. Sarah Anderson

Dr. Shu-Hua Wang
Abstract

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a significant cause of healthcare- and community-acquired infections. The emergence and spread of MRSA strains resistant to commonly prescribed antibiotics has made successful treatment conditional on having detailed knowledge of the antimicrobial susceptibility profile. Medical factors such as a history of hospitalization or previous MRSA infections affect patients’ risk of developing an MRSA infection. Prior work in social epidemiology suggests that social factors likely influence which patients may contract resistant strains. I develop a theoretical framework in which the type of MRSA strain mediates the effect of individual and community level social factors such as gender, age, race, and residence location on the phenotype of antibiotic resistance. Using data on 798 cases from Ohio hospitals, I perform logistic regression to identify social and medical factors significantly associated with having a resistant MRSA strain (p≤0.05). Patients ages 45-59 years and patients age ≥60 years have increased odds of having a resistant MRSA strain compared to patients younger than 45 years (OR=2.12, 95% CI=1.03-4.39 and OR=3.27, 95% CI=1.64-6.45, respectively). After adjusting for medical risk factors associated with having a resistant strain, patient age ≥ 60 years (OR=2.44 95% CI=1.20-5.00) remains significantly associated with odds of having a resistant MRSA strain. In conclusion, prevention and treatment efforts targeting resistant MRSA strains should focus on populations of older adults and those with medical risk factors.
Acknowledgments

I would like to acknowledge Dr. Kurt Stevenson, Dr. Sarah Anderson, and Dr. Shu-Hua Wang for their support and guidance throughout this project. I would also like to acknowledge Lisa Hines and Yosef Khan for their help with maintaining and accessing the data set.
Vita

2005.........................................................Greely High School

2009..........................................................B.S. Biology, University of Virginia

2009..........................................................B.A. Interdisciplinary Applied Statistics, Biostatistics, University of Virginia

2009 to 2010 ...............................................Graduate Fellow, Department of Epidemiology, The Ohio State University

2010 to present .............................................Graduate Associate, Department of Epidemiology, The Ohio State University

Fields of Study

Major Field: Public Health
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Chapter 1: Introduction

Methicillin-resistant *Staphylococcus aureus* (MRSA) causes over half of all *S. aureus* infections in United States hospitals,\(^1\) and its prominence as a cause of skin and soft tissue infections has increased dramatically over the past decade.\(^2,\)\(^3\) Since many MRSA strains exhibit resistance to additional antibiotics,\(^4\) drug susceptibility testing on isolates identified as MRSA is necessary to ensure patients receive the best antibiotic treatment regime. Receiving an initial antibiotic treatment that is not active against the MRSA infection is associated with increased odds of mortality among patients with complicated skin and soft tissue infections,\(^5\) bacteremia,\(^6\) and sterile-site infections.\(^7\) The average length of stay at the hospital can also be longer\(^8\) and treatment failure is more likely in patients with community-acquired MRSA.\(^9\)

When patients first present with a suspected MRSA infection, the prescribing physician must begin antibiotic treatment without any knowledge of potential drug resistance. On average, four to five days may elapse before the antibiotic susceptibility data are available. Patients with resistant MRSA infections may therefore receive little or no benefit from the initial antibiotic treatment. Thus, identifying patient characteristics linked to these resistant strains could help physicians select an antibiotic that would have the greatest likelihood of successfully treating the MRSA infection before the susceptibility testing results are available. This knowledge of high risk patient
characteristics could also be applied in public health settings to design and implement programs intended to prevent the transmission of resistant MRSA strains.

The patient characteristics most commonly studied have been medical risk factors associated with MRSA infections and social factors associated with contracting MRSA rather than methicillin-susceptible \textit{S. aureus} infections. I add to these findings by identifying social risk factors that predispose patients to contracting resistant MRSA strains. The epidemiological literature indicates some social factors may predict which patients contract particular MRSA strains or the severity of the strains contracted. At the individual level, age\textsuperscript{10-13} and race/ethnicity\textsuperscript{13} are associated with the type or severity of the strain patients contract. At the community level, the incidence rate of MRSA varies by residence location as defined by zip code\textsuperscript{13} and the proportion of MRSA isolates resistant to at least three antibiotics varies by geographic region in the United States.\textsuperscript{14}

These results suggest some patients may be at greater risk for contracting susceptible or resistant strains. Information on the social factors associated with MRSA infections is limited, as infectious disease epidemiology typically studies proximal rather than distal causes of disease.\textsuperscript{15} In the next section, I propose a framework for identifying social factors associated with having a resistant strain.
Social factors at the individual and community level affect the development of many health conditions. Individual factors such as socioeconomic status, age, race, and gender are associated with the development of cancer, mental illness, and chronic disease. These factors can also affect where, when or how often someone is exposed to MRSA. People of different ages tend to engage in different daily activities and these activities may imply different probabilities of exposure to MRSA. Community factors include the effect of neighborhood socioeconomic status on individual health and population prevalence of an infectious disease on an individual's risk of contracting it. Community factors can affect which strain types, and thus which antibiotic resistance profiles, are present in a community.

For example, antibiotic use among some members of a community can reduce the overall prevalence of antibiotic susceptible MRSA strains. With this decrease in the prevalence of susceptible MRSA strains, the proportion of MRSA strains that are resistant to antibiotics must increase. When exposed to an MRSA strain, community members now have a higher probability that the strain they encounter will be resistant to antibiotics. As population density increases, the overall antibiotic burden in the community may increase. This in turn could remove a greater percentage of the susceptible strains from circulation, leaving only the antibiotic resistant MRSA strains in the community. A similar effect has been documented in a hospital, where high levels of
overall penicillin use correlate with an increase in the incidence of MRSA cases, regardless of the patients’ use of penicillin.  

Medical factors mediate the relationship between social factors and the type of strain a person contracts. Medical factors include dialysis, hospitalization, and recent antibiotic use. Patients with these factors tend to contract different MRSA strains than those without medical risk factors, and the strains contracted sometimes have different antibiotic susceptibility patterns. Medical risk factors are also socially patterned: people with certain social characteristics may be at a greater risk for these risks. Yet many MRSA infections occur in patients without any known medical risk factors, suggesting social factors affect strain type through other pathways, too. Thus, I expect the effect of social factors on the strain type contracted to be partially mediated by medical factors.  

Individual and community social factors affect which strain someone contracts and that strain type then determines the antibiotic phenotype, or how susceptible or resistant the infection is to different antibiotics. Three different methods exist for classifying MRSA infections into strain types and each method has a unique classification scheme that assigns isolates to groups. Although similar isolates are grouped together, considerable variation may persist within each of these groups. Thus, not all isolates of one strain type may have the same resistance pattern to antibiotics.  

One potential solution to address this remaining within-group variability could be to use the antibiotic phenotype, instead of the strain type, as the outcome. However, this ignores the proposed mechanism in which social factors affect antibiotic susceptibility
only through their effect on strain type. Additionally, the antibiotic phenotype only indicates if the isolate is resistant to antibiotics. Antibiotic phenotype does not differentiate between isolates from frequently resistant strains and from strains that are typically not resistant. This differentiation is important because treatment and prevention efforts should target those MRSA strains most likely to be resistant to common antibiotics. The most informative approach for this purpose is to examine how social factors affect the probability of having MRSA strains that are commonly resistant to select antibiotics. The most relevant method for classifying MRSA strains is that which best predicts the antibiotic phenotype.

To better understand the transmission of MRSA in Ohio, MRSA cases were collected from the eight member hospitals of the Ohio State Health Network Infection Control Collaborative. In this research, I use data on antibiotic phenotype and genotype of MRSA strains to test which genotyping method best predicts the antibiotic phenotype. I also use patient-level data on social and medical factors to test the hypothesis that social factors predict having a resistant MRSA strain independent of medical risk factors. This approach will allow me to identify social factors that should be considered when initiating antibiotic treatment without direct knowledge of antibiotic susceptibility.
Chapter 3: Methods

Data Source

The data have been collected as part of the Ohio State Health Network (OSHN) Infection Control Collaborative – Understanding Transmission of Methicillin-Resistant Staphylococcus aureus project. MRSA isolates were collected at multiple hospitals throughout Ohio. A sample of all MRSA isolates at The Ohio State University Health System (OSUHS) was collected from January 1, 2007 through June 30, 2010. The isolates from January 1, 2007 to November 1, 2008 consisted of MRSA isolates that had already been collected and frozen. No active sampling of MRSA cases was done during this time period. From November 1, 2008 through June 30, 2010, MRSA isolates were collected twice a week at OSUHS. All of the blood cultures were collected, as were isolates from patients classified as being in the catchment area of the other OSHN member hospitals. The remainder of the allotment comprised a random sample of MRSA isolates. Isolates from all MRSA cases were collected at seven other hospitals in the OSHN: Barnesville Hospital, Madison County Hospital, Wyandot Memorial Hospital, Mary Rutan Hospital, Bucyrus Community Hospital, Mercer Community Hospital, and Twin City Community Hospital. These isolates were collected from March 1, 2009 through June 30, 2010.
Antibiotic Susceptibility Testing

Multiple laboratory facilities performed the antibiotic susceptibility testing, with different hospitals utilizing different labs. The number of antibiotics tested also varied by hospital. This study uses data on isolate susceptibility to the antibiotics clindamycin, tetracycline, and gentamicin, because among cases with complete data on social and medical factors, these antibiotics had a large number of susceptible and resistant cases compared to other antibiotics. Susceptibility testing was performed using one of three methods: broth dilution, disk diffusion, or E-tests. Although different tests were used, all lab facilities reported whether the isolates were susceptible, intermediate, resistant, or indeterminate to each antibiotic. Indeterminate means the antibiotic is not an appropriate treatment option for the type of MRSA infection the patient has.

I exclude isolates categorized as indeterminate on any of the three antibiotics (n = 12 isolates). In the primary analysis, I also exclude isolates categorized as intermediate because it is uncertain if the antibiotic would have resolved the infection (n = 12 isolates). Thus it is unclear whether the isolates should be classified as susceptible or resistant to the antibiotic. I treat susceptibility as a dichotomous variable: resistance to all three antibiotics versus susceptibility to at least one.

Genotyping

I consider three genotyping methods: staphylococcal cassette chromosome mec (SCCmec) typing, pulsed-field gel electrophoresis (PFGE) and repetitive element Polymerase Chain Reaction (rep-PCR). The SCCmec is a portion of the S. aureus genome and contains the mecA gene, which provides resistance to methicillin. There are
currently eight SCC\textit{mec} types.\textsuperscript{27} For PFGE, the bacterial genome is cut into fragments and the DNA fragments are separated out on a gel by size.\textsuperscript{28} The pattern of the DNA bands on the gel are used to classify isolates into nationally defined strain categories. For rep-PCR, only sections of the genome are amplified and the patterns of amplified DNA are used to classify isolates into strain categories. Standard definitions are not currently used for the rep-PCR categories.\textsuperscript{29} Similar strains are grouped together, but categories may not refer to the same strain type across studies.

All isolates were sent to the Ohio State University Medical Center Clinical Microbiology Department, where rep-PCR was performed. Rep-PCR analysis was completed using the DiversiLab Microbial Typing system by Biomeriux Durham, NC. Based upon the rep-PCR type, the DiversiLab library also provides the SCC\textit{mec} type and PFGE type for each isolate. PFGE typing was performed on selected isolates predominantly at the Ohio Department of Health, using published methods.\textsuperscript{30, 31} Some isolates were also sent to the Centers for Disease Control and Prevention for confirmation.

In this analysis, the individual strains from each genotyping method are identified as resistant if half or more of the isolates within each strain type have a resistant phenotype. For example, rep-PCR strain type 6 has three isolates that are susceptible to the antibiotics and thirty-three that are resistant. This means 91.67\% of the isolates in strain type 6 have a resistant phenotype, and this rep-PCR strain is therefore classified as resistant. Strain types where less than 50\% of the isolates have a resistant antibiotic phenotype are classified as susceptible. I use this classification system to generate a
binary variable for each of the three genotyping methods by which strains are classified as susceptible or resistant.

Social and Medical Factors

The social and medical factor variables are derived from chart reviews of the patients with MRSA infections. The individual level social factor variables include: age, gender, race (American Indian or Alaska native, Asian, African American, Native Hawaiian or Other Pacific Islander, White), and social history (history of injection drug use, tobacco use, incarceration). Age, recorded in years, is treated as a categorical variable with three categories: ≤44, 45-59 and ≥60. These cut points are the approximate tertiles of the age distribution. I treat race as a binary variable in the analysis, classifying patients as white or non-white. I use the collective count of the social history variables to create a binary variable for social history, comparing patients who have at least one social history measure to those who have none. The frequency of patients with a history of injection drug use or incarceration is too low to consider these variables separately.

I use zip code data to create a measure of community-level social factors. I use version 2.0 of the Rural-Urban Commuting Area Codes \(^{32}\) to generate a measure of population density that classifies residence location as urban or not urban. My definition of urban is consistent with the RUCA code definition of urban in Categorization C.\(^ {33}\) Since the data on social factors come from chart reviews, they do not include some measures of social factors commonly found in survey data, such as individual socioeconomic status.
The medical factor variables are defined as having any of the following in the 12 months preceding the MRSA infection: an invasive medical device, previous MRSA colonization or infection, surgery, hospitalization, dialysis, or residence in a long-term care facility. I create a separate variable for each of the six medical factors, classifying patients as having or not having each of the medical factors.

Data Analysis

I analyze the data using SAS version 9.2 (SAS Institute Inc, Cary, NC) and use only the isolates with complete data on all of the described variables. For each social and medical factor I compare the percent of isolates that are classified as having a susceptible or resistant antibiotic phenotype using a two-tailed $\chi^2$ test. I fit three logistic regression models predicting the odds of having an isolate with a resistant antibiotic phenotype as a function of each genotyping method. I determine which measure of genotype best fits the antibiotic phenotype data by comparing the odds ratio and log likelihood from each model.

I use the data on strain resistance from the best genotyping method as the dependent variable, and regress strain resistance on the social factors. I first consider each social factor individually, and then add variables to the model using an alpha of 0.05 as the cut-point for variable inclusion. Finally, I determine which medical factors predict strain resistance, using the same model building process. I then add those medical factors to the model that already contains the social factors to examine if they mediate the effect of social factors on the odds of having a resistant genotype. The medical factors mediate
this relationship if the odds ratio for the social factors decreases or if social factors are no longer significant predictors of having a resistant genotype (p-value > 0.05).
Chapter 4: Results

This analysis considers 798 isolates, collected from OSUHS and six of the seven outreach hospitals. The sample is predominantly white and two-thirds of patients are 45 or older (Table 1). The minority race group consists primarily of African Americans. Approximately half of the patients are male, have at least one social history measure, or live in an urban environment. Sixty-three percent of patients have at least one of the six medical factors. Among the six factors, previous hospitalization is the most common and dialysis is the least common (Table 2). The antibiotic phenotype classification of resistance yields 68 resistant cases. Using the phenotypic data, one PFGE strain (Portuguese), one SCCmec type (III) and five rep-PCR types (6, 19, 53, 78, and 97) are classified as resistant. Within each strain type, the percentage of isolates with a resistant phenotype ranges from 92-100%. Each genotyping method has 67 resistant cases.
Table 1. Distribution of social factors in full sample and by PFGE strain resistance.

<table>
<thead>
<tr>
<th>Social Factor</th>
<th>% Total</th>
<th>% Susceptible</th>
<th>% Resistant</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Individual Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>55.64</td>
<td>55.13</td>
<td>61.19</td>
<td>0.34</td>
</tr>
<tr>
<td>Race</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>White</td>
<td>79.57</td>
<td>79.21</td>
<td>83.58</td>
<td>0.40</td>
</tr>
<tr>
<td>Age (years)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0-44</td>
<td>35.34</td>
<td>36.94</td>
<td>17.91</td>
<td>0.002</td>
</tr>
<tr>
<td>45-59</td>
<td>31.95</td>
<td>31.87</td>
<td>32.84</td>
<td>0.87</td>
</tr>
<tr>
<td>60 and older</td>
<td>32.71</td>
<td>31.19</td>
<td>49.25</td>
<td>0.003</td>
</tr>
<tr>
<td>Social History ≥ 1 of 3 measures</td>
<td>47.87</td>
<td>48.02</td>
<td>46.27</td>
<td>0.78</td>
</tr>
<tr>
<td><strong>Community Level</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Residence</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Urban</td>
<td>51.88</td>
<td>51.30</td>
<td>58.21</td>
<td>0.28</td>
</tr>
<tr>
<td><strong>Total Number of Cases (N)</strong></td>
<td>798</td>
<td>731</td>
<td>67</td>
<td></td>
</tr>
</tbody>
</table>

Table 2. Distribution of medical factors in full sample and by PFGE strain resistance.

<table>
<thead>
<tr>
<th>Medical Factor</th>
<th>% Total</th>
<th>% Susceptible</th>
<th>% Resistant</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Presence of an invasive device</td>
<td>29.07</td>
<td>27.22</td>
<td>49.25</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Previous MRSA colonization or infection</td>
<td>16.79</td>
<td>15.18</td>
<td>34.33</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Surgery</td>
<td>26.57</td>
<td>24.29</td>
<td>49.25</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Hospitalization</td>
<td>45.49</td>
<td>42.68</td>
<td>76.12</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Dialysis</td>
<td>8.77</td>
<td>8.07</td>
<td>16.42</td>
<td>0.02</td>
</tr>
<tr>
<td>Residence in long-term care facility</td>
<td>19.42</td>
<td>18.19</td>
<td>32.84</td>
<td>0.004</td>
</tr>
<tr>
<td><strong>Total Number of Cases (N)</strong></td>
<td>798</td>
<td>731</td>
<td>67</td>
<td></td>
</tr>
</tbody>
</table>
I first determine which of the genotyping methods best predicts having a resistant antibiotic phenotype. I predict the odds of having an isolate resistant to antibiotics as a function of whether the strain is classified as resistant. I do this for each of the three genotyping methods. All three genotyping methods fit the phenotypic data equally well. Each method generates the same estimate of the natural log of the odds ratio (7.7347) and the log likelihood (-45.0595). I select PFGE as the genotyping method for the remaining analysis because it is a common method for typing MRSA isolates and the strain types are nationally defined. Tables 1 and 2 stratify social and medical factors by resistant PFGE strain. Younger patients are less likely to have a resistant strain. Older patients and those with medical factors are more likely to have a resistant strain.

Age is the only social factor significantly associated with the odds of having a resistant PFGE strain (Table 3, Model 1). The odds of having a resistant strain among patients 60 years and older are 3.27 times those of patients younger than 45 years. Out of the six medical factors, hospitalization and previous MRSA infection or colonization are significantly associated with the odds of having a resistant PFGE strain (Table 3, Model 2). After adjusting for previous MRSA infection or colonization, hospitalization within the preceding twelve months is associated with approximately four times the odds of having a resistant strain, compared to patients who were not hospitalized. Previous MRSA infection or colonization is associated with more than twice the odds of having a resistant strain, compared to patients who do not have this risk factor and after adjusting for hospitalization.
Table 3. Social and medical factors significantly associated with odds of having a resistant PFGE strain. Odds ratio estimate (OR), 95% confidence intervals (95% CI).

<table>
<thead>
<tr>
<th>Social Factor</th>
<th>Model 1</th>
<th>Model 2</th>
<th>Model 3</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>OR</td>
<td>95% CI</td>
<td>p-value</td>
</tr>
<tr>
<td>Age (years)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>45-59</td>
<td>2.12</td>
<td>(1.03, 4.39)</td>
<td>0.04</td>
</tr>
<tr>
<td>60 and older</td>
<td>3.27</td>
<td>(1.64, 6.45)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Medical Factor</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hospitalization</td>
<td>3.79</td>
<td>(2.10, 6.83)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Previous MRSA in</td>
<td>2.25</td>
<td>(1.29, 3.94)</td>
<td>0.004</td>
</tr>
<tr>
<td>or colonization</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

In the model that contains both social and medical factors (Table 3, Model 3), the social factor age remains significantly associated with the odds of having a resistant PFGE strain ($\chi^2 (2)$, p=0.040), after adjusting for the two medical factors. Patients age 60 years and older now have about 2.5 times the odds of having a resistant strain compared to patients younger than 45 years, after adjusting for the other variables. Both medical factors remain significantly associated with the odds of having a resistant PFGE strain.
Chapter 5: Discussion

The increasing prevalence of resistant MRSA infections has made the successful treatment of infections more complicated. I identify social factors associated with having a resistant MRSA strain that can be used to inform treatment and prevention efforts. In this study, the three genotyping methods are similarly associated with the resistant phenotype. I find the individual factor patient age is associated with odds of having a resistant PFGE strain, after adjusting for the medical factors of hospitalization and previous MRSA infection or colonization.

No one genotyping method is better than the others in this population. I anticipated rep-PCR would be the best genotyping method because it has the largest number of strain types and thus should create better separation of resistant and susceptible infections than the other two methods. The limited number of resistant cases may have hampered efforts to tease out the differences in the association between resistant phenotype and the resistant strains from each genotyping method. This comparability among genotyping methods may also change depending on the antibiotics considered when defining the phenotypic resistance. This study only considers resistance to clindamycin, tetracycline, and gentamicin, and using other antibiotics to define resistance may alter which strains from each genotyping method are classified as resistant.
One benefit of the strong association between phenotypic resistance and genotyped strains classified as resistant is that strain type could probably be used as an additional tool to identify patients who likely have resistant infections before susceptibility testing has been completed. This link is only beneficial if the genotyping can be completed well before the susceptibility data are available. Although PFGE is the gold standard for typing *S. aureus*, it is time consuming, labor intensive, and results take two or three days.\textsuperscript{34} Rep-PCR instead requires significantly less resources and provides results in less than 24 hours. The adoption of a universal rep-PCR strain classification system could allow rep-PCR typing to serve as an indicator of antibiotic resistance after a patient presents with an infection but before the susceptibility data are available.

Strain typing as a proxy for antibiotic resistance would only benefit those who already have an MRSA infection and cannot directly improve efforts to prevent resistant MRSA infections. Identifying the social factors associated with having a resistant strain, independent of healthcare-associated risk factors, could improve both patient care and infection prevention. Age is the only social factor that is significantly associated with having a resistant PFGE strain, both before and after adjusting for medical factors. This finding is consistent with findings from other studies. In Northeastern Ohio, the MRSA infections with resistant antibiotic profiles were more common in older populations,\textsuperscript{10} and at the University of Chicago Hospitals, community-associated MRSA (CA-MRSA) isolates collected from adults were more likely to be resistant to three or more antibiotics than pediatric isolates.\textsuperscript{12} Naimi et al. do not explicitly test if younger patient age is associated with more susceptible MRSA infections in their Minnesota-based study.\textsuperscript{35}
However, they find that patients with CA-MRSA are younger than those with healthcare-associated MRSA (HA-MRSA) and CA-MRSA infections are more susceptible to antibiotics than HA-MRSA infections.

In this study, older patients have higher odds of having a resistant strain compared to the youngest patient group. This older patient group likely engages in activities that pose a greater risk of involving exposure to resistant MRSA strains. One possibility is that these older individuals are more likely to have friends or family members in the hospital or a long-term care facility and are thus more likely to visit these places. The older individuals are therefore exposed to settings that may harbor resistant infections, but these individuals do not personally have medical risk factors.

Other studies demonstrate the importance of considering community-level variables. However, in this study the community measure of living in an urban environment as classified by zip code is not a significant predictor of having a resistant strain. Other community-level measures may still be significant in this population. Determining the proper definition and measure of community is a common challenge in research that studies community effects. Liu et al. group cases in San Francisco by zip code and find the zip codes with high MRSA incidence rates also have areas of low median family income or a population of men who have sex with men. The authors propose these community characteristics reflect an increased presence of common MRSA transmission mechanisms or exposures in these areas. Defining community level variables differently could uncover a similar association between geographic location and resistant strains in this study population of Ohio residents.
Finally, both previous hospitalization and previous MRSA infection or colonization are strongly associated with the odds of having a resistant strain, after adjusting for patient age. This significant association is not surprising given these variables are known risk factors for MRSA infections. As all six medical risk factors have a significantly higher prevalence among those with a resistant MRSA strain, all six should be considered when evaluating patients. The magnitude of the odds ratio estimates for hospitalization and previous MRSA infection compared to those for age highlights that the individuals at greatest risk are those who have medical risk factors. Prevention efforts targeting persons with these established medical risk factors may be most appropriate in areas with limited resources.

These results may have limited generalizability to other populations given the nature of the sample. This study only includes MRSA cases identified in a hospital setting. Patients who present with MRSA infections at physicians’ private offices or at clinics are not captured here. The cases collected from the OSUHS are not a random sample of the MRSA cases at the health system. Although the outreach hospitals aimed to collect all cases, the sometimes high rate of missing information on key variables resulted in some hospitals having only a few cases eligible for inclusion in this analysis. However, I do not expect the association between social and healthcare factors and the odds of having a resistant strain to drastically differ across populations. I expect healthcare-associated factors will still exhibit a strong association with the odds of having a resistant strain, but the specific social or healthcare factors in the model may vary from population to population.
Future research could actively collect the independent variable information and should consider other individual and community level measures. This study draws all of the information about the independent variables from chart reviews. The absence of information in patients’ charts regarding behaviors such as smoking or recent healthcare exposures does not guarantee the patient does not have any of those factors. Some patients are therefore likely misclassified as not having social predictors of MRSA when in fact they do. A more active data collection process in which the patient is asked to verify the information or provides all of the information at the time of the MRSA diagnosis might reduce the amount of missing information and reduce misclassification.

Active data collection would also allow researchers to collect patient information not routinely found in patient charts, such as annual income or level of education. Other studies find measures of household income are significantly lower among those with CA-MRSA infections, compared to individuals with HA-MRSA or community-associated MSSA. Similarly, individuals with CA-MRSA may have lower levels of educational attainment. Information concerning community level factors not associated with zip code could also be collected.

In conclusion, this study supports considering age and medical factors when selecting an initial antibiotic treatment for MRSA patients or designing programs to reduce the incidence of resistant MRSA infections in a community. As MRSA strains become increasingly resistant to the available antibiotics, understanding who is at an increased risk for contracting these potentially deadly strains will be very important.
Additional research with other populations or on other social factors can help tailor these efforts to improve population health.
References


