High-Density Livestock Operations, Crop Field Application of Manure, and Risk of Community-Associated Methicillin-Resistant *Staphylococcus aureus* Infection in Pennsylvania

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**IMPORTANCE** Nearly 80% of antibiotics in the United States are sold for use in livestock feeds. The manure produced by these animals contains antibiotic-resistant bacteria, resistance genes, and antibiotics and is subsequently applied to crop fields, where it may put community members at risk for antibiotic-resistant infections.

**OBJECTIVE** To assess the association between individual exposure to swine and dairy/veal industrial agriculture and risk of methicillin-resistant *Staphylococcus aureus* (MRSA) infection.

**DESIGN, SETTING, AND PARTICIPANTS** A population-based, nested case-control study of primary care patients from a single health care system in Pennsylvania from 2005 to 2010. Incident MRSA cases were identified using electronic health records, classified as community-associated MRSA or health care–associated MRSA, and frequency matched to randomly selected controls and patients with skin and soft-tissue infection. Nutrient management plans were used to create 2 exposure variables: seasonal crop field manure application and number of livestock animals at the operation. In a sub study, we collected 200 isolates from patients stratified by location of diagnosis and proximity to livestock operations.

**MAIN OUTCOMES AND MEASURES** Community-associated MRSA, health care–associated MRSA, and skin and soft-tissue infection status (with no history of MRSA) compared with controls.

**RESULTS** From a total population of 446,480 patients, 1,539 community-associated MRSA, 1,335 health care–associated MRSA, 2,895 skin and soft-tissue infection cases, and 2,914 controls were included. After adjustment for MRSA risk factors, the highest quartile of swine crop field exposure was significantly associated with community-associated MRSA, health care–associated MRSA, and skin and soft-tissue infection case status (adjusted odds ratios, 1.38 [95% CI, 1.13-1.69], 1.30 [95% CI, 1.05-1.61], and 1.37 [95% CI, 1.18-1.60], respectively); and there was a trend of increasing odds across quartiles for each outcome (P < .01 for trend in all comparisons). There were similar but weaker associations of swine operations with community-associated MRSA and skin and soft-tissue infection. Molecular testing of 200 isolates identified 31 unique spa types, none of which corresponded to CC398 (clonal complex 398), but some have been previously found in swine.

**CONCLUSIONS AND RELEVANCE** Proximity to swine manure application to crop fields and livestock operations each was associated with MRSA and skin and soft-tissue infection. These findings contribute to the growing concern about the potential public health impacts of high-density livestock production.

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Manure From Antibiotic-Treated Livestock and MRSA

ORIGINAL INVESTIGATION RESEARCH

Manure From Antibiotic-Treated Livestock and MRSA

The US Food and Drug Administration reports that 80% of antibiotics in the United States are used in food animals, mainly to promote growth of livestock in high-density production. In this industrial model, thousands of livestock animals are housed together and fed subtherapeutic doses of antimicrobial agents. This can select for antibiotic-resistant bacteria like methicillin-resistant Staphylococcus aureus (MRSA). About 75% of administered antibiotics are not absorbed by the animal and end up in manure. In addition to antibiotics, antibiotic-resistant bacteria and resistance genes have been isolated from manure and are known to persist in the environment. Application of manure to crop fields close to human dwellings may lead to increased risk of antibiotic-resistant infections.

High prevalence of MRSA colonization among pig farmers was first noted in the Netherlands in 2005. Transmission of MRSA among cows, calves, and humans has also been reported. A US study reported that 45% of workers were colonized, which is 30 times the national average. Few studies have assessed risk of MRSA infection. A Danish case-control study found that living or working on a farm was a risk factor for MRSA infection. Other studies of MRSA infection have described the spread of infection within pig farming families. To our knowledge, the impact of proximity to high-density livestock production on risk of MRSA infection has not been evaluated. Two studies assessed community livestock density and found no association with MRSA colonization. Most studies have implicated clonal complex 398 (CC398) as the most common variant harbored by swine.

In the United States, community-associated MRSA (CA-MRSA) now accounts for more than half of all noninvasive MRSA infections. CA-MRSA often occurs as a skin and soft-tissue infection (SSTI) in young, otherwise healthy individuals who lack common health care risk factors. In contrast, health care–associated MRSA (HA-MRSA) generally occurs in older individuals with comorbidities. Now, the epidemiology and microbiology of 2 epidemics previously considered distinct are merging.

The possible contribution of high-density livestock production to these epidemics has been inadequately studied. US data are needed to evaluate which livestock species pose risk, what aspects of the operations and manure handling are involved, and the magnitude of the risk. We conducted a population-based, nested case-control study using electronic health record (EHR) data from the Geisinger Health System, an integrated health services organization with 4 hospitals and 41 outpatient clinics. We evaluated residential proximity to swine and dairy/veal high-density livestock operations and manure-applied crop fields in relation to CA-MRSA, HA-MRSA, and SSTI (without a history of MRSA infection or colonization) case status.

Methods

Data Sources
To select cases and controls, we used EHR data from January 1, 2005, to February 9, 2010, from 446 480 patients with a Geisinger primary care provider. Geisinger’s primary care patients represent the general population in the region. The study area comprised the health system’s primary care market and bordering counties totaling 38 counties in Pennsylvania (Figure 1); approximately 3.8 million people resided in these counties according to the 2000 US Census. The study was approved by institutional review boards at the Geisinger Health System and the Johns Hopkins Bloomberg School of Public Health.

Pennsylvania Act 38 of 2005 requires high-density livestock operations to develop and implement nutrient management plans (NMPs) for manure handling. We defined high-density livestock operations as agricultural operations where animal density exceeded 2 animal equivalent units (AEUs, 1000 pounds of live weight) per acre and where total AEUs exceeded 8; or operations that exceeded 300 AEUs. When livestock operations have insufficient land for manure application, manure is exported to other areas and applied to crop fields. We focused on swine and dairy/veal operations because of previously identified links with MRSA. The NMPs provided data on livestock operation location, animal type, livestock quantity (AEUs), amount of manure applied to crop fields by season, and crop field area and location. We obtained NMPs from the Pennsylvania Department of Environmental Protection and County Conservation Districts.

Case Ascertainment and Control Selection
Incident MRSA cases were identified primarily using laboratory cultures and secondarily by diagnosis codes (eg, International Classification of Diseases, Ninth Revision [ICD-9]) that indicated MRSA infection, as previously described. Cases were then classified as either CA-MRSA or HA-MRSA based on presence of health care risk factors (eg, hospitalization, surgery, dialysis, nursing home residence, indwelling device) or diagnosis more than 2 days after hospital admission using ICD-9 codes and Current Procedural Terminology codes. We then randomly selected patients with SSTI but no history of MRSA using 29 ICD-9 codes (eg, carbuncle, furuncle, abscess) and controls with no history of MRSA, and we frequency matched both groups with case patients by age (0-6, 7-18, 19-45, 46-62, 62-74, ≥75 years), sex, and diagnosis or an outpatient encounter in the same year as MRSA diagnosis. The SSTI cases were evaluated as a separate case group because some SSTIs occurring during the study period were likely to have been caused by MRSA but not diagnosed as such, and high-density livestock production could cause SSTIs from other bacteria. Therefore, we selected patients with SSTIs without reference to any specific pathogen. If a control had multiple outpatient encounters during the year, a single encounter was randomly selected as the date for exposure assignment.

Geographic Location of Patients, Livestock Operation, and Crop Fields
We identified the latitude and longitude of patient addresses using ArcGIS, version 10 (Esri), and calculated MRSA rates by community (Figure 1). The latitude and lon...
Exposure Assessment

We estimated each individual’s exposure to livestock operations and to manure-applied crop fields, for swine and dairy/veal, using an inverse distance-squared approach\(^34\) in R, version 2.14.2 (R Foundation for Statistical Computing). For livestock operations, we used the equation

\[
\text{Exposure for patient } j = \sum_{i=1}^{n} \frac{a_i}{d_{ij}^2}
\]

where \(n\) is the number of operations, \(a_i\) is AEUs of livestock at operation \(i\), and \(d_{ij}^2\) is the squared distance (in meters) between the operation and the patient. For manure application during the season of diagnosis or visit, we used the equation

\[
\text{Exposure for patient } j = \sum_{i=1}^{n} \frac{c_i}{d_{ij}^2}
\]

where \(n\) is the number of crop fields, \(c_i\) is the concentration of manure (gallons per square meter) applied during the season of diagnosis or visit at field \(i\), and \(d_{ij}^2\) is the squared distance (in meters) between the crop field centroid \(i\) and patient \(j\). This resulted in exposure units of gallons per quartic meter (\(m^4\)). For missing seasonal application data (40% of fields), we used the regional seasonal average. Exposure variables were modeled as quartiles because they were not normally distributed.

Genetic Typing of MRSA Isolates

In a prospective substudy that occurred from January to December 2012, we identified all primary care patients with a culture-confirmed MRSA infection. We then randomly selected isolates from patients stratified by location of diagnosis (in-
patient or outpatient) and presence or absence of a livestock operation or crop field in their zip code of residence. We oversampled outpatient isolates from zip codes with high-density livestock production. All isolates were characterized by DNA sequence analysis of the protein A gene variable repeat region (spa typing). The spa types were also assigned a Ridom StaphType, using the Ridom SpaServer database (available at http://www.spaserver.ridom.de). Panton-Valentine leukocidin (PVL) genes were detected by polymerase chain reaction.

**Statistical Analysis**

To compare the 4 study groups, we used Kruskal-Wallis tests for comparisons of means and χ² tests for comparisons of proportions. We used multilevel multinomial (2 MRSA groups and controls) and multilevel logistic regression (SSTI cases and controls) to assess the association between exposure and case status. We adjusted models for predictors obtained from the EHR: age, sex, race/ethnicity (non-Hispanic white, non-Hispanic black, Hispanic, and other); ever-smoking status using ICD-9 codes; antibiotic order in the 2 years preceding diagnosis; and Medical Assistance for health insurance, residential community (city, borough, or township), and community socioeconomic deprivation. *Medical Assistance* is a means-tested program, which we used as a surrogate indicator for low socioeconomic status. It was identified for each encounter by 1 of 24 codes and modeled as ever received (if received for >2 encounters) vs never received. The livestock operation model was additionally adjusted for season of infection or visit. Final models were selected based on associations reported in our group's earlier article, and adequate model fit was confirmed using Pearson goodness-of-fit tests and likelihood ratio tests. Semivariograms were used to determine that spatial autocorrelation did not account for the results. We used a 2-sided type 1 error rate of 0.05 as the threshold for statistical significance and made no adjustments for multiple comparisons. Logistic and multinomial logistic regression analyses were completed using Stata statistical software version 11.2 (StataCorp Inc) and the GLLAMM program (www.gllamm.org).
We calculated population attributable fraction (PAF) for CA-MRSA and SSTI cases by using the adjusted odds ratios (AORs) for the third and fourth quartile of crop field swine manure exposure obtained from the final multivariable logistic regression model using the formula PAF = (AOR - 1)/AOR × (proportion of cases exposed to risk factor).\(^4\) The PAF for the third and fourth quartiles were summed to calculate the final PAF. Confidence intervals were computed using the delta method with the postestimation command nlcicom in Stata.

We performed several sensitivity analyses. First, we evaluated 2 other time windows for crop field manure exposures: a 1-year and a 30-day window before either the date of MRSA diagnosis or the date of a preceding SSTI diagnosis. Second, models were repeated using different methods to identify crop fields (Figure 2). Third, we evaluated effect modification by community type and season. Fourth, analysis was performed to evaluate whether distance to nearest crop field, independent of manure application, was associated with disease outcomes. Finally, we repeated analyses using only culture-confirmed MRSA cases.

### Results

**Patients, Farms, and Crop Fields Included in the Study**

A total of 1734 CA-MRSA and 1519 HA-MRSA cases were identified between January 2005 and February 2010. Most cases (72.3%) were identified by a positive MRSA culture. We frequency matched 3336 SSTIs and 3336 controls to the cases. Of the 9925 patients, we were able to identify latitude and longitude coordinates for home addresses for 87.5%. Thirty-one percent of patients were excluded because they did not reside in counties for which we collected NMPs. This resulted in a total of 1539 CA-MRSA, 1335 HA-MRSA, and 2895 SSTI cases and 2914 controls with residences in 32 counties and 574 communities defined by minor civil divisions, ie, census-designated divisions of a county.

We collected NMPs and identified the location of 326 high-density livestock operations, 123 swine and 203 dairy/veal operations, in 27 counties and 168 townships. Ninety-eight of the swine operations (79.7%) and 71 of the dairy/veal farms (35.0%) exported at least a portion of their manure to a total of 424 crop fields. Crop fields were located in 29 counties, 8 boroughs, and 218 townships, for an average of 3.4 crop fields per township. A reported 637 266 595 gallons of manure was applied to crop fields annually. Among those in the highest quartiles of swine livestock operation exposure and swine crop field manure exposure, the median (IQR) distance to the nearest farm or field was 4.6 km (3.1-6.7 km) and 4.0 km (2.6-7.5 km), respectively. The Pearson r correlation between the individual-level exposure assignments from the 2 models was 0.59 (both log transformed).

**Demographic Characteristics of Cases and Controls**

There were no differences in demographic characteristics between patients included in the study and those excluded because we could not map their home address (n = 1211), except that patients with SSTIs who were included were significantly more likely to have ever smoked than were those who were excluded (eTable 1 in the Supplement). Compared with controls, patients in the CA-MRSA group were significantly younger; they were more likely to be black, to smoke, and to receive Medical Assistance; and they lived in communities with greater socioeconomic deprivation (Table 1). White race/ethnicity (95.3% of the study population) was associated with higher levels of swine and dairy/veal crop field manure exposure (Table 2). Exposures to manure were also the lowest among those who had not received an antibiotic prescription in the 2 years prior to diagnosis or visit, those who had received Medical Assistance, and those residing in cities.

**Association of Crop Field Manure Exposure With Case Status**

After adjusting for potential confounding variables, we found a significantly increased odds of CA-MRSA, HA-MRSA, and SSTI with higher swine manure exposure (fourth vs first quartile AORs, 1.38 [95% CI, 1.13-1.68], 1.30 [95% CI, 1.05-1.61], and 1.37 [95% CI, 1.18-1.60], respectively; \(P = .01\), \(P < .001\), and \(P < .001\) for trend, respectively) (Table 3). The fourth quartile (vs first quartile) of dairy/veal exposure was also associated with increased odds of CA-MRSA (AOR, 1.24 [95% CI, 1.01-1.52]). The PAFs (95% CI) for the highest 2 quartiles of swine crop field manure exposure for CA-MRSA infection and SSTI were 10.7% (5.0-16.4%) and 11.5% (7.0-16.0%), respectively.

**Association of High-Density Livestock Operations With Case Status**

The fourth quartile vs first quartile of swine livestock operation exposure was associated with increased odds of CA-MRSA and SSTI (AORs, 1.25 [95% CI, 1.09-1.50] and 1.27 [95% CI, 1.08-1.50], respectively; \(P = .04\) and \(P = .002\), respectively) but not HA-MRSA (Table 3). No associations were seen with dairy/veal operations. Receipt of Medical Assistance remained independently associated with MRSA and SSTI outcomes in all adjusted analyses.

**MRSA Isolate Substudy**

A total of 200 isolates were randomly selected from 1128 patients with isolates (Table 4). Of these, 133 (66.5%) were common community strains (spa types t008, t024, t064, t206, t211); 33 (16.5%) were common health care strains (t002, t010, t062, t105); and the remainder were divided among 22 additional types. Notably, none was a spa type associated with CC398. A total of 27 community-onset isolates were PVL-negative.

**Sensitivity Analyses**

Evaluation of the 2 other time windows for manure application revealed slightly attenuated but otherwise similar results, except in the case of annual dairy/veal exposure, where the association strengthened for both CA-MRSA and SSTI cases (fourth vs first quartile AORs, 1.41 [95% CI, 1.13-1.77] and 1.26 [95% CI 1.08-1.48], respectively; \(P = .01\) and \(P = .02\), respectively) (eTable 2 in the Supplement). Exclusion of crop fields without aerial photographs and/or addresses, including interaction terms for community type...
or season, and restricting analysis to culture-confirmed MRSA cases did not alter results. Distance to nearest crop field, independent of manure application, was not associated with MRSA or SSTI.

Discussion

High-density swine production was an independent risk factor for CA-MRSA and HA-MRSA infection and SSTI in patients without a history of MRSA. There was evidence that both a crop field manure application model that incorporated distance, swine manure volume, season of application, and field area, as well as a livestock operation model that incorporated distance and swine count, were each associated with increased risk of infection. Exposure assignments from these 2 models were moderately correlated, suggesting 2 independent sources of risk. Furthermore, while livestock operations are easily identifiable and fixed, manure-applied crop fields are not necessarily easily identifiable, are scattered, and may change from year to year. Associations with dairy/veal operations were less consistent and weaker than those for swine operations, which

Table 1. Patient Demographic and Clinical Characteristics

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Study Participants, No. (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CA-MRSA (n = 1539)</td>
</tr>
<tr>
<td>Male</td>
<td>715 (46.5)</td>
</tr>
<tr>
<td>Age at infection or visit, median (IQR), y</td>
<td>23.5 (10-47)</td>
</tr>
<tr>
<td>Race/ethnicity</td>
<td></td>
</tr>
<tr>
<td>Non-Hispanic white</td>
<td>1446 (94.0)</td>
</tr>
<tr>
<td>Non-Hispanic Black</td>
<td>49 (3.2)</td>
</tr>
<tr>
<td>Hispanic</td>
<td>31 (2.0)</td>
</tr>
<tr>
<td>Other</td>
<td>13 (0.8)</td>
</tr>
<tr>
<td>Smoking</td>
<td></td>
</tr>
<tr>
<td>Never</td>
<td>1288 (83.7)</td>
</tr>
<tr>
<td>Season of onset</td>
<td></td>
</tr>
<tr>
<td>Winter</td>
<td>352 (22.9)</td>
</tr>
<tr>
<td>Spring</td>
<td>269 (17.5)</td>
</tr>
<tr>
<td>Summer</td>
<td>412 (26.8)</td>
</tr>
<tr>
<td>Fall</td>
<td>506 (32.9)</td>
</tr>
<tr>
<td>Any antibiotic prescription in 2 years prior</td>
<td>1125 (73.1)</td>
</tr>
<tr>
<td>Medical assistance</td>
<td></td>
</tr>
<tr>
<td>Never</td>
<td>1056 (68.6)</td>
</tr>
<tr>
<td>City</td>
<td>250 (16.2)</td>
</tr>
<tr>
<td>Borough</td>
<td>550 (35.7)</td>
</tr>
<tr>
<td>Township</td>
<td>739 (48.0)</td>
</tr>
</tbody>
</table>

Abbreviations: CA-MRSA, community-associated methicillin-resistant Staphylococcus aureus; CPT, Current Procedural Terminology; HA-MRSA, health care-associated MRSA; ICD-9, International Classification of Diseases, Ninth Revision; IQR, interquartile range; SSTI, skin and soft-tissue infection.

a Based on 29 ICD-9 codes: 680.0-680.9, 681.00-681.02, 681.9-6811, 682.0-682.9, 035, 684, and 686.9.

b P < .001 vs control.

c Race/ethnicity was missing for 4 HA-MRSA cases and 1 control.

P < .05 vs control.

d Based on presence of ICD-9 codes 305.1 (tobacco use disorder), V15.82 (history of tobacco use), or 649.0 (tobacco use complicating pregnancy) or CPT codes 99406 or 99407 (smoking cessation counseling).

e Spring, March through May; summer, June through August; fall, September through November; and winter, December through February.

f P < .01 vs control.

g Indicates receipt of antibiotic prescription in the 730 to 14 days prior to diagnosis or visit.

h Based on the health insurance carrier for each encounter, identified with 24 separate codes, and “ever” was defined as more than 2 encounters with Medical Assistance.

i Community socioeconomic deprivation was assigned at the township, borough, or census tract level and was based on 6 indicators (all percentages) derived from US Census 2000 data: combined less than high school education, not in the labor force, in poverty, on public assistance, civilian unemployment, and does not own a car; a higher score represents a more deprived community; quartile 1 values, less than −2.22; quartile 2 values −2.23 through 0.46; quartile 3 values, 0.47 through 3.05; and quartile 4 values 3.06 or greater.
was not surprising, given the limited number studies on the topic. Our data also suggest that approximately 11% of CA-MRSA and SSTI cases in the study population could be attributed to crop field application of swine manure.

The association with SSTIs is notable because there were more than 50,000 such cases, compared with 4000 MRSA cases, in the region since 2001. We cannot attribute these infections to any single pathogen. Sub-analysis of 258 SSTI cases (9%) identified from culture data as methicillin-susceptible Staphylococcus aureus (MSSA) revealed an association with swine livestock exposure (AOR, 1.70 [95% CI, 1.15-2.52]) that was stronger than for all SSTIs together. The public health burden of SSTIs warrants future study of links to high-density livestock production. Concerning the association with HA-MRSA, this finding does not imply that livestock-associated strains are in hospitals. Rather, these older patients.
may have been colonized in the community with livestock strains and then had healthcare contact (eg, hospitalization, surgery, dialysis, indwelling device) before infection. To our knowledge, no studies have examined the association between high-density livestock operations and MRSA infection in the community, and only 2 studies have assessed risk of colonization.\textsuperscript{16,17} Study of colonization may not be useful when evaluating the risk of MRSA infection associated with industrial agriculture because, first, environmental exposure or direct contact may more often lead to CA-MRSA infection than does colonization\textsuperscript{43} and second, MRSA colonization may not persist for more than 24 hours after livestock exposure.\textsuperscript{44} Prior studies limited their ability to identify risk from high-density livestock exposure by including only patients with CC398,\textsuperscript{13,45} by studying only people who lived or worked on farms,\textsuperscript{9,12,46-48} and by not including crop field manure exposure.

A unique aspect of this study is the consideration of risk from manure application to crop fields. Sensitivity analyses across time (eg, annual, seasonal, and 30-day exposure) and across space (eg, restricting analysis to fields with aerial photographs or maps) did not substantively change results. Our findings are likely not an artifact of rural residents in the study population.

### Table 3. Association of Seasonal Crop Field Manure Exposure and Livestock Operation Exposure With CA-MRSA, HA-MRSA, and SSTI From Full Multilevel Multivariate Model\textsuperscript{a}

| Characteristic | CA-MRSA | | | HA-MRSA | | | SSTI | | |
|---------------|---------|---------|---------|---------|---------|---------|---------|---------|
|               | Univariate | Adjusted | | Univariate | Adjusted | | Univariate | Adjusted | |
| Seasonal Crop Field Manure Exposure | | | | | | | | |
| Swine\textsuperscript{b} | | | | | | | | |
| Quartile 2 | 1.11 (0.93-1.32) | 1.09 (0.90-1.31) | | 1.15 (0.96-1.38) | 1.21 (0.98-1.48) | | 1.03 (0.89-1.20) | 1.03 (0.88-1.20) | |
| Quartile 3 | 1.12 (0.94-1.33) | 1.26 (1.04-1.52) | | 1.09 (0.90-1.31) | 1.27 (1.03-1.57) | | 1.15 (1.00-1.33) | 1.22 (1.05-1.41) | |
| Quartile 4 | 1.34 (1.13-1.60) | 1.38 (1.13-1.69) | | 1.26 (1.05-1.51) | 1.30 (1.05-1.61) | | 1.34 (1.16-1.55) | 1.37 (1.18-1.60) | |
| P value\textsuperscript{c} | <.001 | .01 | | .04 | <.001 | | <.001 | <.001 | |
| Dairy/veal\textsuperscript{d} | | | | | | | | |
| Quartile 2 | 0.93 (0.78-1.12) | 0.95 (0.78-1.16) | | 0.76 (0.64-0.92) | 0.82 (0.67-1.02) | | 0.90 (0.78-1.04) | 0.90 (0.77-1.05) | |
| Quartile 3 | 0.94 (0.79-1.13) | 0.90 (0.74-1.09) | | 0.94 (0.79-1.12) | 0.92 (0.76-1.13) | | 0.84 (0.72-0.97) | 0.85 (0.73-0.99) | |
| Quartile 4 | 1.25 (1.05-1.48) | 1.24 (1.01-1.52) | | 0.74 (0.62-0.90) | 0.78 (0.62-0.98) | | 1.02 (0.88-1.18) | 1.01 (0.87-1.19) | |
| P value\textsuperscript{c} | .01 | .06 | | .03 | .08 | | .96 | .92 | |
| Livestock Operation Exposure | | | | | | | | |
| Swine\textsuperscript{e} | | | | | | | | |
| Quartile 2 | 0.85 (0.72-1.02) | 0.96 (0.77-1.20) | | 0.78 (0.65-0.94) | 0.96 (0.76-1.21) | | 0.91 (0.79-1.06) | 1.00 (0.85-1.18) | |
| Quartile 3 | 0.91 (0.77-1.09) | 1.05 (0.84-1.32) | | 0.83 (0.69-0.99) | 0.88 (0.70-1.12) | | 0.95 (0.82-1.10) | 1.05 (0.89-1.23) | |
| Quartile 4 | 1.03 (0.87-1.23) | 1.25 (0.99-1.58) | | 1.04 (0.87-1.25) | 1.18 (0.93-1.50) | | 1.19 (1.03-1.38) | 1.27 (1.08-1.50) | |
| P value\textsuperscript{c} | .60 | .04 | | .57 | .19 | | .01 | .002 | |
| Dairy/veal\textsuperscript{f} | | | | | | | | |
| Quartile 2 | 0.80 (0.67-0.95) | 0.90 (0.72-1.12) | | 0.79 (0.66-0.94) | 0.83 (0.66-1.05) | | 1.02 (0.88-1.18) | 1.10 (0.93-1.30) | |
| Quartile 3 | 1.04 (0.88-1.24) | 1.18 (0.94-1.48) | | 0.95 (0.79-1.13) | 1.00 (0.79-1.26) | | 1.07 (0.92-1.24) | 1.17 (0.99-1.39) | |
| Quartile 4 | 0.86 (0.73-1.03) | 1.07 (0.85-1.35) | | 0.62 (0.52-0.75) | 0.80 (0.62-1.02) | | 0.99 (0.87-1.15) | 1.12 (0.95-1.32) | |
| P value\textsuperscript{c} | .51 | <.001 | | .24 | .97 | | .18 | | |

Abbreviations: AEU, animal equivalent unit; CA-MRSA, community-associated methicillin-resistant Staphylococcus aureus; HA-MRSA, health care-associated MRSA; SSTI, skin and soft-tissue infection.

\* For multinomial models, n = 5783, and for binomial model, n = 5808; crop field model adjusted for sex, age, race/ethnicity, ever-smoking status, antibiotic prescription in the prior 2 years, receipt of Medical Assistance, residential minor civil division, and community socioeconomic deprivation; livestock model further adjusted for season of infection or visit.

\* Quartile 1 values, less than 75,494 gal/m\textsuperscript{2}/km\textsuperscript{2}; quartile 2 values, 76,500 through 188,466 gal/m\textsuperscript{2}/km\textsuperscript{2}; quartile 3 values, 188,467 through 390,474 gal/m\textsuperscript{2}/km\textsuperscript{2}; quartile 4 values, 390,475 gal/m\textsuperscript{2}/km\textsuperscript{2} or greater.

\* Quartile 1 values, less than 29,205 gal/m\textsuperscript{2}/km\textsuperscript{2}; quartile 2 values, 29,206 through 60,623 gal/m\textsuperscript{2}/km\textsuperscript{2}; quartile 3 values, 60,624 through 104,717 gal/m\textsuperscript{2}/km\textsuperscript{2}; quartile 4 values, 104,718 gal/m\textsuperscript{2}/km\textsuperscript{2} or greater.

\* Quartile 1 values, less than 6.3 AEU/km\textsuperscript{2}; quartile 2 values, 6.4 through 17.9 AEU/km\textsuperscript{2}; quartile 3 values, 17.9-34.7 AEU/km\textsuperscript{2}; quartile 4 values, 34.8 AEU/km\textsuperscript{2} or greater.

\* Quartile 1 values, less than 7.1 AEU/km\textsuperscript{2}; quartile 2 values, 7.2 through 21.0 AEU/km\textsuperscript{2}; quartile 3 values, 21.1 through 44.9 AEU/km\textsuperscript{2}; quartile 4 values, 44.9 AEU/km\textsuperscript{2} or greater.

\* P value for linear trend (quartiles included as a single variable with values 1, 2, 3, and 4).
Table 4. Summary of MRSA Genetics

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Community (n = 123)*</th>
<th>Healthcare (n = 33)**</th>
<th>Other Types, No. (%) (n = 34)**</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age at infection, median (IQR), y</td>
<td>29 (13-48)</td>
<td>65 (45-77)</td>
<td>46 (14-61)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Location of onset</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Inpatient***</td>
<td>8 (6.0)</td>
<td>20 (60.1)</td>
<td>7 (20.6)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Outpatient****</td>
<td>125 (94.0)</td>
<td>13 (39.9)</td>
<td>27 (79.4)</td>
<td></td>
</tr>
<tr>
<td>Community type</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>City</td>
<td>18 (13.5)</td>
<td>1 (3.0)</td>
<td>5 (14.7)</td>
<td>0.25</td>
</tr>
<tr>
<td>Borough</td>
<td>34 (25.6)</td>
<td>13 (39.4)</td>
<td>12 (35.3)</td>
<td></td>
</tr>
<tr>
<td>Township</td>
<td>81 (60.9)</td>
<td>19 (57.6)</td>
<td>17 (50.0)</td>
<td></td>
</tr>
<tr>
<td>PVL-positive</td>
<td>131 (98.5)</td>
<td>1 (3.0)</td>
<td>17 (50.0)</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Swine operation exposure, fourth quartile†</td>
<td>27 (20.3)</td>
<td>10 (30.3)</td>
<td>13 (38.2)</td>
<td>0.36</td>
</tr>
</tbody>
</table>

Abbreviations: AEU, animal equivalent unit; IQR, interquartile range; MRSA, methicillin-resistant Staphylococcus aureus; PVL, Panton-Valentine leukocidin genes.

* Includes spa types t008 (n = 123), t024 (n = 7), t064, 1206, and t121.
** Includes spa types t002 (n = 27), t105 (n = 3), t010 (n = 2), and t606.
*** Includes spa types t121 (n = 4), novel varieties (n = 3), t088 (n = 3), t622 (n = 3), t045 (n = 2), t068 (n = 2), t012, t125, t126, t304, t306, t316, t437, t539, t681, t692, t6856, t948, t1754, t1761, t6564, t9964, and unknown.
**** Inpatient isolates collected more than 2 days after hospital admission.
† Isolates collected in the outpatient setting or within the first 2 days of hospitalization.
†† Quartile 4 values, 33.4 AEU/km² or greater.

We did not find any spa types associated with clonal complex CC398. Most MRSA found on farms or in farmers has been characterized as CC398, though other types have been identified. However, few studies have assessed MRSA infection, instead focusing on MRSA carriage, and those that do come from Europe14 and/or deal exclusively with CC398. The most common strains on US farms are not well known. In Ohio, the closest state to Pennsylvania for which there are data, common health care strains were most often isolated from swine; CC398 was secondary.53 We were limited in that genetic data did not come from the same time period as the main study, and isolate strains could have changed over time.

We used ICD-9 codes to classify MRSA cases as CA or HA and to derive the predictor variables used in the analysis. The primary HA epidemiologic factors are well captured by the EHR. Ever-smoking status can also be effectively obtained using ICD-9 codes.51 Unfortunately, the EHR did not directly capture data on individual-level socioeconomic status or occupation, so our results could have been due to these variables. To evaluate this potential confounding, we adjusted the final models for 2 surrogates for socioeconomic status: Medical Assistance at the individual level and community socioeconomic deprivation at the community level. As expected, patients with CA-MRSA were more likely to receive Medical Assistance and more likely to live in more deprived communities than controls, associations that persisted in the adjusted models.62,63 Previous literature has suggested increased prevalence of MRSA colonization in livestock workers. However, given the low prevalence of this employment (1% of population in any agricultural work, according to US Census data) even in towns and rural areas, it seems unlikely that farming occupation could account for the reported associations. Moreover, inclusion of community-level percentage of agri-
cultural workers in the multilevel model did not change associations.

In conclusion, proximity to and size of high-density livestock production were associated MRSA infection and SSTI, and the population-attributable fraction of crop field manure application exceeded 10% for CA-MRSA and SSTI. The findings contribute to the growing concern about the potential public health impacts of high-density livestock production.

REFERENCES


28. Tattevin P, Schwartz BS, Graber CJ, et al. Concurrent epidemics of skin and soft tissue...


