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Prospective multicenter surveillance identifies *Staphylococcus aureus* infections caused by livestock-associated strains in an agricultural state

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Abstract

We conducted a surveillance study to investigate the epidemiology of *Staphylococcus aureus* infections in Iowa, using a convenience sample. Diagnostic laboratories submitted 20 *S. aureus* isolates per month for a 20-month period between 2011 and 2013. Of the 2226 isolates analyzed, 73.6% were methicillin-resistant *S. aureus* (MRSA) and 26.4% were methicillin-susceptible *S. aureus* (MSSA). *S. aureus* infections in 25 patients (1%) were caused by ST398- and ST9-associated strain types, and appeared to be a common occurrence in areas of the state with the highest numbers of hogs and hog farms. Twenty nine (5.1%) of MSSA isolates and 10 (40.0%) livestock-associated strains were multi-drug resistant.

Keywords

Staphylococcus aureus; Surveillance; Infection; Methicillin resistant; Methicillin susceptible; Livestock

1. Introduction

Staphylococcus aureus (*S. aureus*) is a common commensal and highly adaptable organism of humans and animals that causes a wide range of infections, from superficial skin and soft tissue infections (SSTIs) to life-threatening invasive diseases (Fitzgerald, 2012). In the 1990s, new strains of community-associated (CA-) methicillin-resistant *S. aureus* (MRSA) were identified as a cause of infections among previously healthy people and were

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occasionally fatal (David and Daum, 2010; Herold et al., 1998). A 6-month nationwide surveillance study conducted in 2011 observed a predominance of the USA300/t008 strain type as a healthcare associated pathogen in all tested regions and infection sites, particularly wounds and skin infections (Diekema et al., 2014). Although invasive CA-MRSA infections are tracked by the Centers for Disease Control and Prevention's Active Bacterial Core Surveillance, a great majority of CA-MRSA infections are not invasive such as SSTIs and would not be captured by the surveillance program (Dukic et al., 2013; Klevens et al., 2007). A recent meta-analysis of studies conducted in the US noted an increase in CA-MRSA infections between 1990 and 2012 and, speculate that these infections could be endemic and at unprecedented levels in many regions (Dukic et al., 2013). However, this meta-analysis was modeled largely on studies from urban populations and may not accurately reflect the trajectory of CA- infections in a rural region.

More recently, a novel *S. aureus* sequence type (ST) 398 was reported to colonize livestock. Human carriage and infection caused by ST398 were first reported in Europe (Fitzgerald, 2012; Smith and Pearson, 2011). It was suggested that these *S. aureus* strain types associated with livestock production were responsible for the increase in incidence of CA-MRSA since the MRSA strains were isolated from farmers and their livestock (Harrison et al., 2013; Hasman et al., 2010). Swine are observed to be the most common reservoir for the ST398; however, it has also been found to colonize other livestock. Typical human strains belonging to ST5, ST8, ST22, ST97, and ST1 have also been isolated from livestock (Fitzgerald, 2012; Hasman et al., 2010; Osadebe et al., 2013). Severe infections due to ST398 strains have emerged globally (Monaco et al., 2013; Verkade and Kluytmans, 2013). Increased rates of colonization with livestock-associated (LA-) MRSA in areas with high density of livestock such as the Netherlands and Germany, could potentially lead to increased transmission and infection by these strains (Kock et al., 2013; Wulf et al., 2012). A population-based study conducted in Iowa observed that swine farmers are at an increased risk of colonization with not only *S. aureus* but also livestock strains with varying antibiotic resistance, such as multidrug-resistant *S. aureus* and tetracycline resistant strains (Wardyn et al., 2015). In addition, studies conducted in USA and Europe have identified ST398 as an increasing cause of disease among people with potentially no livestock contact (Larsen et al., 2015; Mediavilla et al., 2012; Uhlemann et al., 2013).

Little is known regarding the epidemiology of *S. aureus* infections in Iowa—a rural population with exposure to hospitals, nursing homes, and livestock, all of which are implicated in *S. aureus* acquisition. The aim of our surveillance study is to characterize pathogenic *S. aureus* strains, and determine the prevalence of resistance to tested antibiotics. We included both methicillin-susceptible *S. aureus* (MSSA) and MRSA strains to be able to capture a regional perspective on *S. aureus* evolution. We anticipated ST398 infections in our population, as there is evidence of circulation of these strains in Iowa (Leedom Larson et al., 2010; O'Brien et al., 2012; Wardyn et al., 2015).

2. Materials and methods

A prospective, multi-laboratory *S. aureus* infection surveillance study was conducted between June 1, 2011 and February 28, 2013. A waiver of consent was obtained from The

University of Iowa Human Subjects Office (HSO) since isolates were obtained for surveillance and personal identifiers were not collected.

2.1. Participating laboratories

The Iowa State Hygienic Laboratory (SHL), Coralville coordinated recruitment of laboratories that participated in a MRSA statewide surveillance system, as reported in a previous study (Van De Griend et al., 2009). Of these, 13 diagnostic laboratories serving 23 hospitals in and around Iowa volunteered participation in our study. One laboratory did not submit any isolates during the study period. Eleven laboratories were hospital-affiliated and one was an independent laboratory, affiliated with healthcare centers in Iowa and Illinois. As per the 2012 US Census data and report available from the Iowa Hospital Association, we estimate that the participating laboratories cumulatively served roughly one-third of Iowa's population (Table A.1).

2.2. Surveillance data and *S. aureus* isolate collection

All isolates were de-identified and assigned study-defined identifiers. A short data collection form was developed to obtain patient information not designated as Personal Health Information. Data was obtained on exposures such as hospitalization including admission to an intensive care unit (ICU), antimicrobial exposure, dialysis, occupational exposure to healthcare-settings, and correctional facility in the past one year. Data on patients past and/or current comorbidities, presence of indwelling catheter and/or other medical devices, type of infection and source of the isolate was also acquired. The Infection Control Preventionist for each participating lab filled the data collection form using information available with isolates; patient medical records were not accessed for data collection.

Laboratories were asked to submit twenty clinically significant MRSA and/or MSSA infection isolates (only 1 isolate per patient) per month, collected at any time in a month (Table A.2). Laboratories were instructed not to send isolates representing colonization. Isolates from nasal, throat or oral swabs, and nasopharyngeal aspirate or drainage were presumed to be colonizers and excluded from final analysis (n=29). Isolates were classified as invasive *S. aureus* infections based on previously published and validated definitions (Klevens et al., 2007). We developed this protocol for feasibility of the study but anticipate the potential for selection bias due to the convenience sampling methodology.

2.3. Molecular analysis

All *S. aureus* isolates were cultured and re-confirmed to be *S. aureus* at the Center for Emerging Infectious Diseases (CEID), as described previously (O'Brien et al., 2012). Presence of methicillin-resistance (*mecA*) and Panton-Valentine leukocidin (PVL) genes, and determination of *spa* type was performed using published methods and primers (Bosgelmez-Tinaz et al., 2006; Lina et al., 1999; Shopsin et al., 1999). Isolates were classified as MRSA or MSSA based on presence of the *mecA* gene. The Based-Up on Repeat Pattern (BURP) analysis to identify *spa* cluster complexes (*spaCC*) was conducted using the Ridom StaphType software using default parameters (version 2.2.1; Ridom GmbH, Würzburg, Germany) (Mellmann et al., 2008). Positive and negative controls were used in all molecular assays.

2.4. Antimicrobial susceptibility testing

The antibiogram for *S. aureus* isolates were obtained from corresponding diagnostic laboratories tested in accordance with the Clinical Laboratory Standards Institute (CLSI) standards (Clinical Laboratory and Standards Institute, 2012). Multidrug resistance (MDR) was defined as isolates determined to be MRSA or observed to be resistant to at least three discrete non beta-lactam antimicrobial classes (Magiorakos et al., 2012). Antimicrobial susceptibility percentages were analyzed for individual antibiotics using antibiogram classification of isolates as resistant or susceptible as determined by laboratories. Isolates with intermediate or inducible resistance were analyzed as a separate category.

2.5. Data analysis

Analyses were performed using the SAS software (Version 9.3, SAS Institute Inc., Cary, NC). Prevalence of *S. aureus* infections during the study period was calculated using the 2012 mid-year population for Iowa. The chi-square test for equal proportions or Fisher's exact test was used to analyze categorical variables. *P* values ≤ 0.05 were considered statistically significant.

2.6. Spatial analysis

Lab locations were geocoded and isolates were mapped according to the submitting lab in ArcMap10.3 (ESRI, Redlands, CA). Isolates were assigned to the three-digit leading prefix of the home address ZIP code in order to understand how the lab samples are representative of Iowa *S. aureus* isolates. The locations and numbers of swine animal units (swine AU) in concentrated animal feeding operations (CAFOs) were accessed from the Iowa Department of Natural Resources (DNR) and the number of swine AU per square kilometer in each three-digit ZIP code was calculated. Animal Units (AU) are a measure developed by the Iowa DNR to compare manure production across species and ages of animals. One fully grown hog equals 0.4 AU, immature hogs are smaller portions of AU.

3. Results

Of the 2226 *S. aureus* infection isolates analyzed, 73.6% were MRSA and 26.4% were MSSA by *mecA* presence. Interestingly, 1.1% ($n = 25$) of the isolates were noted to be *spa* types with previously known livestock association (Ballhausen et al., 2014; Cuny et al., 2013; David et al., 2013; Hasman et al., 2010; Kock et al., 2013; Normanno et al., 2015; Silva et al., 2014). Patient characteristics were significantly different by hospitalization at the time of infection culture, prior antibiotic use, prior surgery, and exposure to long-term care facility between MRSA, MSSA, and LA infections (Table 1). Population demographics in participating three-digit ZIP code areas were noted to be homogeneous in the proportion of people over 65 years of age and white race. Four ZIP codes (503, 507, 524, 528) had less than 10% population residing in rural areas and majority ZIP code areas had greater than 10% households in poverty (Table A.1).

Nine confirmed *S. aureus* isolates were identified as "non-typable" after at least two attempts to sequence the *spa* gene. These isolates were typed as ST15 ($n = 6$) and one each of ST25, ST683, and ST97 by MLST. Three hundred distinct *spa* types were identified, of

which 194 *spa* types were among MSSA isolates. Most infections were caused by *spa* types t008 (n = 837, 37.6%) and t002 (n = 509, 22.9%). Of the ST398-associated *spa* types, t034 (n = 11, 44%) and t571 (n = 5, 20%) were observed to be the major cause of LA infections among Iowans. Other *spa* types observed to cause infections were t337 (ST9-associated, n = 3, 12%) and one infection episode each caused by ST398 associated *spa* types t011, t3446, t5883, and t7880 (Table 2). These isolates were from both MRSA (n=3, 12%) and MSSA (n=22, 88%) infections. The LA strains were most commonly isolated from SSTI in our sample set, particularly *spa* type t034. None of the LA *spa* types were positive for the PVL genes. Fifty-three percent of MRSA isolates and 13% of MSSA isolates were positive for the PVL genes.

Table 3 summarizes the susceptibility testing results for commonly tested antibiotics (>80% isolates) in MRSA and MSSA.

Clindamycin resistance was inducible in 181 (11%) of the 1026 MRSA isolates tested using the D-test. Low resistance prevalence to the following antibiotics was noted among MRSA isolates: rifampin (0.4%), linezolid (0.1%), and nitrofurantoin (0.1%). Inducible clindamycin resistance was tested in 58.5% MSSA isolates; of these, 70 (12.4%) demonstrated the phenotype. A small proportion of MSSA isolates were resistant to TMP/SMX (0.4%) and rifampin (0.2%). Twenty nine (5.1%) of the MSSA isolates were observed to be MDR. Of the 25 LA isolates, 10 (40.0%) were MDR based on presence of the *mecA* genotype and phenotypic antibiotic susceptibility. All *S. aureus* isolates were susceptible to vancomycin, daptomycin, quinupristin-dalfopristin, and tigecycline in this surveillance study.

The state of Iowa has twenty six three-digit ZIP code area. The northwestern and central portions of the state have the highest swine AU density per square kilometer in these three-digit ZIP code areas (Fig. 1A). The 12 participating laboratories are widely distributed across the state of Iowa, and sent samples from twenty two of the three-digit ZIP code prefixes of the state (Fig. 1B). Some samples lacked this three-digit ZIP prefix (n = 124) or had a prefix from a state other than Iowa (n = 49) and are not included in panel B.

While t002, t008, and associated *spa* types are the most common types in all labs, LA *spa* types were found only in the three labs in the far northwest corner of the state and the two furthest to the southeast (Fig. 1, Panel A; Table A.2). The northwest portion of the state has the highest number of swine farms and highest swine AU density in the state.

4. Discussion

The current surveillance study evaluated *S. aureus* isolates in Iowa, a state with a significant rural population. During our two-year surveillance period, the prevalence of MRSA and MSSA infections was observed to be 73.6% and 26.4% respectively. In addition, 75% of the *S. aureus* strains isolated during the study period were MDR, including MRSA. *S. aureus* strain types previously isolated from pigs, cattle, and poultry, including MDR strains were identified to be associated with clinical infections among humans. The physician's decision to culture a patient indicates that these infections are either perceived to be severe or did not respond to prior antibiotic treatment. Our study adds important data on such *S. aureus*

infections in a rural area of the US. While infectious disease epidemiologists contend that infection due to CA-MRSA is on the decline, our study results suggest that this could be due to replacement of CA-MRSA by other strains such as LA *S. aureus*.

A similar surveillance study conducted in Iowa between 1999 and 2006 did not identify infections due to confirmed LA strains (Van De Griend et al., 2009). This study did not include any SSTI (the main origin of ST398 in our study) and included only invasive MRSA isolates. LA strains have been primarily known to cause SSTIs that could potentially be undiagnosed or under-diagnosed, depending on the severity of the infection (Verkade and Kluytmans, 2013). A previous study by our group to examine MRSA infections in pigs and pork producers observed that 3.7% of the participants self-reported being previously diagnosed with a MRSA SSTI (Leedom Larson et al., 2010). However, this was a cross-sectional study and we did not have access to the study specimens in order to confirm livestock association of the strain types. A prospective study conducted in Italy to investigate the prevalence of LA-MRSA colonization and proportion of infections in an area with dense livestock farming identified one infection episode (1/20, 5%) due to ST398 (Monaco et al., 2013). This study investigated and characterized only MRSA isolates and may have overlooked LA-MSSA infections. The current surveillance study broadened our scope of identifying the proportion of LA-SA infections in Iowa by providing access to a wide range of MSSA and MRSA infection samples.

A population-based prospective cohort study conducted by our study group reported an incidence rate of 2.7 infections per 1000 person-months (95%CI 1.8–3.9) for *S. aureus* SSTIs among individuals with livestock contact over a period of 17 months in Iowa (Osadebe et al., 2013). LA *S. aureus* infections are generally SSTIs and often MSSA, hence there is potential for missed diagnosis or under-diagnosis and increased risk for transmission. In addition, there is a possibility of other strains such as t002 arising in livestock production (Casey et al., 2014; Frana et al., 2013; Molla et al., 2012). Findings from our study suggest that LA strains are responsible for infections in Iowa, possibly due to concentration, duration of exposure, and residential proximity to livestock among the population (Bhat et al., 2009; Carrel et al., 2014; Casey et al., 2013; Mediavilla et al., 2012; Schinasi et al., 2014; Uhlemann et al., 2013). The low rates of ST398/ST9 infections in the overall study could potentially be due to low transmission potential (Verkade et al., 2014; Wassenberg et al., 2011) in the presence of other competing *S. aureus* strains such as t002/ST5 and t008/ST8, or to the hypothesized decreased virulence of these strains (van Cleef et al., 2013), making them less likely to cause symptomatic infections even in those colonized with LA *S. aureus*.

Our study had several limitations. A major limitation is not having access to detailed patient risk exposures, such as occupation, environment, and exposure to pets or livestock that would be important to consider when evaluating LA infections. Residential proximity to livestock is also observed to be a risk factor for colonization (Feingold et al., 2012), suggesting other potential reservoirs or mechanisms of transmission such as the environment. However, our study was unable to do a detailed spatial analysis due to lack of exact home address or ZIP code level data. Our study included a convenience sample of *S. aureus* isolates. In addition, some labs submitted only MRSA isolates, possibly due to

hospital infection reporting policies. Hence, results from this surveillance study have limited generalizability to other populations in Iowa or the US. We conducted *S. aureus* molecular characterization based on *spa* typing. While this could have potentially resulted in misclassification of infection isolates, previous studies have shown that *spa* typing reliably correlates with other, more expensive methods, including MLST (Strommenger et al., 2006). We did not have complete information on antibiotic susceptibility due to differences in antibiotic panels tested in the regional laboratories. In addition, classification of MRSA and MSSA was based on the *mecA* genotype due to missing data on ceftazidime susceptibility. This could have resulted in misclassification of isolates, as observed by the 4.3% oxacillin-resistant MSSA isolates. Despite limitations, conducting *S. aureus* surveillance at a local level is relatively more feasible and, provides better understanding of the distribution of *S. aureus* strains and antibiotic susceptibility.

5. Conclusions

In conclusion, surveillance in Iowa observed regional distribution of *S. aureus* (MRSA and MSSA) strain types. We identified multidrug resistance among 75% of *S. aureus* infection isolates. LA-SA strains, both MRSA and MSSA, were responsible for non-invasive and invasive infections in Iowa. These findings reinforce the importance of including direct or indirect livestock exposure as a potential risk factor when assessing patients with confirmed *S. aureus* infections.

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Appendix

Table A.1.

ZIP Code Areas	Total Population	Percent 65+	Percent White	Percent Rural	Total Households	Percent HH in Poverty
500	226135	0.12	0.946	0.29	88403	0.132
501	176553	0.15	0.952	0.46	68541	0.099
502	214923	0.14	0.951	0.38	84964	0.085
503	284484	0.11	0.843	0.01	113955	0.126
504	104558	0.19	0.972	0.53	45541	0.111
505	124100	0.19	0.944	0.48	51972	0.122
506	172119	0.17	0.974	0.57	67608	0.112
507	77857	0.14	0.826	0.07	32539	0.154
510	88325	0.18	0.972	0.68	35554	0.078

ZIP Code Areas	Total Population	Percent 65+	Percent White	Percent Rural	Total Households	Percent HH in Poverty
512	43946	0.15	0.971	0.61	16465	0.095
513	47413	0.21	0.979	0.41	21054	0.100
514	47695	0.19	0.967	0.62	19407	0.113
515	148149	0.16	0.969	0.41	58694	0.122
520	141435	0.16	0.975	0.42	57018	0.101
521	59250	0.18	0.976	0.72	23828	0.107
522	167696	0.12	0.904	0.34	66803	0.156
523	155750	0.14	0.958	0.49	62062	0.075
524	134783	0.13	0.907	0.04	55602	0.114
525	111556	0.18	0.959	0.49	45457	0.163
526	106209	0.17	0.949	0.44	42697	0.142
527	169062	0.15	0.951	0.34	66978	0.098
528	102811	0.12	0.861	0.03	42196	0.161

Data Source: Population total by age, white only race, total households and percent households in poverty from the 2008–2012 American Community Survey. Data on the percent of population residing in rural areas from the 2010 population, using 2010 population as the denominator Abbreviation: HH, household.

Table A.2.

Lab Identifier	Associated ZIP codes	MRSA	MSSA	SSTI	Blood	ST5/ t002	ST8/ t008	ST398/ t034
Number of isolates (%)								
02	500, 505, 506, 510, 512, 513, 514, 521	160 (9.8)	194 (32.9)	285 (16.5)	12 (14.3)	122 (17.2)	87 (8.5)	8 (32)
03	503, 504, 506, 507, 521, 522, 524	371 (22.7)	10 (1.7)	323 (18.7)	14 (16.7)	134 (18.9)	204 (19.9)	2 (8)
04	500, 501, 502, 525,	111 (6.8)	4 (0.7)	88 (5.1)	2 (2.4)	31 (4.4)	77 (7.5)	0 (0)
05	520, 526, 527	114 (6.9)	2 (0.3)	78 (4.5)	4 (4.8)	52 (7.3)	56 (5.5)	0 (0)
06	510, 512	33 (2.1)	19 (3.2)	43 (2.5)	1 (1.2)	15 (2.1)	24 (2.4)	1 (4)
07	501, 503, 520, 522, 523, 526, 527, 528	290 (17.7)	129 (21.9)	332 (19.2)	23 (27.4)	126 (17.7)	196 (19.2)	4 (16)
08	506, 525, 526	77 (4.7)	49 (8.3)	94 (5.4)	7 (8.3)	30 (4.2)	57 (5.6)	2 (8)
09	510, 515	3 (0.2)	3 (0.5)	4 (0.2)	1 (1.2)	3 (0.4)	1 (0.1)	0 (0)
10	501, 503, 504, 506, 507, 513, 520, 522, 523, 524, 525	342 (20.9)	2 (0.3)	264 (15.3)	7 (8.3)	105 (14.8)	231 (22.6)	0 (0)
11	505, 507, 513, 510, 512, 514	111 (6.8)	151 (25.6)	184 (10.6)	11 (13.1)	71 (9.9)	77 (7.5)	8 (32)
12	521	5 (0.3)	2 (0.3)	2 (0.1)	2 (2.4)	2 (0.3)	2 (0.2)	0 (0)
13	506	20 (1.2)	24 (4.1)	33 (1.9)	0 (0)	20 (2.8)	10 (0.9)	0 (0)
Total	-	1637	589	1730	84	711	1022	25

Note: Lab 01 did not submit any isolates during the study period.

Abbreviations: MRSA, methicillin-resistant *S. aureus*; MSSA, methicillin-susceptible *S. aureus*; SSTI, skin and soft tissue infection; ST, sequence type.

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Fig. 1.

Maps of *Staphylococcus aureus* infection isolates in Iowa, 2011–2013. (A) Location of labs and the density of swine animal units per square kilometer in each three-digit ZIP code area. (B) Location of labs and the number of isolates from each three-digit ZIP code of patient residence (excludes non-Iowa isolates and those without a three-digit ZIP).

Table 1
Patient and pathogen characteristics in *Staphylococcus aureus* infections in Iowa, 2011–2013.

Characteristics	MRSA (n = 1634)	MSSA (n = 567)	L.A-SA (n = 25)	P-value
Frequency (Column %)				
Age ≥ 65 years	536 (32.8)	193 (34.1)	5 (20.0)	0.33
*Male	800 (49.1)	286 (50.7)	17 (68.0)	0.15
SSTIs	1276 (78.1)	454 (80.1)	18 (72.0)	0.45
**Invasive infections	85 (5.2)	43 (7.6)	2 (8.3)	0.07
***Hospitalized at time of culture	391 (25.7)	82 (15.4)	5 (20.0)	<0.01
***ICU exposure at time of culture	42 (4.0)	7 (1.6)	0 (0)	0.06
Permanent indwelling catheter	12 (0.7)	2 (0.4)	0 (0)	0.61
Percutaneous medical device	6 (0.4)	1 (0.2)	0 (0)	0.71
Participation in sports/athlete	4 (0.2)	2 (0.4)	0 (0)	0.67
Previous culture positive for MRSA	22 (1.4)	3 (0.5)	0 (0)	0.37
Antibiotic use	65 (3.9)	7 (1.2)	1 (4.0)	0.003
Surgery	90 (5.5)	15 (2.7)	1 (4.0)	0.02
Dialysis	12 (0.7)	3 (0.5)	0 (0)	0.81
Exposure to correctional facility	0 (0)	1 (0.2)	0 (0)	0.27
Exposure to LTCF as patient or visitor	79 (4.8)	8 (1.4)	0 (0)	0.0004
Occupational exposure to healthcare setting	8 (0.5)	5 (0.9)	1 (4.0)	0.08
PVL positivity	860 (52.5)	74 (12.6)	0 (0)	<0.01
MDR	1637 (100)	29 (5.1)	10 (40)	–

Missing:

* n = 9,

** n = 15,

*** n = 143,

**** n = 725

Significant at $P < 0.05$

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Abbreviations: ICU, intensive care unit; LA-SA, livestock-associated *S. aureus*; LTCF, long-term care facility; MDR, multidrug-resistant; MRSA, methicillin-resistant *S. aureus*; MSSA, methicillin-susceptible *S. aureus*; PVL, Pantone-Valentine leukocidin; SSTIs, skin and soft tissue infections

Table 2

Characteristics of livestock-associated *Staphylococcus aureus* strains infection in Iowa, 2011–2013.

Antibiotic resistance	<i>mecA</i>	<i>spa</i>	PVL	Exposures	Description of infection
T	(-)	t034	(-)	Antibiotic use, hospitalization, surgery	SSTI
T	(-)	t034	(-)	Previous culture positive for MRSA, antibiotic use	SSTI
O, CX, T	(+)	t034	(-)	Unknown	Synovial fluid
T	(-)	t034	(-)	Unknown	SSTI
T	(-)	t034	(-)	Surgery	Maxillary sinus
G(i), C, LEVO(i), E, CL, T	(-)	t571	(-)	Unknown	SSTI
C, LEVO(i), E, CL, T	(-)	t571	(-)	Unknown	SSTI
T	(-)	t011	(-)	Unknown	SSTI
G, T	(-)	t034	(-)	-	SSTI
T	(-)	t034	(-)	Unknown	Sputum
T	(-)	t034	(-)	Unknown	SSTI
T	(-)	t034	(-)	Unknown	SSTI
T	(-)	t7880	(-)	Unknown	SSTI
O, C, LEVO(i), E	(+)	t5883	(-)	None	SSTI
T	(-)	t571	(-)	Unknown	SSTI
O, E, CL(i), T	(+)	t034	(-)	Unknown	Sputum
T, TMP-SMX	(-)	t034	(-)	-	SSTI
G, C, LEVO(i), CL, T, TMP-SMX	(-)	t571	(-)	Unknown	SSTI
C, LEVO(i), G, TMP-SMX, T	(-)	t571	(-)	Unknown	SSTI
E, CL, IC, T	(-)	t337	(-)	Unknown	SSTI
E, CL, IC, T	(-)	t337	(-)	Unknown	SSTI
CL, E, T	(-)	t337	(-)	Unknown	Unknown
AM/KC, A/S, CL, E, T	(-)	t3446	(-)	-	SSTI
P, O, AM/KC, A/S, CZ, IM, MO	(+)	t12359	(-)	-	SSTI
NONE	(-)	t193	(-)	-	Urine

Note: Diagnostic laboratories reported only available patient exposure information. Information on livestock exposure not available from surveillance

Abbreviations: AM/KC, amoxicillin-k-clavulanate; A/S, ampicillin-sulbactam; C, ciprofloxacin; CL, clindamycin; CX, ceftriaxone; CZ, cefazolin; E, erythromycin; F, Female; G, gentamicin; IC, inducible clindamycin resistance; IM, imipenem; (i), intermediate susceptibility; LEVO, levofloxacin; M, Male; MO, meropenem; None, susceptible to all tested antimicrobials; O, oxacillin; P, penicillin; T, tetracycline; TMP-SMX, trimethoprim/sulfamethoxazole; (+), gene present; (-), gene absent; SSTI, skin and soft tissue infection; * indicates missing information

Table 3
Antimicrobial Susceptibility in *Staphylococcus aureus* infection isolates in Iowa, 2011–2013.

Antimicrobial	Range	MRSA (n = 1634)		MSSA (n = 567)			
		T	R	I	T	R	I
		Number of isolates (%)					
Oxacillin	0.25->16	1623 (99.3)	1596 (98.3)	0 (0)	564 (99.5)	24 (4.3)	0 (0)
TMP/SMX	0.25- 320	1632 (99.9)	24 (1.5)	0 (0)	566 (99.8)	2 (0.4)	0 (0)
Levofloxacin	0.12->32	1611 (98.6)	751 (46.6)	246 (15.3)	563 (99.3)	62 (11.1)	21 (3.7)
Erythromycin	0.25->32	1554 (95.1)	1396 (89.8)	8 (0.5)	553 (97.5)	201 (36.3)	5 (0.9)
Clindamycin	0.12->16	1556 (95.2)	568 (36.5)	11 (0.7)	544 (95.9)	111 (20.4)	5 (0.9)
Tetracycline	0.1-32	1630 (99.8)	118 (7.2)	4 (0.2)	557 (98.2)	53 (9.4)	6 (1.1)
Vancomycin	0.5- 32	1622 (99.3)	0 (0)	0 (0)	564 (99.5)	0 (0)	0 (0)

Note: MRSA and MSSA does not include LA strain types.

Abbreviations: I, intermediate; MRSA, methicillin-resistant *S. aureus*; MSSA, methicillin-susceptible *S. aureus*; R, resistant; TMP/SMX, trimethoprim/sulfamethoxazole; T, tested