Models to predict prevalence and transition dynamics of methicillin-resistant *Staphylococcus aureus* in community nursing homes

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**Key Words:** USA300 MRSA, non-USA300 MRSA, colonization, prevalence, risk factors, acquisition rates

**Background:** Recent spread of USA300 methicillin-resistant *Staphylococcus aureus* (MRSA) to nursing homes has been of particular concern. We sought to predict the ultimate prevalence of USA300 and non-USA300 MRSA and to examine the influence of potential risk factors on MRSA acquisition in community nursing homes.

**Methods:** The data were collected during a longitudinal MRSA surveillance study that involved 449 residents in 6 community nursing homes in Wisconsin. The subjects were screened every 3 months for up to 1 year. Markov chain models were employed to predict strain-specific prevalence of MRSA at steady state, and to assess the influence of potential risk factors, including recent hospitalizations, invasive medical devices, and antibiotic exposure on MRSA acquisition rates and average duration of colonization.

**Results:** At steady state, 20% (95% confidence interval [CI], 15%-25%) of residents were predicted to remain colonized with non-USA300 and 4% (95% CI, 2%-7%) with USA300 MRSA. Residents who used antibiotics during the previous 3 months were twice more likely to acquire MRSA than those who did not (acquisition rates, 0.052; 95% CI, 0.038-0.075 and 0.025; 95% CI, 0.018-0.037, respectively).

**Conclusions:** Non-USA300 was predicted to remain the dominant MRSA strain in community nursing homes. The higher rate of MRSA acquisition among residents with recent antibiotic exposure suggests that antibiotic stewardship may reduce MRSA colonization in this setting.

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*Methicillin-resistant* *Staphylococcus aureus* (MRSA) is a common cause of infection in community and health care settings.1,2 These infections are responsible for substantial patient morbidity and mortality and significantly increase health care use relative to infections caused by susceptible strains.3-5 Consequently, there has been great interest in understanding the dynamics and epidemiology of MRSA in health care facilities.6-11

Nursing homes are major reservoirs of MRSA with prevalence of colonization among residents approaching 50% in some settings.12-16 Residents in these facilities transition frequently between community and other health care settings, and nursing homes likely play a critical role in the regional spread of multidrug-resistant organisms, including MRSA.17-19 Whereas a number of mathematical models have been used to describe the dynamics of MRSA in acute-care settings7,10,11,20 and to predict the role of nursing homes in the regional spread of MRSA,17,20-22 their use in describing the dynamics of MRSA within nursing homes remains limited.

A number of factors could influence the dynamics of MRSA within nursing homes. Prior studies have shown that invasive medical devices, recent antibiotic use, chronic wounds, comorbidity, and...
frailty are risk factors for colonization with MRSA when residents with prevalent MRSA colonization are compared with noncolonized residents in cross-sectional or case-control studies. Whether these same conditions and exposures are also risk factors for acquisition of MRSA while residing in a nursing home and whether different strains of MRSA have an influence on the dynamics of spread in nursing homes remains poorly understood. Whereas health care-associated strains (eg, Centers for Disease Control and Prevention USA100 pulsotype) have been the dominant MRSA clones identified in most settings, an increasing number of studies suggest that community-associated strains (particularly, the Centers for Disease Control and Prevention USA300 pulsotype) are becoming more common in these facilities. This is of particular concern because community-associated MRSA strains may be more virulent and easily spread between individuals compared with health care-associated strains.

Given these gaps in knowledge, we sought to describe the transition dynamics of MRSA within nursing homes and assess the influence that MRSA strain type and potentially modifiable resident characteristics have on this process using a mathematical modeling approach. We hypothesized that resident acquisition of community-acquired MRSA (defined in this study as colonization with any USA300 pulsotype strain) differs from acquisition of health care-associated MRSA (defined in this study as colonization with any pulsotype strain other than USA300). We further hypothesized that resident characteristics that influence acquisition of USA300 and non-USA300 MRSA are distinct. To test these hypotheses, we employed Markov chain models to predict the distribution of residents colonized with USA300 and non-USA300 MRSA in the long run and to assess how potentially modifiable resident risk factors influence MRSA acquisition stratified by pulsotype strain.

MATERIALS AND METHODS

Sources of data

Data employed in this research were derived from a prospective longitudinal study of MRSA colonization performed in 6 community nursing homes between February 2008 and October 2010. The 6 nursing homes were located in 5 counties in south central Wisconsin. Subjects participating in this study were screened for MRSA colonization during a baseline examination and every 3 months thereafter for a period of up to 1 year or until they were discharged from the study facility, whichever occurred sooner. Surveillance cultures were collected from multiple anatomic locations of each subject, including surface cultures of the nares, skin of the axilla, groin, and perirectal region. Additional cultures were obtained from open wounds and the insertion sites of invasive devices, when applicable. A urine specimen was collected from subjects with indwelling urinary devices. Additional data were abstracted from health records during these visits to ascertain subject exposure to risk factors that might potentially influence their colonization status. Subject comorbidity, functional status, and cognitive status were assessed at baseline. A Charlson Comorbidity Index score ≥ 3, a Katz Activities of Daily Living score < 2, and Minimum Data Set Cognitive Performance Scale score ≥ 5 were used to stratify subjects into severe levels of comorbidity, function, and cognition, respectively, and none severe otherwise. Additional exposure to other potential risk factors, including presence of a chronic wound, invasive medical devices, hospitalization, and antibiotic exposure within the preceding 3 months were ascertained at baseline and each subsequent assessment and used as dichotomous variables in our study. This study was reviewed and approved by the Health Sciences Institutional Review Boards of the University of Wisconsin-Madison.

MRSA colonization patterns observed

Four hundred forty-nine subjects were screened for MRSA colonization at baseline, and 319 of these subjects were screened for MRSA colonization during subsequent follow-up on at least 1 occasion (Table A1). A subject’s MRSA status during a particular assessment was considered evaluable only if the results of cultures obtained from the nares, stool, or perirectal skin, and skin of the axilla or groin was not missing. Of the 1,468 subject assessments performed over the course of this study, 12 were considered nonevaluable (0.8% of total sample) due to missing data at 1 of the 3 screening body sites (Table A1). A total of 446 subjects contributed evaluable observations to the study. Ninety-five of the 446 subjects (21.3%) were colonized with MRSA at baseline: 79 subjects (17.7%) were colonized with non-USA300, 13 subjects (2.9%) with USA300, and 3 subjects (0.7%) were co-colonized with both strain types. An additional 52 subjects (11.7%) who were not identified as colonized at baseline had positive MRSA cultures during 1 or more of the follow-up assessments. MRSA was never recovered from the remaining 298 subjects (66.8%). In total, 72 MRSA acquisitions were observed over the course of the study: 68 events in subjects who were MRSA-colonized following a prior assessment in which they were noncolonized and 4 events in which subjects became colonized with a MRSA strain that was genetically distinct from isolates recovered during prior assessment.

For the purposes of this study, MRSA-positive subjects were classified as colonized with USA300 if an organism with this pulsotype was recovered from culture; otherwise, they were classified as being colonized with a non-USA300 strain (eg, subjects from whom USA700 was recovered were classified as being colonized with a non-USA300 strain of MRSA). MRSA was recovered from 663 of the cultures. Upon molecular typing, 495 of the isolates were identified as belonging to the USA100 CDC pulsotype group, 114 were assigned to the USA300 pulsotype group, and the remaining 24 isolates were assigned to other pulsotype groups. The distribution of the different MRSA strain types, stratified by facility, is included in Figure A1.

Models overview

We used Markov chain models with the assumption of nonstate-dependent acquisition rates to describe the dynamics of MRSA in nursing homes. Markov chain models are ideal tools for describing processes in which individuals move through a number of states (eg, noncolonized and colonized with non-USA300 or colonized with USA300) in discrete or continuous time. They allow modeling of transition rates between the states and predict the population distribution at steady state. The states of our models represented a subject’s possible MRSA colonization status. Colonization data observed in our study were used to fit discrete and continuous time models of differing complexity. Theoretically, a subject in our sample could be free of any MRSA, colonized with USA300 only, colonized with non-USA300 only, or colonized with both strains. Consequently, the model that would describe such a system most closely would have 4 states. However, due to the low number of transitions observed between some states, models with a smaller number of states (either 2 or 3) were employed in this study (Fig 1A and 1B). Over time, a subject could transition to another state or remain in the same state. The probability of a subject’s MRSA colonization status at a particular time point was assumed to only depend on the subject’s MRSA status during the immediate prior assessment and not on the full history of MRSA colonization or the present amount of colonized in the facilities. All computations and data analyses were performed in the R software environment, version 3.1.0 or higher (R Foundation for Statistical Computing, Vienna Austria).
that was used to calculate the steady-state ability matrix were characterized as USA300 in the models. The transition probabilities of co-colonized individuals observed in the study sample could be noncolonized (ie, negative) or colonized either with a non-USA300, irrespective of USA300. Similarly, in the USA300 model, Positive stands for colonized with non-USA300 MRSA, whereas Negative represents free of colonization with any MRSA strain or a specific strain, either non-USA300 or USA300. In the strain-independent model, Positive represents colonized with any MRSA strain and Negative stands for noncolonized with MRSA. In the non-USA300 model, Positive represents colonized with non-USA300, whereas Negative represents free of non-USA300, irrespective of USA300. In the USA300 model, Positive stands for colonized with USA300 and Negative represents free of USA300, irrespective of non-USA300 strain-type.

**Predicting steady-state distribution of MRSA in study nursing homes**

To predict the steady-state distribution of MRSA in nursing homes, a discrete-time Markov chain model with 3 states was employed (Fig 1A and Table A2). Due to the small number of transitions observed in each facility, the data from the 6 study nursing homes were combined, so that the estimated parameters would be representative of the hypothetical “average” nursing home (the characteristics of the individual facilities were published elsewhere). Models to predict the steady state of MRSA in individual nursing homes, although underpowered, were fit separately. In these models, subjects could be noncolonized (ie, negative) or colonized either with a USA300 or non-USA300 MRSA strain, but not both. The small numbers of co-colonized individuals observed in the study sample were characterized as USA300 in the models. The transition probability matrix that was used to calculate the steady-state distribution is shown in Table A2. Standard errors and 95% confidence intervals around the point estimates were computed by means of bootstrapping with 1,000 resampling runs and based on approximate normality.

**Influence of resident risk factors on predicted MRSA transition rates and average duration of colonization in study nursing homes**

Continuous-time Markov chain models were used to estimate MRSA transition rates and average duration of colonization (ie, the average time during which the same MRSA strain remained recoverable from a study subject) in our study of nursing homes. Similar to the approach used for predicting a steady-state distribution, data from the 6 study nursing homes were combined to increase precision of the estimated model parameters (the characteristics of the participating facilities can be found elsewhere). A mixture of 2- and 3-state models was employed (Fig 1A and Table A2). A strain-independent 2-state model (Fig 1B), in which a subject was either MRSA positive or MRSA negative, was used to explore the influence of individual candidate risk factors on MRSA transition rates. Strain-specific models were subsequently fit to identify interaction effects between individual candidate risk factors and strain type (USA300 and non-USA300). Three-state strain-specific models (Fig 1A) failed to converge for most of the candidate risk factors due to the scarcity of data. Consequently, simplified strain-specific 2-state models (Fig 1B and Table A2) were employed. In these simplified 2-state models, a subject was designated as noncolonized (negative) if he or she did not harbor the MRSA strain being evaluated in the current model and colonized (positive), otherwise (ie, a resident colonized with non-USA300 but free of USA300 was considered negative in the USA300 2-state model). The R package MSM (version 1.3) was used for model fitting.

**RESULTS**

**Predicted steady-state distribution of MRSA in study nursing homes**

For all facilities combined; that is, for our hypothetical typical nursing home, the significant differences in the distribution of residents colonized with USA300 and non-USA300 at steady state were observed (Fig 2). In the long run, 4% (95% confidence interval [CI], 2%-7%) of nursing home residents were predicted to be colonized with USA300 (and possibly co-colonized with non-USA300), 20% (95% CI, 15%-25%) would be colonized with non-USA300, and 75% (95% CI, 70%-81%) would remain free of MRSA. Facility-level models predicted that non-USA300 MRSA would dominate over USA300 strains in 4 of the 6 study facilities, including Facility 5, which did not have any residents colonized with USA300 over the course of the study. Although the predicted prevalence of USA300 exceeded that of non-USA300 in facilities 3 and 6, these differences were not statistically significant.

**Influence of resident risk factors on predicted MRSA transition rates**

In the strain-independent 2-state continuous-time Markov model (subjects either MRSA positive or MRSA negative), antibiotic use in the past 3 months doubled the acquisition rate of MRSA from 0.025 (95% CI, 0.018-0.037) to 0.052 (95% CI, 0.038-0.075) (Table 1). None of the other candidate risk factors examined in the study had a statistically significant influence on the transition rates of strain-independent MRSA (Table 1). It is worth noting that the difference between the point estimates of the levels of previous hospitalizations and cognitive status was quite pronounced, although statistical significance at the 95% confidence level was not achieved in our sample, which had low numbers of observations for some subgroups. In the strain-specific 2-state models (Fig 1B), recent antibiotic use remained a risk factor for colonization with non-USA300 MRSA, increasing its acquisition rate 2-fold, from 0.020 (95% CI, 0.013-0.030) to 0.042 (95% CI, 0.030-0.060) (Fig 3A). No other potential risk factors influenced the acquisition rates for strain-specific MRSA at the 95% confidence level (Fig 3B-G).

**Average duration of colonization**

The average duration of colonization with either strain type was longer than one year for most of the candidate risk factors considered (Fig 4). Furthermore, no significant differences were observed in the average duration of colonization between non-USA300 and USA300, regardless of the risk factors being examined (Fig 4). For example, for the subjects who used antibiotics during the past 3 months, the average duration of colonization with non-USA300 was not significantly different from the duration of colonization with USA300. Furthermore, the use of antibiotic agents did not significantly...
influence the duration of colonization for residents colonized with either strain.

**DISCUSSION**

The emergence of community-associated MRSA and subsequent introduction into health care settings, including nursing homes, has become a growing concern in recent years. To our knowledge, our study represents the first attempt to model strain-specific long-term prevalence of MRSA, its acquisition rates, and the duration of colonization in community nursing homes while accounting for factors that potentially influence these dynamics.

Our study results show that, on average, health care-associated strains of MRSA will continue to dominate in nursing homes in our region, although we could not exclude the possibility that USA300 could achieve dominance in individual facilities. These findings are consistent with other studies demonstrating a preponderance of health care-associated MRSA strains in nursing homes within the same region. In these studies, USA300 was identified as the dominant circulating strain only rarely, even in regions with high levels of community-acquired strains circulation in the surrounding population.

Antibiotic exposure within the previous 3 months was the only factor that, when entered into our model, significantly increased the acquisition rate of strain-independent MRSA. It also increased the acquisition rates of strain-specific MRSA, although statistical significance at a 95% confidence level was only achieved for non-USA300. This finding is consistent with other studies that have found that recent antibiotic use increased nursing home resident risk of MRSA acquisition. Antibiotic agents are among the most frequently prescribed medications in nursing homes and much of this use is inappropriate. Our findings in this study suggest that antibiotic stewardship may represent a powerful tool to reduce the spread of MRSA in nursing homes.

**Table 1**

<table>
<thead>
<tr>
<th>Risk factor</th>
<th>Level of risk factor</th>
<th>Negative to positive</th>
<th>Positive to negative</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Estimate (95% CI)</td>
<td></td>
</tr>
<tr>
<td>Antibiotic use in the past 3 mo</td>
<td>Nonexposed</td>
<td>0.025 (0.018-0.037)*</td>
<td>0.122 (0.086-0.172)</td>
</tr>
<tr>
<td></td>
<td>Exposed</td>
<td>0.052 (0.038-0.075)*</td>
<td>0.099 (0.069-0.146)</td>
</tr>
<tr>
<td>Hospitalizations in the past 3 mo</td>
<td>Nonexposed</td>
<td>0.034 (0.026-0.044)</td>
<td>0.108 (0.081-0.132)</td>
</tr>
<tr>
<td></td>
<td>Exposed</td>
<td>0.056 (0.028-0.109)</td>
<td>0.126 (0.059-0.255)</td>
</tr>
<tr>
<td>Invasive device</td>
<td>Nonexposed</td>
<td>0.036 (0.028-0.047)</td>
<td>0.112 (0.085-0.146)</td>
</tr>
<tr>
<td></td>
<td>Exposed</td>
<td>0.038 (0.017-0.087)</td>
<td>0.099 (0.051-0.187)</td>
</tr>
<tr>
<td>Wound</td>
<td>Nonexposed</td>
<td>0.035 (0.028-0.045)</td>
<td>0.121 (0.091-0.159)</td>
</tr>
<tr>
<td></td>
<td>Exposed</td>
<td>0.049 (0.022-0.105)</td>
<td>0.069 (0.034-0.146)</td>
</tr>
<tr>
<td>Comorbidity</td>
<td>Nonsevere</td>
<td>0.033 (0.023-0.048)</td>
<td>0.121 (0.082-0.181)</td>
</tr>
<tr>
<td></td>
<td>Severe</td>
<td>0.039 (0.027-0.054)</td>
<td>0.103 (0.073-0.143)</td>
</tr>
<tr>
<td>Functional status</td>
<td>Nonsevere</td>
<td>0.032 (0.020-0.053)</td>
<td>0.131 (0.074-0.227)</td>
</tr>
<tr>
<td></td>
<td>Severe</td>
<td>0.038 (0.028-0.050)</td>
<td>0.105 (0.079-0.142)</td>
</tr>
<tr>
<td>Cognitive status</td>
<td>Nonsevere</td>
<td>0.038 (0.030-0.050)</td>
<td>0.121 (0.092-0.158)</td>
</tr>
<tr>
<td></td>
<td>Severe</td>
<td>0.024 (0.012-0.047)</td>
<td>0.048 (0.018-0.126)</td>
</tr>
</tbody>
</table>

*The difference is statistically significant at the 95% CI.
In contrast to other studies, anumber of candidate risk factors we examined in this study did not achieve statistical significance at a 95% confidence level. For example, the increase in MRSA colonization predicted by our model in the presence of recent hospitalizations (acquisition rate, 0.034-0.056) or a wound (acquisition rate, 0.035-0.049) was substantial in absolute terms but did not achieve statistical significance. Likewise, impaired cognition appeared to be associated with a reduced risk of MRSA acquisition (transition rate, 0.038-0.024) but, again, this did not achieve statistical significance. It is possible that a number of these risk factors that did not achieve statistical significance could become significant in larger studies with more power.

Fig 3. Predicted acquisition rates for non-USA300 and USA300 (relative frequency per 3 months) and their 95% confidence intervals (CL) by potential risk factors. The candidate risk factors are (A) antibiotic use in the past 3 months, (B) previous hospitalizations in the past 3 months, (C) presence of invasive device, (D) wound, (E) comorbidity, (F) functional status, and (G) cognitive status. The levels of the candidate risk factors are indicated parenthetically and represent absence (Non-exposed) or presence (Exposed) of the risk factor for antibiotic use, previous hospitalizations, invasive device, and wound as well as severity (Non-severe or Severe) for comorbidity, functional status, and cognitive status.
factors would have achieved statistical significance using models based on a larger dataset or those that incorporated a multivariate approach rather than the bivariate approach employed in this study.

The limitations of our study were mainly driven by modeling assumptions and scarcity of data. For example, whereas MRSA acquisition rates were facility-specific, the data from the 6 facilities were combined due to its paucity in separate facilities. Hence,
our estimates would be representative of a hypothetical typical nursing home. Likewise, we examined 1 candidate risk factor at a time. Such model simplifications allowed comparisons within each risk factor but restricted comparisons across the risk factors. Furthermore, due to the scarcity of data, all of the potential risk factors were considered as dichotomous variables in our models. This was likely to reduce the discriminatory power of the models to detect the true level of association between the candidate risk factors and acquisition of MRSA. Thus, the true level of association between recent antibiotic exposure and MRSA acquisition was likely to be attenuated by dichotomizing its variable (exposed or non-exposed), because residents who received a single dose of an antimicrobial agent and those who received a long course of antibiotics over the previous 3 months were assigned to the same group. Similarly, residents were classified into noneverse and severe levels of comorbidity, functional status, and cognitive status based on the arbitrarily chosen cutoffs for the associated raw scores. This may have resulted in assigning residents with similar amounts of exposure to different levels of the respective candidate risk factors. Moreover, our study did not account for changes in the admission prevalence of strain-specific MRSA that may occur over time; for example, due to changes in the prevalence of MRSA in referring hospitals or the surrounding community. Such changes may affect the epidemiology of MRSA in the nursing homes over time.

Additional work is needed to better understand the transmission dynamics of MRSA in community nursing homes. It includes determining the conditions under which MRSA could be reduced or eliminated from the facilities and evaluating the risk of a MRSA outbreak in this setting. Understanding associations between potentially modifiable resident characteristics and acquisition and persistence of MRSA strains may contribute to adopting better-informed infection control strategies aimed at decreasing the burden of MRSA in nursing homes.

CONCLUSIONS

Our study results suggest that under current conditions non-USA300 MRSA will continue to dominate USA300 in community nursing homes. Antibiotic exposure during the previous 3 months was the only factor associated with a significant increase in MRSA acquisition rates in the study facilities. Consequently, antibiotic stewardship may reduce the burden of MRSA in nursing homes.

Acknowledgments

The authors thank Drs Vicki Bier, Molly Carnes, and David Zim-merman for their constructive suggestions, invaluable feedback, and support during different stages of the study. The authors also thank Dr Bret Hanlon for providing methodology advice and Helena Tsotis for helping with data retrieval.

References


APPENDIX

Table A1

<table>
<thead>
<tr>
<th>Time point</th>
<th>No. of subjects screened for MRSA at assessment</th>
<th>No. of subjects evaluable* at assessment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Baseline</td>
<td>449</td>
<td>444†</td>
</tr>
<tr>
<td>3 mo</td>
<td>319</td>
<td>316</td>
</tr>
<tr>
<td>6 mo</td>
<td>271</td>
<td>268</td>
</tr>
<tr>
<td>9 mo</td>
<td>238</td>
<td>238</td>
</tr>
<tr>
<td>12 mo</td>
<td>191</td>
<td>190</td>
</tr>
</tbody>
</table>

MRSA, methicillin-resistant Staphylococcus aureus.

*MRSA status of a subject at a particular assessment was considered evaluable for the purpose of the study if all 3 culture results obtained from nares, stool, or perirectal skin and skin of the axilla or groin were valid (eg, if a subject’s cultures obtained from nares and skin of the axilla or groin were both negative for MRSA, whereas if the culture obtained from stool or perirectal skin was missing, the assessment was considered not evaluable).

†Two subjects with nonevaluable observations at baseline had at least 1 evaluable observation during subsequent assessments (1 subject had an evaluable observation at 3 months, and the other subject had evaluable observations at 3, 6, and 9 months). That is, the total of 446 subjects had evaluable observation during the study period.

Table A2

<table>
<thead>
<tr>
<th>From state</th>
<th>To state</th>
<th>3-State model*</th>
<th>USA300</th>
<th>Non-USA300</th>
</tr>
</thead>
<tbody>
<tr>
<td>Negative</td>
<td>Negative USA300</td>
<td>711 (0.913)</td>
<td>13 (0.017)</td>
<td>55 (0.071)</td>
</tr>
<tr>
<td>USA300</td>
<td>Non-USA300</td>
<td>10 (0.222)</td>
<td>30 (0.667)</td>
<td>5 (0.111)</td>
</tr>
<tr>
<td>Non-USA300</td>
<td>USA300</td>
<td>52 (0.278)</td>
<td>2 (0.011)</td>
<td>132 (0.711)</td>
</tr>
</tbody>
</table>

2-State strain-specific models

<table>
<thead>
<tr>
<th>From state</th>
<th>To state</th>
<th>USA 300 Model†</th>
<th>Negative USA300</th>
<th>Non-USA300 Model‡</th>
<th>Negative Non-USA300</th>
</tr>
</thead>
<tbody>
<tr>
<td>Negative</td>
<td>USA 300</td>
<td>950 (0.984)</td>
<td>15 (0.016)</td>
<td>NA</td>
<td>58 (0.071)</td>
</tr>
<tr>
<td>USA 300</td>
<td>Non-USA300</td>
<td>15 (0.333)</td>
<td>30 (0.667)</td>
<td>NA</td>
<td>136 (0.716)</td>
</tr>
<tr>
<td>Non-USA300</td>
<td>Negative</td>
<td>762 (0.929)</td>
<td>NA</td>
<td>58 (0.071)</td>
<td>NA</td>
</tr>
<tr>
<td>Non-USA300</td>
<td>Non-USA300</td>
<td>54 (0.284)</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

NOTE. Values are presented as n (probability).

MRSA, methicillin-resistant Staphylococcus aureus; NA, not available.

*In the 3-state model, subjects can be MRSA-free (Negative), colonized with USA300 and possibly co-colonized with non-USA300 (USA300) or colonized with non-USA300 only (non-USA300).

†In this model, a subject can be either colonized with USA300 (USA300) or non-colonized with USA (Negative). Subjects classified as Negative in this model can be colonized with non-USA300 strains.

‡In this model, a subject can be either colonized with non-USA300 (non-USA300) or free from non-USA300 (Negative). Subjects classified as Negative in this model can be colonized with USA300.

Fig A1. Counts of residents colonized with strain-independent and strain-specific methicillin-resistant Staphylococcus aureus (MRSA) in each facility over time. Rows represent MRSA strains: MRSA (any strain of MRSA), non-USA300, and USA300. Columns represent facilities. Bars show the number of subjects colonized with the corresponding MRSA strain (Positive) or noncolonized with this MRSA strain (Negative).