**Supplemental materials**

**Supplemental methods**

*Counties*

For this paper, data were used from the following Emerging Infections Program continuously under surveillance for invasive methicillin-resistant *Staphylococcus aureus* during 2005–2013: California (Contra Costa, Alameda, and San Francisco counties), Georgia (DeKalb, Fulton, Douglas, Clayton, Gwinnett, Cobb, Newton, and Rockdale counties), Minnesota (Ramsey county), New York (Monroe County), Tennessee (Davidson county). Compared to the United States as a whole, minority races are overrepresented in this five site population area.

*Isolate collection*

As noted in the methods section of the manuscript, a subset of clinical laboratories in each of the above EIP sites was identified from which either >50% of MRSA blood isolates from cases were submitted and tested at CDC or a systematic sample of blood isolates was submitted and tested (New York site only). All laboratories from Minnesota were included because isolate submission occurs throughout the county. Of 5614 bloodstream infection cases identified from these clinical laboratories from 2005–2013, isolates had been submitted and tested for 68%.

*Multiple imputation*

To perform imputation, first a multinomial logistic regression model was created using strain type (“USA100”, “USA300”, or “other”) as the dependent variable with backwards stepwise selection and a stay criteria of P<0.05 to select variables significantly associated with different strain types. Candidate variables were age, sex, state, year, infection type (e.g., bloodstream infection, osteomyelitis), culture source, comorbid conditions (HIV infection, recurrent boils, prior CVA, chronic liver disease, diabetes, congestive heart failure, injection drug use, obesity, peptic ulcer disease, peripheral vascular disease, chronic renal disease, smoking, dementia, chronic pulmonary disease, homelessness, connective tissue disease, other drug use), and healthcare exposure data (prior hospitalization, dialysis, or long-term facility stay; overall epidemiologic classification; recent central venous catheter use), date of admission when specimen was collected, where the specimen was collected (e.g., intensive care, unit, emergency department) and whether the infection represented a recurrence. Variables independently associated with different strain types were age, sex, state, year, cellulitis, pneumonia, traumatic wound infection, skin abscess, AIDS, recurrent boils, congestive heart disease, hematologic malignancy, injection drug use, obesity, current smoker, chronic pulmonary disease, dementia, other drug use, hemiplegia, prior long-term care facility residence, prior surgery, location of specimen collection, epidemiologic class, and admission date of culture.

Second, multiple imputation was performed using these variables. Twenty-five imputation datasets were created with the SAS PROC MI procedure using a monotone logistic method.

**Supplemental Tables**

**Table S1**: Completeness of blood isolates submitted by selected laboratories in five Emerging Infections Program sites, by year (*P*<0.0001 overall)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 |
| Cases with isolates submitted, n | 520 | 502 | 518 | 539 | 419 | 344 | 344 | 310 | 294 |
| Cases with no isolate submitted, n | 280 | 339 | 203 | 168 | 203 | 167 | 185 | 153 | 126 |
| Cases with isolates submitted, % of total | 65.0% | 59.7% | 71.8% | 76.2% | 67.4% | 67.3% | 65.0% | 67.0% | 70.0% |

**Table S2**: Completeness of blood isolates submitted by selected laboratories in five Emerging Infections Program site (*P*<0.0001 overall)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | CA | GA | MN | NY | TN |
| Cases with isolates submitted, n | 317 | 1762 | 553 | 755 | 403 |
| Cases with no isolate submitted, n | 123 | 798 | 74 | 771 | 58 |
| Cases with isolates submitted, % of total | 72.1% | 68.8% | 88.2% | 49.5% | 87.4% |