Methicillin-resistant Staphylococcus aureus (MRSA) with reduced vancomycin susceptibility has been reported from many countries. Whether resistance is evolving regularly in different genetic backgrounds or in a single clone with a genetic predisposition, as early results suggest, is unclear. We have studied 101 MRSA with reduced vancomycin susceptibility from nine countries by multilocus sequence typing (MLST), characterization of SCCmec (staphylococcal chromosomal cassette mec), and agr (accessory gene regulator). We found nine genotypes by MLST, with isolates within all five major hospital MRSA lineages. Most isolates (88/101) belonged to two of the earliest MRSA clones that have global prevalence. Our results show that reduced susceptibility to vancomycin has emerged in many successful epidemic lineages with no clear clonal disposition. Increasing antimicrobial resistance in genetically distinct pandemic clones may lead to MRSA infections that will become increasingly difficult to treat.

Materials and Methods

We collected 101 isolates of MRSA with reported heterogeneous or homogeneous resistance to vancomycin (MIC $\geq$ 8 mg/L) from China (n = 1), France (31), Japan (2), Norway (14), Poland (13), Sweden (1), United Kingdom (28), and the United States (11). Antimicrobial susceptibility tests were performed by the agar dilution method of the National Committee for Clinical Laboratory Standards. Isolates were described as VISA if they fulfilled the three criteria adopted by the Centers for Disease Control and Prevention, that is, broth microdilution vancomycin MIC of 8 to 16 mg/L, MIC $>6$ mg/L on E-test, and growth on brain-heart infusion agar containing 6 mg/L vancomycin (12). Isolates with heterogeneous resistance to vancomycin were confirmed by using population analysis profiling followed by measuring the area under the curve (PAP-AUC), as described previously (13). The prototypic
hVISA strain MU3 was used as a standard, and isolates with an AUC ≥ 0.9 compared to MU3 were described as hVISA.

MLST was performed as described previously (10). The seven housekeeping gene sequences were compared to known alleles in the MLST database (available from http://www.mlst.net), and the resulting allelic profiles (which define sequence types, STs) were used to interrogate the databases for matches within records of the 988 isolates held there. The MLST databases contain molecular and epidemiologic data on S. aureus isolates from carriage and disease, including examples of all major MRSA clones (10). Data from this study were added to the S. aureus MLST database, and the entire dataset was analyzed by using the BURST algorithm to assign isolates to clonal complexes (CCs), which are lineages containing genetically related isolates (sharing 100% genetic identity at ≥ 5/7 loci used). Polymerase chain reaction (PCR) analysis of the ccr (chromosomal cassette recombinase) and mec (methicillin resistance) regions was performed to discriminate the four main SCCmec types (I–IV) on the basis of the combinations of the two regions. PCR was used to detect SCCmec I–III by using the primers described in Ito et al. (14) and SCCmec IV by using those described by Daum et al. (15). These results were confirmed using the multiplex method of Oliveira et al. (16). Detection of agr subgroups I–IV was performed by PCR of the region surrounding agrD, which codes for an autoinducing peptide, according to the method of Peacock et al. (17).

**Results and Discussion**

The results are shown in the Table. PAP-AUC values for the isolates varied from 0.9 to 3.0 and 91/101 isolates were designated hVISA on the basis of a PAP-AUC value ≥ 0.9. Nine isolates were designated as VISA.

From the genotyping results, strains were divided into clonal complexes, which can be subdivided according to sequence type (ST) and SCCmec differences. The clonal complexes CC5, CC8, CC22, CC30, and CC45 represent the five pandemic MRSA lineages that have been previously described (10). Our results show that hVISA has arisen in all five of these pandemic clones and that VISA has so far developed in CC5 and CC8. The three most common MRSA clones present in the United Kingdom (EMRSA-3, EMRSA-15, EMRSA-16) (18) are included within these lineages, and reduced vancomycin susceptibility has been identified in all of these clones. All lineages displayed resistance to multiple antimicrobial classes, and only the new oxazolidinone linezolid was active against all strains.

Only agr subgroups (alleles) I and II were found in isolates in this study with 7/9 VISA and 57/92 hVISA having

### Table. Characteristics of study isolates with reduced vancomycin susceptibility

<table>
<thead>
<tr>
<th>CC</th>
<th>ST</th>
<th>SCCmec</th>
<th>Clonal type</th>
<th>agr type</th>
<th>Vancomycin resistance phenotype (no. of strains)</th>
<th>PAP-AUC</th>
<th>Country of origin</th>
<th>Antimicrobial susceptibility</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>5</td>
<td>I</td>
<td>EMRSA-3</td>
<td>I or II</td>
<td>VISA (3)</td>
<td>1.4–1.92</td>
<td>Japan, Sweden, France, Poland, UK, USA, Norway</td>
<td>Lzd Syn Gen Cip Rif</td>
</tr>
<tr>
<td>5</td>
<td>5</td>
<td>II</td>
<td>New York/Japanese</td>
<td>I or II</td>
<td>VISA (3)</td>
<td>1.19–1.32</td>
<td>UK</td>
<td>S S S R R R</td>
</tr>
<tr>
<td>8</td>
<td>8</td>
<td>I</td>
<td>II</td>
<td>I or II</td>
<td>VISA (3)</td>
<td>0.92–1.2</td>
<td>France, UK, Norway</td>
<td>S S S R R R</td>
</tr>
<tr>
<td>8</td>
<td>8</td>
<td>II</td>
<td>Irish-1</td>
<td>I or II</td>
<td>VISA (3)</td>
<td>1.04–1.2</td>
<td>France, USA, Norway</td>
<td>S S S R S/R S/R</td>
</tr>
<tr>
<td>22</td>
<td>22</td>
<td>IV</td>
<td>EMRSA-15</td>
<td>I or II</td>
<td>VISA (7)</td>
<td>0.9–1.25</td>
<td>UK</td>
<td>S S S R R R</td>
</tr>
<tr>
<td>25</td>
<td>25</td>
<td>NT</td>
<td>EMRSA-16</td>
<td>I</td>
<td>VISA (1)</td>
<td>0.92–1.17</td>
<td>UK</td>
<td>S S S R R R</td>
</tr>
<tr>
<td>30</td>
<td>36</td>
<td>II</td>
<td>EMRSA-16</td>
<td>I</td>
<td>VISA (1)</td>
<td>1</td>
<td>USA</td>
<td>S S S R S S</td>
</tr>
<tr>
<td>45</td>
<td>45</td>
<td>II</td>
<td>Brazilian/Portuguese</td>
<td>I or II</td>
<td>VISA (10)</td>
<td>0.9–1.22</td>
<td>France, Poland, China, Norway, UK</td>
<td>S S S R S/R S/R</td>
</tr>
<tr>
<td>8</td>
<td>239</td>
<td>I or II</td>
<td>Portuguese</td>
<td>I or II</td>
<td>VISA (7)</td>
<td>1.44–3.01</td>
<td>France, Poland, UK</td>
<td>S S/R R R R S/R</td>
</tr>
<tr>
<td>8</td>
<td>239</td>
<td>NT</td>
<td></td>
<td>I</td>
<td>VISA (1)</td>
<td>0.92</td>
<td>France</td>
<td>S S R R R R</td>
</tr>
<tr>
<td>8</td>
<td>246</td>
<td>NT</td>
<td></td>
<td>I</td>
<td>VISA (1)</td>
<td>1.13</td>
<td>Norway</td>
<td>S S R R R R</td>
</tr>
<tr>
<td>8</td>
<td>247</td>
<td>I</td>
<td>Iberian</td>
<td>I</td>
<td>VISA (1)</td>
<td>1.57</td>
<td>UK</td>
<td>S S R R R R</td>
</tr>
</tbody>
</table>

*S, susceptible; R, resistant; NT, nontypeable; PAP-AUC, population analysis profiling followed by measuring the area under the curve; Lzd, linezolid; Syn, synercid; Gen, gentamicin; Cip, ciprofloxacin; Rif, rifampin; CC, clonal complex; ST, sequence type; EMRSA, methicillin-resistant Staphylococcus aureus found in the United Kingdom (UK); hVISA, heterogeneous vancomycin-intermediate S. aureus; USA, United States of America.
agr I. Within the 14 clones in this study, the proportion of isolates with particular agr alleles was variable. The presence of both agr I and agr II among VISA/hVISA, even in genetically similar isolates, suggests that the genes for the agr system are horizontally transferred. Sakoulas et al. reported an association of agr II with the development of vancomycin resistance (11). Our results show that VISA/hVISA also emerged in strains with agr I.

Molecular analyses of VISA isolates to date have focused on isolates from the United States and Japan, and results have indicated that all strains belong to the New York/Japanese MRSA clone. In our study, we found that hVISA isolates have emerged from every lineage that has produced pandemic MRSA clones, and VISA isolates have emerged in two of five lineages, in all likelihood from hVISA precursor isolates.

Increasing drug resistance in clones that are multidrug resistant and adapted to spread and cause serious disease can do much damage in the modern hospital environment. We have shown that reduced vancomycin susceptibility has emerged in genetically and phenotypically diverse MRSA clones throughout the world. This finding suggests that vancomycin resistance has the potential to become a widespread problem in MRSA strains already resistant to multiple antimicrobial agents.

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Dr. Howe is a consultant microbiologist at Southmead Hospital, Bristol, and Clinical Lecturer at Bristol University. His research interests include many areas of clinical microbiology, particularly the mechanisms of antimicrobial resistance in bacterial pathogens.

References


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