Genetic diversity and antimicrobial susceptibility profiles among mastitis-causing Staphylococcus aureus isolated from bovine milk samples

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Objective—To determine whether particular antimicrobial susceptibility profiles of bovine mastitis-causing Staphylococcus aureus isolates were associated with specific S aureus genotypes.

Sample Population—357 S aureus isolates recovered from milk samples submitted for diagnostic bacteriologic testing from 24 dairy herds.

Procedures—Antimicrobial susceptibility of S aureus isolates was assessed by determining minimum inhibitory concentrations (MICs) to 14 antimicrobial agents. After digestion of S aureus genomic DNA by Smal, electrophoretic patterns were obtained via pulsed-field gel electrophoresis (PFGE) and used to classify isolates into types. Gels were analyzed, and data were used to prepare dendrograms.

Results—308 of 357 (86%) S aureus isolates were susceptible to all antimicrobials evaluated. Forty-nine S aureus isolates were resistant to 1 or more antimicrobials; of these isolates, 37 were resistant only to penicillin, 9 were resistant to penicillin and erythromycin, 2 were resistant to tetracycline, and 1 was resistant to erythromycin. Isolates were assigned to 7 PFGE types. An association was found between PFGE type and antimicrobial susceptibility profile. Organisms with resistance to at least one of the tested antimicrobial agents were identified in only 4 of the 7 types of S aureus.

Conclusions and Clinical Relevance—Antimicrobial resistance was uncommon among the mastitis-causing S aureus isolates identified in the milk samples. A limited number of genotypes were associated with mastitis in these herds. Antimicrobial resistance phenotypes were associated with particular S aureus PFGE types; this association may have implications for future treatment and control of S aureus-associated mastitis in cattle. (Am J Vet Res 2006;67:1185–1191)

Staphylococcus aureus is a common cause of chronic subclinical mastitis in many dairy herds. One notable characteristic of S aureus–associated mastitis is that it is often refractory to antimicrobial treatments. Failure of treatment occurs for multiple reasons, including antimicrobial resistance and the inability of antimicrobials to gain access to the bacterium by virtue of the intracellular location of S aureus or the formation of microabscesses. Antimicrobial resistance is often cited as a major reason for failure of antimicrobial treatment in cattle with chronic S aureus–associated mastitis. Several recent reports have considered the antimicrobial resistance patterns of S aureus isolates from cattle with mastitis. In general, the consensus from these reports is that among S aureus isolates from mastitis-affected cows, there is little to moderate resistance to most commonly used antimicrobials, with the exception of penicillin and ampicillin and, to a much lesser extent, tetracycline and erythromycin. Approximately 30% to 50% of isolates have been reported as resistant to either penicillin or ampicillin in various studies. However, there are some exceptions. As an example, a report regarding S aureus isolates from Israel reveals a much higher degree of resistance, with 97% of 319 isolates being resistant to penicillin. Conversely, less resistance among S aureus isolates has been determined in some studies in countries such as Switzerland and Denmark. Disparate results from different countries highlight the importance of continued antimicrobial susceptibility monitoring of S aureus and other bovine udder pathogens.

Several phenotypic and molecular techniques have been used to classify mastitis–causing S aureus in attempts to investigate the molecular epidemiology of S aureus–associated mastitis. The most commonly used phenotypic methods include phage typing, biotyping, and use of antibiograms. Molecular techniques used to classify S aureus include PFGE; binary typing; coagulase gene typing; restriction enzyme fragmentation pattern analysis; ribotyping; multilocus enzyme elec-
Most of the molecular epidemiology reports of mastitis-causing *S. aureus* isolates in cattle suggest clonal populations characterized by dominant strain types and an overall low strain diversity. The consensus of most studies is that a limited number of clones (sometimes also referred to as strains or types) of *S. aureus* usually cause mastitis in a given dairy herd and that some types or strains may be distributed widely in herds across geographic regions. Particular *S. aureus* type dominance may be associated with specific virulence properties, however, the correlation between genotype and antimicrobial resistance phenotype has yet to be fully investigated.

The purpose of the study reported here was to determine whether particular antimicrobial susceptibility profiles of mastitis-causing *S. aureus* isolates obtained from bovine milk samples were associated with specific *S. aureus* genotypes. Further investigation of the role of *S. aureus* genotype relative to antimicrobial susceptibility phenotype should contribute to a greater understanding of the molecular epidemiology of *S. aureus*-associated mastitis and could lead to the development of more effective mastitis infection control strategies.

**Materials and Methods**

**Bacterial isolates**—Bacterial isolates (*n* = 454) identified as *S. aureus* were obtained from bovine milk samples submitted for diagnostic testing for mastitis from farms in North Carolina and Virginia. Procedures for bacteriologic culture of milk were consistent with those described by the National Mastitis Council. Freshly collected milk samples were plated within 24 hours or frozen for ≤1 week at –20°C and then quick-thawed and plated. Milk samples were vortexed, and 0.01 mL of milk was plated on trypticase soy agar with 5% sheep blood. Plates were incubated at 36°C and examined after 24 and 48 hours. Cream- or golden-yellow–pigmented colonies of catalase- and coagulase-positive gram-positive cocci that were capable of complete, incomplete, or both complete and incomplete hemolysis were identified as *S. aureus*. Similar colonies with no hemolysis were confirmed as *S. aureus* by use of a standardized identification system for staphylococci. Only 1 isolate/cow was used, unless > 1 *S. aureus* PFGE-derived EP was detected in milk from the same cow. Only those PFGE types with ≥5 isolates were considered in this study. Further analysis was performed on the 357 isolates that fit these criteria.

**Antimicrobial susceptibility testing**—Antimicrobial MICs for *S. aureus* isolates were determined by use of a semiautomated antimicrobial susceptibility system according to the manufacturer’s instructions and interpreted according to the Clinical and Laboratory Standards Institute standards for broth microdilution methods. The antimicrobial agents of veterinary and human importance tested were as follows: amoxicillin-clavulanic acid, cephalothin, chlindamycin, gentamicin, oxacillin, trimethoprim-sulfamethoxazole, vancomycin, ceftriaxone, cefuroxime, erythromycin, penicillin, tetracycline, penicillin-novobiocin, and pirlimycin. Minimum concentrations of antimicrobial agents required to inhibit the growth of at least 50% and 90% of the bacteria tested were also derived. Quality-control organisms were obtained from the American Type Culture Collection (Escherichia coli ATCC 25,922 and *S. aureus* ATCC 29,213); data from all quality-control organisms were within appropriate Clinical and Laboratory Standards Institute quality-control ranges.

**PFGE**—Preparation of bacterial genomic DNA and digestion by *Smal*, as well as PFGE, were performed as previously described, with minor modifications. The DNA was prepared according to the method of Shimizu et al. except that 5 μL of lysostaphin solution was added to the cell suspension rather than 10 μL and 40 units of *Smal* was used rather than 20 units. Digested fragments were separated by use of a PFGE system with a ramped pulse of 15 to 55 sec.

Figure 1—Composite gel of all EPs of 357 *Staphylococcus aureus* isolates obtained from milk samples submitted for mastitis diagnosis from 24 dairy herds. The dendrogram shows the percentage similarity at each node. The EPs clustered above a similarity value of 80% were considered to be the same PFGE type.
Table 1—Antimicrobial resistance profiles and MIC values of 357 Staphylococcus aureus isolates obtained from milk samples submitted for diagnostic bacteriologic testing from 24 dairy herds.

<table>
<thead>
<tr>
<th>Antimicrobial agent</th>
<th>Resistance break point (μg/mL)</th>
<th>MIC range (μg/mL)</th>
<th>MIC&lt;sub&gt;mic&lt;/sub&gt; (μg/mL)</th>
<th>MIC&lt;sub&gt;90&lt;/sub&gt; (μg/mL)</th>
<th>No. of resistant organisms (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amoxicillin-clavulanic acid</td>
<td>8/4</td>
<td>0.06/0.3–1.0/0.5</td>
<td>0.25/0.12</td>
<td>0.5/0.25</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Cephalothin</td>
<td>32</td>
<td>0.06–0.5</td>
<td>0.25</td>
<td>0 (0)</td>
<td></td>
</tr>
<tr>
<td>Clindamycin</td>
<td>4</td>
<td>0.03–0.25</td>
<td>0.12</td>
<td>0 (0)</td>
<td></td>
</tr>
<tr>
<td>Erythromycin</td>
<td>8</td>
<td>0.12–0.2</td>
<td>0.25</td>
<td>1/357 (3)</td>
<td></td>
</tr>
<tr>
<td>Gentamicin</td>
<td>16</td>
<td>0.12–1.0</td>
<td>0.25</td>
<td>0 (0)</td>
<td></td>
</tr>
<tr>
<td>Oaxacillin</td>
<td>4</td>
<td>0.12–1.0</td>
<td>0.25</td>
<td>0 (0)</td>
<td></td>
</tr>
<tr>
<td>Penicillin</td>
<td>0.25</td>
<td>0.06–2</td>
<td>0.06</td>
<td>1/357 (13)</td>
<td></td>
</tr>
<tr>
<td>Tetracycline</td>
<td>16</td>
<td>0.01–0.16</td>
<td>0.25</td>
<td>2/357 (0.5)</td>
<td></td>
</tr>
<tr>
<td>Trimethoprim-sulfamethoxazole</td>
<td>4/76</td>
<td>0.5–0.95</td>
<td>0.5/0.95</td>
<td>0 (0)</td>
<td></td>
</tr>
<tr>
<td>Vancomycin</td>
<td>32</td>
<td>0.5–1</td>
<td>0.5</td>
<td>0 (0)</td>
<td></td>
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<tr>
<td>Ceftiofur</td>
<td>8</td>
<td>0.12–2</td>
<td>1</td>
<td>0 (0)</td>
<td></td>
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<tr>
<td>Enrofloxacin</td>
<td>4</td>
<td>0.03–0.25</td>
<td>0.12</td>
<td>0 (0)</td>
<td></td>
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<tr>
<td>Penicillin-novobiocin</td>
<td>4/8</td>
<td>0.06/0.06–0.06/0.12</td>
<td>0.03/0.06</td>
<td>0 (0)</td>
<td></td>
</tr>
<tr>
<td>Pirlimycin</td>
<td>4</td>
<td>0.12–1.0</td>
<td>0.5</td>
<td>0 (0)</td>
<td></td>
</tr>
</tbody>
</table>

*According to Clinical and Laboratory Standards Institute resistant break points for S aureus. †No Clinical and Laboratory Standards Institute resistant break point.

Table 2—Association of S aureus PFGE type with antimicrobial resistance phenotype among S aureus isolates obtained from 357 milk samples submitted for diagnostic bacteriologic testing from 24 dairy herds.

<table>
<thead>
<tr>
<th>S aureus type</th>
<th>No. of isolates</th>
<th>No. of resistant isolates %</th>
<th>No. of farms which types were isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>49</td>
<td>32 (65.3)†</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>174</td>
<td>0 (0)</td>
<td>13</td>
</tr>
<tr>
<td>3</td>
<td>73</td>
<td>0 (0)</td>
<td>11</td>
</tr>
<tr>
<td>4</td>
<td>5</td>
<td>4 (80.0)†</td>
<td>2</td>
</tr>
<tr>
<td>5</td>
<td>11</td>
<td>2 (18.2)</td>
<td>3</td>
</tr>
<tr>
<td>6</td>
<td>34</td>
<td>0 (0)</td>
<td>12</td>
</tr>
<tr>
<td>7</td>
<td>11</td>
<td>11 (100.0)†</td>
<td>1</td>
</tr>
<tr>
<td>Total*</td>
<td>357</td>
<td>49 (13.9)</td>
<td>24</td>
</tr>
</tbody>
</table>

*Of the 357 isolates, 308 (86.3%) were susceptible to all antimicrobials used in the study. †All resistant to penicillin only; resistant isolates obtained from farm B. ||Both resistant to tetracycline only; resistant isolates obtained from farm H. §Both resistant to erythromycin and penicillin; 1 isolate resistant to penicillin only; 1 isolate resistant to erythromycin only; all obtained from farm B.

Results

Three hundred fifty-seven of the original 454 S aureus isolates met the study criteria. Of the 97 isolates that were not considered, 81 were removed because they were duplicates and 16 were removed because their types had fewer than 5 isolates. The 357 isolates comprised 351 isolates from 19 farms in North Carolina (designated as farms A through P and R through T) and 6 isolates from 5 farms in Virginia (designated as farms Q and U through X). Via broth microdilution, antimicrobial agent susceptibilities to 14 antimicrobial agents that are important in veterinary and human medicine were determined. Of the 357 isolates, 308 (86%) were susceptible to all antimicrobial agents tested (Tables 1 and 2). Resistant phenotypes were infrequently detected and included penicillin (13%), erythromycin (3%), and tetracycline (0.5%). Nine of 10 erythromycin-resistant S aureus isolates also had coreistance to penicillin. The MIC<sub>50</sub> and MIC<sub>90</sub> for most antimicrobial agents tested were similar or within 1 doubling dilution of each other. A notable exception among S aureus isolates was high MIC<sub>90</sub> values, compared with MIC<sub>50</sub> values, for penicillin (1 μg/mL vs ≤ 0.06 μg/mL).

Pulsed-field gel electrophoresis was used to assess genetic relatedness among the S aureus isolates. By use of PFGE, 50 banding patterns were identified among the 357 S aureus isolates, which grouped into 7 types (Figure 1; Table 2). One hundred forty-nine of the 357 (42%) S aureus isolates grouped into 1 of 3 EF subtypes (1a1, 2a1, and 3a1 [data not shown]); these subtypes were included within PFGE types 1, 2, and 3, respectively. One hundred seventy-four of the 357 isolates (49%) were grouped into type 2; these 174 isolates were also the most genetically diverse, comprising 21 different subtypes. The PFGE clusters had good correlation with the antimicrobial susceptibility profiles. Staphylococcus aureus isolates with resistance to at least 1 tested antimicrobial agent were only found in PFGE types 1, 4, 5, and 7 in 32 of 49, 4 of 5, 2 of 11, and 11 seconds at 200 V for 22 hours at 14°C. Gels were stained in a 0.1% ethidium bromide solution for 15 minutes and destained in distilled water for 2 hours.

Stained gels were photographed, and the photographs were scanned into a computer. Scanned photographs were processed and dendrograms made by use of gel analysis and comparison software. Similarity coefficients were calculated and dendrograms constructed by use of the Dice coefficient and unweighted pair group method with arithmetic means, and dendrograms constructed by use of the Dice coefficient and unweighted pair group method with arithmetic means, respectively, with an optimization value of 0.50% and a position tolerance of 1.0%."
of 11 isolates, respectively (Table 2 and 3). Resistant isolates were found in milk samples from only 3 of the 24 farms. Among the 4 PFGE types that included resistant *S aureus* isolates, 2 (types 1 and 7) were found only in samples from farm B. *Staphylococcus aureus* isolates included in PFGE types 2, 3, and 6 were also found on farm B; these 3 PFGE types were composed of *S aureus* isolates that were susceptible to all 14 antimicrobial agents. *Staphylococcus aureus* isolates resistant to at least 1 antimicrobial agent from PFGE types 4 and 5 were found only in samples from 1 farm each (farm K and H, respectively). However, pan-susceptible *S aureus* isolates included in PFGE types 3 and 6 were also found in samples from farm H. Antimicrobial-susceptible PFGE types 2, 3, and 6 were more widespread, being detected in samples from 13, 11, and 12 of the 24 dairy farms, respectively. Among PFGE types, combined over farms, there was a significant \( P < 0.001 \) difference in the percentage of *S aureus* isolates resistant to at least one of the antimicrobial agents tested.

**Discussion**

Results of our study identified an association between *S aureus* isolates classified by PFGE and antimicrobial susceptibility phenotypes. Seven PFGE types were identified among the 357 *S aureus* isolates obtained from milk samples, and most of the isolates were susceptible to all antimicrobial agents that were tested. Antimicrobial-resistant *S aureus* isolates were only found among 4 PFGE types recovered from 3 of the 24 farms. Three PFGE types included isolates that were susceptible to all tested antimicrobials and had a broad geographic distribution, being recovered from multiple farms.

It seems reasonable to question whether particular genotypes correlate with specific antimicrobial agent-resistance phenotypes. Results of a limited number of studies indicate that antibiograms are, at best, minimally useful in describing the epidemiology of *S aureus* associated with mastitis in cattle. Antibiograms appear to be most useful only as part of a much larger typing scheme that includes other characteristics. For example, Aarestrup et al\(^\text{13}\) found that plasmid profile analysis and antibiogram typing were less discriminatory in classifying *S aureus* isolates from cows with mastitis in Denmark than were ribotyping, biotyping, and phage typing. Additionally, in a study completed by Sommerhäuser et al\(^\text{14}\), antibiogram typing separated 110 isolates from 7 herds into only 2 types and was much less discriminating than protein A polymorphism, coagulase gene typing, or PFGE methods, which identified 7, 19, and 17 types, respectively. Another study\(^\text{15}\) revealed variations in antibiograms of *S aureus* strains isolated from cattle with subclinical mastitis in Israeli dairy herds, but did not find correlations between antibiogram results, milk yield, or the severity of the disease as indicated by somatic cell concentrations.

However, contrasting data have also been reported. Rivas et al\(^\text{16}\) investigated 50 *S aureus* isolates from 12 herds in New York and determined that some *S aureus* ribotypes had marginal to significant associations with antimicrobial resistance profiles. Gohi et al\(^\text{17}\) typed 50 mastitis-causing strains of *S aureus* from sheep and rabbits in Spain using PFGE, plasmid pattern analysis, and antibiogram typing. Ovine strains were seldom resistant to antimicrobials, and few plasmids were detected, whereas rabbit strains were commonly resistant to antimicrobials, and multiple plasmids were detected per isolate. Those investigators also concluded that particular PFGE types could be further subdivided into antimicrobial-resistant or -susceptible isolates. Our results are in agreement with those of both aforementioned studies, in that it appears there is some type of association between bovine mastitis-causing *S aureus* PFGE type and antimicrobial susceptibility phenotypes.

The *S aureus* isolates investigated in the present study had little resistance to any of the antimicrobial agents tested. Of 357 *S aureus* isolates, 86% were pan-susceptible. Resistant phenotypes were infrequently detected and included resistance to penicillin (13%), erythromycin (3%), and tetracycline (0.5%). Resistance to penicillin appears to be the most commonly reported phenotype among mastitis-causing *S aureus* isolates from cattle.\(^\text{3,4,11,12,19}\) An increase in the incidence of penicillin-resistant *S aureus* over time has been identified in some countries, but major differences between countries do exist.\(^\text{16}\) For example, results of several studies\(^\text{3,11,12,19}\) have indicated that approximately 30% to 70% of mastitis-causing *S aureus* isolates from cattle are resistant to penicillin. Examples of exceptions include reports of resistance to penicillin in 97% of 319 Israeli *S aureus* isolates from cattle with chronic mastitis,\(^\text{32}\) approximately 15% of 105 *S aureus* isolates from cattle in Denmark,\(^\text{33}\) and 10% of 212 *S aureus* isolates from cattle in Canada.\(^\text{34}\)

<table>
<thead>
<tr>
<th>Susceptibility</th>
<th>PFGE type (No. of isolates)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1 (n = 48)</td>
</tr>
<tr>
<td>Resistant to penicillin</td>
<td>22</td>
</tr>
<tr>
<td>Resistant to erythromycin</td>
<td>0</td>
</tr>
<tr>
<td>Resistant to erythromycin</td>
<td>0</td>
</tr>
<tr>
<td>Resistant to tetracycline</td>
<td>0</td>
</tr>
<tr>
<td>Susceptible to all antimicrobials</td>
<td>17</td>
</tr>
</tbody>
</table>

*Antimicrobials used included amoxicillin-clavulanic acid, cephalothin, clindamycin, gentamicin, oxacillin, trimethoprim-sulfamethoxazole, vancomycin, cefotaxin, enrofloxacin, erythromycin, penicillin, tetracycline, penicillin-novobiocin, and pirlimycin.*

Table 3—Antimicrobial resistance patterns (grouped by PFGE type) of *S aureus* isolates obtained from 357 milk samples submitted for diagnostic bacteriologic testing from 24 dairy herds.
The finding of the present study (ie, resistance to penicillin detected in 13% of isolates) is similar to previous reports of resistance to penicillin in 14% and 10% of Staphylococcus aureus isolates. Overall, the geographic differences in penicillin susceptibility may reflect the presence of different S aureus clones within each country and may be associated with particular use patterns of β-lactam antimicrobial agents for treatment of mastitis in cows.29,30

With regard to the other antimicrobials tested, minimal resistance to erythromycin (3%) and tetracycline (0.5%) was detected, and all isolates were susceptible to amoxicillin–clavulanic acid, cephalothin, clindamycin, gentamicin, oxacillin, trimethoprim-sulfamethoxazole, vancomycin, cefotaxim, enrofloxacin, penicillin-novobiocin, and pirlimycin. Values for MIC\textsubscript{50} and MIC\textsubscript{90}, determined in our study were comparable to those in other studies26,31 for penicillin, oxacillin, cefotaxim, clindamycin, penicillin-novobiocin, enrofloxacin, erythromycin, gentamicin, cefotaxim, and pirlimycin. Interestingly, 9 of 10 erythromycin-resistant S aureus isolates were also co-resistant to penicillin, indicating that these isolates may harbor resistance determinants to these antimicrobial agents that may be linked. Resistance determinants in staphylococci can be located on the chromosome or extrachromosomally on plasmids or transposons.30,40 For example, the bla\textsubscript{Z} β-lactamase gene that confers penicillin resistance and several staphylococci-associated erythromycin resistance genes (eg, erm\textsubscript{A}, erm\textsubscript{B}, or erm\textsubscript{C}) have been identified on the chromosome and plasmids.30,40 Further research is warranted to characterize both the associated resistance mechanisms and the locations of the resistance elements within the S aureus isolates.

Clones, or genetically related isolates, are indistinguishable from each other by genotyping methods such as PFGE or ribotyping or are at least sufficiently similar that they are considered to be derived from a common parent organism.29 A strain has been defined as an isolate (or group of isolates) that has genotypic or phenotypic characteristics that can be used to distinguish it from other isolates of the same genus or species.29 In the present study, we used PFGE to assess genetic relatedness among the mastitis-causing S aureus isolates obtained from bovine milk samples. Fifty EPs were detected by use of SmaI. On the basis of similarity with an 80% cluster cutoff, isolates were assigned to 7 PFGE types. Of the 337 isolates, 49% grouped into type 2; these 174 isolates were also the most genetically diverse, comprising 21 different subtypes. The 7 PFGE types of S aureus isolated in our study varied in distribution among herds as well as in antimicrobial susceptibility profiles. Some types were widely distributed across herds. For example, S aureus isolates included in PFGE types 2, 3, and 6 were susceptible to all tested antimicrobial agents and were widely distributed, being present on >10 farms each. By contrast, other PFGE types included isolates that generally had more resistance and were further limited to 1 or a few farms.

Differing results have been reported regarding the pattern and behavior of types of S aureus as causes of mastitis within and among herds. A major portion of the variation is in the number of types within a given herd, which varies from only a few strains per herd to many strains from a given herd.34 Results of several studies have suggested a limited number or widely dispersed types of S aureus as causes of mastitis. For example, Fitzgerald et al23 studied 63 S aureus isolates from bovine sources from the United States and Republic of Ireland and determined that 1 common clone, ET3, was present worldwide. In Korea, Joo et al36 used PFGE to study isolates from 28 herds and determined that approximately two thirds (65%) of the genotypes were restricted to a single herd. In Israel, Younis et al32 detected 1 major type of S aureus within each of 15 herds, with the prevalence of this main type being 54% to 100% of total isolates in the same herd. Other studies31,36,37,39 detected PFGE types widely distributed across multiple farms, whereas PFGE types limited to 1 or a few farms were generally more resistant to antimicrobial agents.

Results of the present study support both scientific views with regard to the diversity of mastitis-causing S aureus isolates because several S aureus PFGE types were widely distributed across multiple farms, whereas other types were limited to 1 or only a few farms. One other interesting finding that would bear further study is that the widely distributed PFGE types identified in our study were susceptible to multiple antimicrobial agents, whereas PFGE types limited to 1 or a few farms generally had more resistance to antimicrobial agents. Overall, our data suggest that a limited number of S aureus clones appear to be responsible for most cases of mastitis.

Findings of additional studies26,31,48 provide further perspective on the issue of type variation in S aureus mastitis. Early work by Aarestrup et al48 revealed a large number of S aureus types among isolates obtained from 5 Nordic countries; however, only a few types predominated within each of the countries. Sommerhauser et al47 monitored S aureus populations in 7 herds during institution of a mastitis control program. Typing results and clinical observations indicated a difference in strains with respect to tendency to spread and ability to infect udders. Differences were also identified in behavior; in 3 herds, a predominant type was found with epidemiologic features of a contagious mastitis pathogen, whereas in other herds, there was no predominant type and the behavior of the S aureus organism was somewhat similar to that of an environmental pathogen.

Results of the present study support both scientific views with regard to the diversity of mastitis-causing S aureus isolates because several S aureus PFGE types were widely distributed across multiple farms, whereas other types were limited to 1 or only a few farms. One other interesting finding that would bear further study is that the widely distributed PFGE types identified in our study were susceptible to multiple antimicrobial agents, whereas PFGE types limited to 1 or a few farms generally had more resistance to antimicrobial agents. Overall, our data suggest that a limited number of genotypes were associated with most of the S aureus mastitis in cattle in North Carolina and Virginia from which milk samples were obtained and that antimicrobial-resistant phenotypes are associated with particular S aureus PFGE types. Investigators attempting to delineate the molecular epidemiology of S aureus–associated mastitis should
consider antimicrobial susceptibility phenotypes and virulence properties among S aureus genotypes to increase our understanding of S aureus–associated mastitis.

a. Becton, Dickinson & Co, Sparks, Md.
b. API-Staph identification system, bioMérieux Vitrek Inc, Hazelwood, Mo.
c. PASCO System, BD Biosciences, Sparks, Md.
d. Chef-DR II pulsed field electrophoresis system, Bio-Rad Laboratories Inc, Hercules, Calif.
g. EXACT option, PROC FREQ, SAS Institute Inc, Cary, NC.

References


