

Clinical Importance of Purulence in Methicillin-Resistant *Staphylococcus aureus* Skin and Soft Tissue Infections

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Background: The so-called community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) strains are more frequently susceptible to non- β -lactam antibiotics (including clindamycin) than health care-associated MRSA strains. We assessed whether predictive clinical characteristics of presumptive MRSA infections can be identified to guide choice of empiric antibiotic therapy.

Methods: A clinical syndrome was assigned to each inpatient and outpatient at the University of Chicago Medical Center with an MRSA infection in 2004 to 2005. Antimicrobial susceptibilities and molecular characteristics of MRSA isolates were assessed. Patients were stratified by lesion characteristics.

Results: Of MRSA isolates from 262 patients with purulent skin and soft tissue infections (SSTIs), 231 (88%) were susceptible to clindamycin, 253 (97%) contained staphylococcal chromosomal cassette *mec* (SCC*mec*) IV, and 245 (94%) contained Panton-Valentine leukocidin (*pvl*) genes, characteristics associated with community-associated MRSA strains. The presence of a purulent SSTI had a positive predictive value of 88% for a clindamycin-susceptible MRSA isolate. Among 87 isolates from a nonpurulent SSTI, 44% were susceptible to clindamycin and 34% contained *pvl* genes. In 179 invasive MRSA disease isolates, 33% were clindamycin-susceptible and 26% carried *pvl* genes.

Conclusions: A purulent MRSA SSTI strongly predicted the presence of a clindamycin-susceptible MRSA isolate. Presence of the *pvl* genes was almost universal among MRSA isolates causing purulent SSTIs; this was less common in nonpurulent SSTIs and other clinical syndromes. (J Am Board Fam Med 2009;22:647–654.)

Methicillin-resistant *Staphylococcus aureus* (MRSA) isolates were first recognized in the 1960s^{1,2} and

were largely confined to patients with certain health care exposures.³ During the past 10 years, novel MRSA isolates have been recognized among previously healthy members of the community who often lack these health care-associated (HA) MRSA risk factors.^{4,5}

Both clinical information and molecular isolate characteristics have been used to distinguish patients with HA MRSA and community-associated (CA) MRSA infections.⁶ HA MRSA isolates are typically resistant to multiple antimicrobial drugs, including clindamycin, and, in the United States, belong to multilocus sequence type (MLST) 5 and contain the methicillin resistance element staphylococcal chromosomal cassette *mec* (SCC*mec*) type II.⁷ In contrast, CA MRSA-type isolates are frequently susceptible to clindamycin (with some exceptions)^{8,9}; belong to MLST 8 or 1; contain SCC*mec* type IV or, rarely, type V; and bear the genes for the Panton Valentine leukocidin (*pvl*).^{10–12}

Skin and soft tissue infections (SSTIs) account for approximately 80% of infections caused by

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CA MRSA strains,¹³ although severe, life-threatening disease syndromes have also been described.^{5,14–16} HA MRSA-type isolates, in contrast, are seldom associated with purulent SSTIs but have instead been associated with catheter-related bacteremia, postoperative wound infections, and infections with onset 48 hours or more after hospitalization.¹⁷

Recent analyses of MRSA infections with onset in the community have revealed a complex epidemiology with both HA and CA MRSA strains circulating in the community.^{18–20} Moreover, nosocomial MRSA infections and MRSA infections among patients with health care-related risk factors have been caused by various isolate types, including CA MRSA strains.^{21–25}

The epidemiologic case definition of CA MRSA used by the Centers for Disease Control and Prevention (CDC) employs the lack of HA risk factors as follows: culture from an outpatient or within 48 hours of hospital admission and no history of hemodialysis, surgery, residence in a long-term care facility, or hospitalization during the previous 12 months; no indwelling catheter or percutaneous device at the time of culture; and no previous isolation of MRSA. We have shown, however, that application of this definition to a patient with an MRSA infection substantially underestimates the prevalence of infection caused by CA MRSA strains.²⁰ Although the CDC criteria do accurately identify a portion of the CA MRSA isolate disease burden in the community, many patients with health care exposures (who would be classified as having HA MRSA) have disease caused by CA MRSA strains. This underestimate of disease caused by CA MRSA strains is important because the CA MRSA isolates are often susceptible to more classes of antimicrobial drugs than are HA MRSA strains.

As the complex epidemiology of MRSA disease has evolved, we hypothesized that there might be identifiable clinical features that would distinguish disease caused by CA MRSA strains from disease caused by HA MRSA strains and that would allow clinicians to choose appropriate initial empiric therapy for putative MRSA infections. In particular, we hypothesized that the presence of a purulent SSTI might be a useful predictor of a CA MRSA strain with clindamycin susceptibility in the era of epidemic MRSA disease.

Methods

Setting

Pediatric and adult patients served by the inpatient, outpatient and emergency department facilities at the University of Chicago Medical Center (UCMC) were asked to participate in this study, as described previously.²⁰ The institution has 577 inpatient beds and 26,200 annual admissions. More than 71,000 visits are made to the emergency department annually. UCMC serves an inner city population and draws tertiary referrals from the surrounding region.

Microbiologic Studies

The UCMC Clinical Microbiology Laboratory prospectively identified all MRSA isolates collected between July 1, 2004, and June 30, 2005, from patients in all clinical settings, as previously reported.²⁰ The antibiotic susceptibility profile of each isolate was determined by Vitek testing (bioMérieux Vitek, Hazelwood, MO) for oxacillin, clindamycin, erythromycin, and gentamicin. Isolates that were resistant to erythromycin but susceptible to clindamycin by Vitek testing underwent a D test to detect inducible clindamycin resistance. All assays were performed in accordance with Clinical and Laboratory Standards Institute guidelines.²⁶

Molecular Studies

For all MRSA isolates, polymerase chain reaction assays for *mecA*, *SCCmec* type, *lukF-PV*, and *lukS-PV* (which encode *pvl*) were conducted and MLST was determined, as described previously.^{20,27,28}

Patient Information

A review of all consenting patients' electronic medical records—including hospital discharge summaries and radiographic, laboratory, pathology, operative, and outpatient clinic reports—was conducted and a clinical syndrome was assigned to each MRSA patient's isolate using all available data by 2 physician investigators (SEC and DG), as described previously.²⁰ The clinical syndrome and molecular type were independently assigned without knowledge of the susceptibility or the molecular testing results on the isolate. This study was approved by the Institutional Review Board of the Biological Sciences Division of the University of Chicago.

Definitions

In a previous report,²⁰ we stratified isolates according to the site from which the culture was obtained, including skin and soft tissue, respiratory, blood, bone and joint, and the urinary tract. For this investigation, each patient's isolate was assigned a more detailed syndrome classification.

Among patients with isolates from SSTIs, a lesion requiring incision and drainage or a lesion with spontaneously draining purulent fluid (as described by the treating physician) was defined as an "abscess." This group included treating clinician-designated diagnoses of abscesses as well as carbuncles, furuncles, boils, and cellulitis with purulent drainage. The diagnosis of "pustule" was assigned when an isolate was obtained from a pus-containing, 1 to 2 mm, superficial skin lesion. A chronic ulcer or an open pressure sore with nonpurulent drainage (if drainage was present) found in a patient with diabetes, peripheral vascular disease, or another underlying disease predisposing to these conditions was termed a "wound."

Patients with an isolate from the respiratory tract were assigned a diagnosis of ventilator-associated pneumonia, pneumonia with empyema, or other pneumonia. Any designation of MRSA pneumonia required the presence of respiratory symptoms such as cough, signs such as tachypnea and rales, consistent findings on a chest radiograph, and the prescription by the treating physician of an antibiotic effective against MRSA. Isolates colonizing the respiratory tract without attendant clinical illness and those obtained from the respiratory tract of patients with cystic fibrosis during routine surveillance were not included for analysis.

Some patients had several foci of infection. An identified anatomic focus of infection was assigned priority in designating the syndrome. For example, a patient with bacteremia and osteomyelitis was categorized as having osteomyelitis. Bacteremia without a focus of infection was termed "bacteremia without focus."

An isolate that was shown to be susceptible to clindamycin by Vitek testing (bioMérieux Vitek), resistant to erythromycin, and showed a positive D test was considered resistant to clindamycin.

Statistical Analysis

Categorical data were compared using the χ^2 or Fisher exact tests, as appropriate. All calculations were performed using Stata 9.0 (StataCorp, Col-

lege Station, TX). $P < .05$ was considered significant.

Results

The UCMC Clinical Microbiology Laboratories identified 1225 MRSA isolates during the study period. After excluding multiple isolates from the same patient, confirming the species as *S. aureus* and the presence of *mecA*, as well as excluding respiratory colonization or skin surveillance culture isolates and the 35 patients who declined to participate, 548 MRSA isolates were designated for further analysis.

Of these 548 MRSA isolates, 362 (66%) contained SCCmec type IV and 321 (89%) of these isolates were *pvl* positive. Three hundred sixteen (87%) of the isolates containing SCCmec type IV were susceptible to clindamycin. Among the 46 SCCmec type IV isolates resistant to clindamycin, 21 (46%) were detected by single-agent testing and 25 (54%) were detected by D test. Among SCCmec IV-bearing isolates, 319 (88%) were ST8, 20 (5%) were ST1, and 11 (3%) were ST5.

One hundred seventy-nine (33%) contained SCCmec type II. None of the 179 were *pvl* positive and 9 (5%) were susceptible to clindamycin. Among the isolates resistant to clindamycin, 152 (85%) were resistant on single-agent testing and 18 (10%) showed a positive D test. By MLST, 154 (86%) SCCmec II-bearing isolates were ST5, 14 (8%) were ST231, and only 3 (2%) were ST8.

Seven isolates had a SCCmec element that could not be classified as SCCmec types I through VI. None of them were *pvl* positive; all belonged to ST5 and were isolated from patients with one or more HA risk factors. One was susceptible to clindamycin.

A site of isolation and specific syndrome was identified for each of the 548 MRSA isolates, as seen in Tables 1 and 2. The designation of "abscess" strongly predicted the presence of a clindamycin-susceptible, SCCmec type IV-containing, *pvl* positive isolate (Table 2). Two hundred eight (89%) of the 234 MRSA abscess isolates were susceptible to clindamycin; SCCmec type IV was found in 229 of these (98%) and *pvl* genes were found in 223 (95%). Of the 229 SCCmec type IV-containing isolates found in abscesses, only 6 (2.6%) lacked the *pvl* genes.

Twenty-eight MRSA isolates were obtained from patients with a purulent SSTI that was not

Table 1. Characteristics of Methicillin-Resistant *Staphylococcus aureus* Isolates from Patients Without Skin and Soft Tissue Infections (n = 199)

Syndrome	Strains Tested (n = 199)	Strains Susceptible to Clindamycin	Strains Containing SCC <i>mec</i> IV	Strains with the <i>PVL</i> Genes
Respiratory tract*	63 (32)	13 (21)	16 (25)	13 (21)
Pneumonia	26	5 (19)	6 (23)	5 (19)
Empyema	4	2 (50)	2 (50)	2 (50)
Ventilator-associated pneumonia	19	4 (21)	5 (26)	4 (21)
Other respiratory isolates†	14‡	2 (14)	3 (21)	2 (14)
Bacteremia syndromes	60 (30)	14 (23)	19 (32)	11 (18)
Bacteremia	18	4 (22)	6 (33)	5 (28)
Line infection	38‡	8 (21)	10 (26)	4 (11)
Endocarditis§	4	2 (50)	2 (50)	2 (50)
Bone and joint	33 (17)	16 (48)	17 (52)	13 (39)
Osteomyelitis	18‡	7 (39)	9 (50)	7 (39)
Septic arthritis	12	7 (58)	7 (58)	5 (42)
Septic bursitis	3	2 (66)	1 (33)	1 (33)
Urinary tract	23 (12)	5 (22)	4 (17)	3 (13)
Other	20 (10)	9 (45)	9 (45)	5 (25)

All data provided as n (%).

*Isolates from the upper respiratory tract designated as colonization isolates were excluded; isolates from patients with cystic fibrosis were also excluded.

†Includes isolates obtained from patients with bronchitis, chronic laryngitis, sinusitis, tracheitis, and acute otitis media.

‡Isolates with an untypeable SCC*mec* element were included.

§As defined by modified Duke criteria.

||Including intra-abdominal fluid, deep intraperitoneal abscess, gall bladder, pericardial fluid, conjunctiva or the external ear canal. *PVL*, Pantan-Valentine leukocidin.

designated as an abscess. The syndromes for these patients were designated as a pustule, paronychia, pyomyositis, or felon. Twenty-three (82%) of these

nonabscess purulent MRSA SSTI isolates were susceptible to clindamycin; 24 (86%) contained SCC*mec* type IV and 22 (79%) were *pvl* positive.

Table 2. Characteristics of Methicillin-Resistant *Staphylococcus aureus* Isolates from Patients with Skin and Soft Tissue Infections (n = 349)

Type of Infection	Strains Tested (n = 349)	Strains Susceptible to Clindamycin	Strains Containing SCC <i>mec</i> IV	Strains with the <i>PVL</i> Genes
Purulent SSTI	262 (75)	231 (88)	253 (97)	245 (94)
Abscess	234	208 (89)	229 (98)	223 (95)
Pustules	16	14 (88)	13 (81)	13 (81)
Paronychia	4	3 (75)	4 (100)	3 (75)
Pyomyositis	6	4 (67)	5 (83)	4 (67)
Felon	2	2 (100)	2 (100)	2 (100)
Nonpurulent SSTI	87 (25)	38 (44)	44 (51)	30 (34)
Postoperative wound infection	42*	15 (36)	16 (38)	10 (24)
Wound	17	8 (47)	9 (53)	5 (29)
Wound and foreign body	18*	12 (67)	13 (72)	9 (50)
Burns	8	2 (25)	5 (63)	5 (63)
Impetigo	2	1 (50)	1 (50)	1 (50)

All data provided as n (%).

*Isolates with an untypeable SCC*mec* element were included.

SSTI, skin and soft tissue infection; *PVL*, Pantan-Valentine leukocidin.

Table 3. Characteristics of Methicillin-resistant *Staphylococcus aureus* Isolates from Patients with Purulent and Nonpurulent Skin and Soft Tissue Infections

Characteristic	Purulent SSTI* (n = 262)	Nonpurulent SSTI* (n = 87)	P
Contains SCCmec IV	253 (97)	44 (51)	<.001
Contains SCCmec II	9 (3)	41 (47)	<.001
Positive for <i>PVL</i> genes	245 (94)	30 (34)	<.001
Susceptibility to:			
Clindamycin	231 (88)	38 (44)	<.001
Ciprofloxacin	237 (90)	31 (36)	<.001
Gentamicin	261 (99)	77 (89)	<.001
Erythromycin	19 (7)	11 (13)	.1
Rifampin	260 (99)	83 (95)	.04
Trimethoprim-sulfamethoxazole†	232 (100)	31 (97)	.1

*Data provided as n (%).

†Two hundred thirty-two isolates from purulent SSTIs and 32 from nonpurulent SSTIs were tested for susceptibility to trimethoprim-sulfamethoxazole.

SSTI, skin and soft tissue infection; *PVL*, Panton-Valentine leukocidin.

When clinical data regarding abscess and non-abscess purulent SSTIs were pooled, 88% were caused by MRSA isolates that were susceptible to clindamycin, 97% contained SCCmec IV, and 94% were *pvl* positive. Eighty-nine percent of purulent SSTI isolates belonged to ST8, 5% belonged to ST1, and 4% belonged to ST5; 2% of isolates belonged to other MLST types. Overall, the positive predictive value of a purulent SSTI for clindamycin susceptibility was 88%. The high percent of clindamycin-susceptible strains in all purulent SSTI isolates did not differ significantly ($P = .37$) among isolates obtained from children or adults.

The 87 MRSA isolates from nonpurulent SSTIs were obtained from patients with infected wounds in the presence or absence of an associated foreign body (eg, nonpurulent drainage at a central venous catheter insertion site), a burn, impetigo, or a post-operative wound infection. The isolates from these patients contained SCCmec types II and IV with approximately equal frequency (47% and 51%, respectively); 38 (44%) were susceptible to clindamycin and 30 (34%) were *pvl* positive. ST5 was represented among 47% of nonpurulent SSTI isolates; ST8 was found in 41% of the isolates and 12% of isolates had other MLST types. Clindamycin susceptibility was not reliably predicted by clinical syndrome among patients with a nonpurulent SSTI (Table 3).

It is noteworthy that 97% of the SCCmec IV-containing isolates found in patients with purulent SSTIs contained the *pvl* genes compared with only

30 of 44 (68%) of the isolates that contained SCCmec IV obtained from patients with nonpurulent SSTIs ($P < .001$).

Among isolates associated with disease from the respiratory tract, bloodstream, bone or joint, or the urinary tract, we found that none of these non-SSTI syndromes were strongly associated with clindamycin susceptibility, *pvl* gene carriage, or SCCmec type IV (Table 1).

A patient with isolation of MRSA from a normally sterile body site—including blood, pleural fluid, joint/synovial fluid, or bone—was considered to have invasive MRSA disease.¹¹ Of the 95 isolates from patients with invasive MRSA disease, 31 (33%) were susceptible to clindamycin, 37 (39%) contained SCCmec type IV, and 25 (26%) carried the *pvl* genes.

Using the CDC case definition for CA MRSA, only 228 of 390 (58%) patients with *pvl*-positive isolates that contained SCCmec type IV would have been classified as CA MRSA, whereas 162 (42%) of the patients with *pvl*-positive isolates that contained SCCmec type IV would have been classified as HA MRSA cases.

Of the patients with a purulent MRSA SSTI (n = 262), 91 (35%) had a health care risk factor that would result in their isolate being classified as HA MRSA by the CDC definition. Of these 91 isolates, 74 (81%) were susceptible to clindamycin, 82 (90%) possessed the *pvl* genes, and 85 (93%) contained SCCmec type IV.

Table 4. Comparison of Purulent and Nonpurulent Skin and Soft Tissue Infections among Patients with One or More Health Care Risk Factors as Defined by the Centers for Disease Control and Prevention (n = 169)

Characteristic	Purulent SSTI* (n = 91)	Nonpurulent SSTI* (n = 78)	P
Contains SCCmec IV	85 (93)	36 (46)	<.001
Contains SCCmec II	6 (7)	40 (51)	<.001
Positive for <i>PVL</i> genes	82 (90)	23 (29)	<.001
Susceptible to clindamycin	74 (81)	32 (41)	<.001

*All data provided as n (%).

SSTI, skin and soft tissue infection; *PVL*, Panton-Valentine leukocidin.

In contrast, among the 87 isolates from patients with a nonpurulent SSTI, 78 (90%) were identified as HA MRSA by CDC criteria. Of these, 32 (41%) were susceptible to clindamycin, 36 (46%) contained SCCmec type IV, and 23 (29%) carried the *pvl* genes. Thus, even among those patients with a CDC-defined health care risk factor, those with a purulent MRSA SSTI were significantly more likely to have a clindamycin-susceptible, *pvl*-positive, SCCmec type IV isolate than patients with nonpurulent SSTIs ($P < .001$; Table 4).

Discussion

The presence of a purulent SSTI strongly predicted the presence of an MRSA isolate that was susceptible to clindamycin, contained SCCmec type IV, and possessed the *pvl* genes, regardless of the presence of CDC health care risk factors. In contrast, among the patients with nonpurulent SSTIs with respiratory, bone and joint, bloodstream, and urinary tract infections from which MRSA was isolated, strains containing both SCCmec types II and IV were responsible for infection.

The absence of a CDC health care risk factor also identified a subset of patients whose MRSA isolate was susceptible to clindamycin and contained SCCmec IV and the *pvl* genes.²⁰ However, the CDC criteria for CA MRSA identified a smaller subset of patients for whom clindamycin therapy would be effective.

Thirteen percent of strains that contained SCCmec type IV and 11% of MRSA isolated from purulent SSTIs were resistant to clindamycin. This rate of clindamycin resistance among CA MRSA strains is comparable with that reported by others,²⁹ but the rate varies geographically and temporally.³⁰ Clindamycin has been suggested as first-line therapy in the treatment of putative staphylococcal SSTIs in areas in which MRSA

strains comprise >10% of *S. aureus* infections.³¹ Clindamycin is often effective in the treatment of infections caused by MRSA strains possessing the inducible form of clindamycin resistance. However, a few failures have been reported,³² and for this reason we considered isolates with a positive D test as resistant to clindamycin. Alternatives for the empiric treatment of CA MRSA SSTIs must be considered should the rate of clindamycin resistance increase; some consider trimethoprim-sulfamethoxazole (TMP/SMX) as first-line therapy for this reason and because of its better tolerability in some cases,³³ although few reported data attest to its efficacy. Indeed, we found TMP/SMX susceptibility to be near universal in isolates tested from both purulent and nonpurulent SSTIs. Therapy with TMP/SMX is not recommended when infection caused by group A *Streptococcus* is likely.

Caution must be used when trying to interpret institution-specific rates of clindamycin resistance among MRSA isolates. Antibigrams often reflect susceptibility among pooled MRSA isolates and do not distinguish between isolates that contain SCCmec IV that are usually susceptible to clindamycin and those isolates that contain SCCmec II that are usually resistant to clindamycin. Institutions may find it helpful to stratify reporting of MRSA antibigrams by clinical syndromes. Such stratification would be helpful for practitioners when monitoring antibiotic susceptibility patterns and serve as a practical guide in the treatment options for MRSA infections.

It has been suggested that *pvl* might be an important virulence factor in CA MRSA disease. However, animal infection studies have provided contradictory results.^{34,35} Our data show near universality of *pvl* genes in isolates from purulent SSTIs and their substantially lower prevalence in all other MRSA clinical syndromes. Of note, we

also found that *pvl* genes were significantly more common among strains that contain SCCmec type IV found in purulent SSTIs than in those strains containing SCCmec IV found in nonpurulent SSTIs or non-SSTI syndromes. This suggests that *pvl* may not solely be a marker for SCCmec type IV strains but that it also may be important in the pathogenesis of purulent lesions characteristic of certain CA MRSA infections.^{35,36} Further studies are needed to delineate the role of *pvl* in the pathogenesis of MRSA infections.

Our study has several limitations. We only studied infections caused by MRSA and did not include those caused by methicillin-sensitive *S. aureus*. Our study represents clinical and isolate data from one center and may not be representative of other areas. The burden of community and hospital disease caused by MRSA was high in our center (approximately 60% of *S. aureus* isolates), but it is also high in many other US medical centers.³⁰ Antibiotic resistance rates among CA MRSA isolates may have changed since this study period. In addition, clinical features of methicillin-sensitive *S. aureus* and MRSA infections have been found to be indistinguishable.³⁷ Therefore, a putative *S. aureus* infection can be presumed to be MRSA and treated as such until culture results are obtained, but this approach may vary geographically.

We relied on physician documentation to assign a clinical syndrome category and assigned these syndromes retrospectively. For example, furuncles, carbuncles, and superficial primary cutaneous abscesses were grouped together as “abscess” because the detail provided by observer description made it difficult to stratify them further. Drainage from a postoperative wound infection or around a central venous catheter or another foreign body was often not described in sufficient detail. Therefore, if purulence was not described, we assigned the designation “nonpurulent.” It is not known if such drainage, if purulent, would also predict the presence of an isolate that was susceptible to clindamycin, that contained SCCmec IV, and that was *pvl* positive.

Conclusion

The diagnosis of a purulent, putative MRSA skin lesion predicts the presence of an MRSA isolate susceptible to clindamycin, bearing the SCCmec type IV element, and carrying *pvl* genes, regardless

of the presence of HA risk factors. Epidemiologic studies of MRSA infections that excluded patients with health care risk factors have probably underestimated the burden of clindamycin-susceptible MRSA disease.¹³ Recognition of a purulent SSTI will permit clinicians to select from a broader range of empiric antimicrobial drugs including clindamycin (when such therapy is deemed necessary), even among patients with CDC-defined, health care-related risk factors.

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