

# Evolutionary Models of the Emergence of Methicillin-Resistant *Staphylococcus aureus*

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**Five major lineages of methicillin-resistant *Staphylococcus aureus* (MRSA) have evolved since the introduction of methicillin for the treatment of infections caused by penicillin-resistant *S. aureus* in 1959. The clones of these lineages are responsible for the vast majority of hospital-acquired MRSA disease globally. We have constructed high-resolution evolutionary models for each lineage using a parsimony approach with 15 partial gene sequences from 147 geographically diverse isolates. On the basis of these models, we infer that MRSA has emerged at least 20 times upon acquisition of the methicillin resistance determinant, which is carried on a mobile genetic element called the staphylococcal cassette chromosome *mec* (SCC*mec*). The acquisition of SCC*mec* by sensitive clones was four times more common than the replacement of one SCC*mec* with another. Notably, SCC*mec* type IV was found in twice as many clones as any other SCC*mec* type, and it is this SCC*mec* type which is commonly found in clones from patients with community-acquired MRSA disease. Our findings suggest that most clones of MRSA arise by the acquisition of SCC*mec* type IV by methicillin-sensitive isolates.**

*Staphylococcus aureus* has a proven ability to adapt to the selective pressure of antibiotics. The emergence of strains with resistance to penicillin and methicillin was reported in 1948 and 1961, respectively (2, 17). In both cases, resistance developed within a few years of the introduction of the antibiotics into clinical medicine. At present, methicillin-resistant *S. aureus* (MRSA) strains with resistance to vancomycin are emerging (4, 13). This trend is a cause of great public health concern, as vancomycin is the antibiotic of last resort for the treatment of MRSA infections. There are indications that the epidemiology of MRSA may also be expanding, from being a major cause of hospital-acquired infections to becoming a cause of community-acquired infections (3, 14). Consequently, there has been keen interest in understanding how natural populations of MRSA have evolved over the past half century.

Our understanding of the evolution of MRSA has benefited from the development of molecular tools that allow characterization of both the strain phylogeny and the methicillin resistance determinant. Strain phylogeny can be resolved by multilocus sequence typing, which identifies a strain unambiguously on the basis of its sequence at seven housekeeping genes (8). The product of the *mecA* gene confers methicillin resistance and is carried on a mobile genetic element called the staphylococcal cassette chromosome *mec* (SCC*mec*). Four main types of SCC*mec*, which differ in size and composition, have been described for *S. aureus* (16, 22). The application of multilocus sequence typing and SCC*mec* typing to international collections of MRSA and methicillin-susceptible *S. aureus* (MSSA) isolates has revealed that (i) methicillin resistance has emerged in five phylogenetically distinct lineages, (ii) methicillin resistance has emerged on multiple occasions within a given phylogenetic lineage, and (iii) most MRSA disease is caused by a relatively small number of pandemic clones (9).

The frequency with which SCC*mec* is acquired in nature is unknown. Are new clones of MRSA sporadically emerging by a frequent acquisition of SCC*mec*, perhaps on a daily basis in the hospital setting, or is SCC*mec* a relatively stable locus that has been acquired on rare historical occasions? To address this question, we developed a high-resolution multilocus typing method that could detect SCC*mec* acquisitions among closely related isolates of *S. aureus*. The data allowed us to construct detailed evolutionary models upon which inferences regarding the acquisition of SCC*mec* could be based.

## MATERIALS AND METHODS

**Bacterial isolates.** A previous study of 912 MRSA and MSSA isolates found that methicillin resistance had emerged in five phylogenetically distinct lineages of *S. aureus* (9). We selected 136 of these isolates, which represented all hospital-acquired MRSA clones with an international distribution, plus related MRSA and MSSA isolates. We also included four MSSA isolates from Cuba and seven historically early MSSA isolates (5). Multiple isolates of the same clone were selected to be geographically diverse. A total of 147 isolates from 18 countries were included in this study, of which 92 were MRSA and 55 were MSSA. All isolates were stored at  $-80^{\circ}\text{C}$  and grown overnight on blood agar plates at  $37^{\circ}\text{C}$ .

**Sequence typing.** We selected seven *S. aureus* surface protein (*sas*) genes that encode the LPXTG cell wall attachment motif. The genes chosen were among the least well-characterized *sas* genes and have been named *sasA*, *sasB*, *sasD*, *sasE*, *sasF*, *sasH*, and *sasI* by Mazmanian et al. (24). *sasB* has homology with *fmfB*, a gene required for methicillin resistance (20). *sasE* has also been named *sai-1*, which encodes a 29-kDa surface protein (GenBank accession number AB042826), and *isdA*, an iron-responsive surface determinant (25). *sasH* has homology with a gene that encodes a 5' nucleotidase. On the basis of the COL genome sequence (<http://www.tigr.org>), *sasA* and *sasF* were located ~11 kb from each other, and all other *sas* loci were >50 kb from each other.

Polymorphic regions of the *sas* genes were identified by using the publicly available *S. aureus* genomic sequences, and primers were designed to amplify ~450-bp fragments (Table 1). The primers of Enright et al. (8) were used for multilocus sequencing of the seven housekeeping genes, *arcC*, *aroE*, *glpF*, *gmk*, *pta*, *tpi*, and *yqiL*. Primers were also designed to amplify the short sequence repeats of the *spa* gene (Table 1). Chromosomal DNA was isolated with a DNeasy kit (Qiagen). The PCR conditions were identical to those of Enright et al. (8), with a few modifications. The PCR mixtures used 10 pmol of the *sas*- and housekeeping gene-specific primers per  $\mu\text{l}$  and 100 pmol of the *spa*-specific primers per  $\mu\text{l}$ . PCR annealing temperatures were  $45^{\circ}\text{C}$  for the *sas* genes and  $55^{\circ}\text{C}$  for the housekeeping and *spa* genes. Sequencing of the DNA of both

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TABLE 1. PCR primers

Primer pair	Sequence (5'-3')
Primary <i>sas</i> -specific primers	
sasAF sasAR	TCAACATCCTCAAAGAATACTACA ATGCGTACTTAAGCCACCAATAC
sasBF sasBR	GTTGCAGCGCTTGTGACT ATTTTTGAGATTTCTTCGTTTTTA
sasDF sasDR	GGCGGAGTAGTACCACAAGGAA AATGCTAAGAATAACCCAGACT
sasEF sasER	TTACAATGCAAACAATCAAGA GTTTAGGCGTTTCGTTATGTTTT
sasFF sasFR	GGATAGCAAAGACAATAAAAGTTC TGATATGTGTAATGTTGCGTTGAG
sasHF sasHR	CGCACCAACTAACAAACCAACTAC TACGCCAATAATTCCATAACGA
sasIF sasIR	ATACTATCACTTTTTTCAGCATCAA TCATTCTTTTTATCGTTAGTATTA
Alternative <i>sas</i> -specific primers	
sasDF4 sasDR4	ATTTTGTGCAATTTCTTT TCACACGATTTTTCTATTAT
sasEF2 sasER2	ACCCTGGTAAAGTGATT CTAAAAGGGCAAGTGTT
sasIF3 sasIR3	CAAACACTGCGAAAACTATCCT TTTACCTTTATCATTTTTTCATTT
<i>spa</i> -specific primers	
spa1095u spa1517d	AGACGATCCTTCGGTGA CAGCAGTAGTGCCGTTTG
<i>mec</i> -specific primers	
mec 3490u 4110Ad 4110Bd	ATGATTCAATGCCTAACCTAATCG (common) GAATTATAACTGGGAATATTTTAAATCCCA (class B <i>mec</i> ) CTTTTTGTTTCAAAGTCATACTATTTTCAAC (class A <i>mec</i> )

strands was performed as described by Enright et al. (8) with an ABI 3700 automated sequencer (PE Applied Biosystems).

For the *sas* and housekeeping genes, unique sequences defined alleles, and the unique series of alleles at each locus defined a sequence type (ST). For the *sas* genes, a database of alleles was compiled and is available upon request. For the housekeeping genes, the alleles were identified by using the MLST database, available at <http://www.mlst.net>. The *spa* repeats were characterized as described by Shopsin et al. (31). The resolution obtained by different typing methods was compared by using Simpson's index of diversity ( $D$ ) and was calculated as  $1 - \{[1/N(N-1)]\sum n_i(n_i-1)\}$ , where  $n_i$  is the number of isolates belonging to the  $i$ th ST and  $N$  is the total number of isolates in the sample (12, 15).

**SCC*mec* typing.** SCC*mec* types were assigned by PCR analysis of the *ccr* and *mec* genes, as described by Okuma et al. (27). The primers of Ito et al. (16) were used for PCR of the *ccr* genes, and new primers (Table 1) were used for PCR of the *mec* genes. Structural variants of SCC*mec* were detected by the multiplex PCR analysis of Oliveira and de Lencastre (28).

**Nomenclature.** This study used a newly proposed nomenclature for MRSA clones that was based on a combination of the STs at seven housekeeping genes and the SCC*mec* type (9). For example, an MRSA clone of ST250 and SCC*mec* type I is referred to as ST250-MRSA-I, and an MSSA clone of ST8 is referred to as ST8-MSSA.

**Phylogenetic analyses.** The alleles of the *sas* and the housekeeping genes were aligned by using the CLUSTALW program (33) with default parameters, fol-

lowed by manual inspection. Insertion and deletion polymorphisms were ignored during phylogenetic analyses. MEGA software (version 2.0) (21) was used to calculate  $d_s/d_n$  ratios by the modified Nei and Gojobori method.  $d_s/d_n$  is the ratio of the number of synonymous or silent nucleotide changes ( $d_s$ ) to the number of nonsynonymous or amino acid-replacing nucleotide changes ( $d_n$ ). The PAUP\* program (version 4.0b10) (32) was used to construct neighbor-joining (NJ) and maximum-parsimony (MP) trees. NJ trees were constructed by using the absolute number of nucleotide differences between STs. MP trees of all STs were constructed with a heuristic search and random addition of taxa. MP trees of specific lineages were constructed with a branch-and-bound search to ensure that all most parsimonious trees were found. Bootstrapping was performed with 1,000 replicates.

**Nucleotide sequence accession numbers.** The *sas* gene sequences reported in this study have been deposited in GenBank under accession numbers AY175407 to AY175464.

## RESULTS

**Development of a high-resolution multilocus typing method.** To develop a multilocus typing method that could detect SCC*mec* acquisitions among closely related isolates, we se-

TABLE 2. Nucleotide sequence variation among alleles of *sas* and housekeeping loci

Gene	Sequence length (bp)	No. of alleles	No. of polymorphic sites <sup>a</sup>	No. of informative sites <sup>a</sup>	$d_s/d_n$
<i>sas</i> genes					
<i>sasA</i>	462	8	59	51	3.9
<i>sasB</i>	462	7	40	20	9.9
<i>sasD</i>	453	7	11	2	
<i>sasE</i>	450	7	41	28	2.0
<i>sasF</i>	439	14	34	24	
<i>sasH</i>	467	8	36	18	5.2
<i>sasI</i>	452	7	43	25	3.0
Housekeeping genes					
<i>arcC</i>	456	6	7	4	6.3
<i>aroE</i>	456	14	19	10	3.4
<i>glpF</i>	465	8	11	4	3.8
<i>gmk</i>	429	10	13	7	6.5
<i>pta</i>	474	9	11	4	5.3
<i>tpi</i>	402	11	13	6	4.0
<i>yqiL</i>	516	9	13	4	4.3

<sup>a</sup> Excludes insertions and deletions at *sasD* and *sasF*.

quenced fragments of seven *S. aureus* surface protein (*sas*) genes, which we expected would accumulate variations more rapidly than the seven housekeeping genes. We sequenced a similar number of nucleotides ( $P = 0.710$ , Mann-Whitney U test) and observed a similar number of alleles ( $P = 0.165$ ) for the *sas* and housekeeping genes (Table 2). However, the *sas* genes provided significantly more polymorphic sites ( $P = 0.011$ ) and parsimony-informative sites ( $P = 0.026$ ) than the housekeeping genes (Table 2). The variation found in *sasD* appeared to be similar to that found in the housekeeping genes. *sasD* and *sasF* both presented alleles with insertion or deletion polymorphisms.

There is reason to suspect that variations in genes encoding surface proteins may be influenced by the selective pressure of the host immune system, but we found no evidence of diversifying selection in the fragments sequenced. When all alleles were considered, the proportion of synonymous nucleotide changes was greater than the proportion of nonsynonymous nucleotide changes (see the  $d_s/d_n$  ratios in Table 2). There were no differences in the  $d_s/d_n$  ratios for the *sas* and housekeeping genes ( $P = 0.530$ ).

The short sequence repeats of the *spa* gene, which encodes immunoglobulin G-binding protein A, provides a highly discriminatory sequence-based method for the typing of *S. aureus* (31). We compared the resolutions of the different typing methods using Simpson's index of diversity, which takes into account the observed numbers of STs and their frequencies of occurrence (12, 15). The diversity resolved by the *spa* repeats was significantly greater than the diversity resolved by either multilocus method (i.e., the 95% confidence intervals did not overlap), and the diversities resolved by the multilocus methods were similar to each other (Table 3). However, the multilocus methods in combination provided a significantly greater resolution than either multilocus method by itself and a resolution similar to that obtained with the *spa* repeats (Table 3).

TABLE 3. Resolution of sequence-based typing methods

Typing method	No. of types	% Most frequent type	Index of diversity (95% CI <sup>a</sup> )
<i>spa</i> repeats	48	11.0	0.959 (0.948–0.970)
<i>sas</i> genes	33	14.4	0.929 (0.927–0.932)
Housekeeping genes	45	15.6	0.927 (0.909–0.946)
Multilocus methods ( <i>sas</i> + housekeeping)	66	11.0	0.965 (0.953–0.977)
All methods ( <i>spa</i> + <i>sas</i> + housekeeping)	84	5.1	0.988 (0.983–0.993)

<sup>a</sup> CI, confidence interval.

**Construction of evolutionary models.** To compare the phylogenetic signals of the *sas* and housekeeping genes, we constructed NJ and MP trees based on the 3,185 nucleotides of the *sas* genes and the 3,198 nucleotides of the housekeeping genes. Previously, it was found that MRSA had emerged in five phylogenetically distinct lineages called clonal complexes (CCs) (9). The *sas* and housekeeping genes classified all but one isolate of ST36 into the same CCs on both NJ and MP trees with high bootstrap support (Fig. 1). The bootstrap support for the CCs was generally higher for the trees based on the *sas* genes, presumably because these genes provided the most polymorphisms (Table 2).

The branching order between the CCs significantly differed between the *sas* and housekeeping genes, as witnessed by the high bootstrap support for conflicting arrangements of CCs (Fig. 1). Thus, no inferences regarding the relationships between CCs are made with these data. Of note, the housekeeping genes grouped the pandemic clones of ST8, ST250, and ST239 and their variants into a single lineage, called CC8 (Fig. 1). The *sas* genes grouped ST8 and ST250 into the same lineage but clearly showed that ST239 was a diverged branch of CC8. Moreover, the *sas* genes were identical for ST235 and some isolates of ST8, but these clones differed at five of seven housekeeping genes (Fig. 1).

To investigate the branching order within CCs, we combined the nucleotide sequences of the 14 *sas* and housekeeping genes into a single data set with 6,383 nucleotides. This total evidence approach is justified, given that the data classified the isolates into the same CCs, with the two exceptions noted above. MP trees were constructed for each CC by using the combined data set. CC5, CC8 (consisting of separate trees for ST8-ST250 and ST239), and CC45 yielded single MP trees with perfect consistency. CC22 yielded two MP trees that differed in the placement of a single ST. CC30 yielded 17 MP trees. Evolutionary models for each CC were constructed by expanding the MP trees to include SCCmec type and *spa* type and assuming the fewest additional changes to the trees (Fig. 2).

Of the 59 steps depicted in our evolutionary models (Fig. 2), the housekeeping genes and SCCmec type resolved 21 steps, the *spa* repeats and *sas* genes resolved 24 steps, and a combination of these two categories of typing methods resolved 14 steps. While the *spa* repeats and *sas* genes provided a modest but significant increase in typing resolution of 6.1% (98.8% diversity – 92.7% diversity) over that of the housekeeping genes (Table 3), these markers provided a large increase in phylogenetic resolution of 40.7% (24/59 steps, respectively)

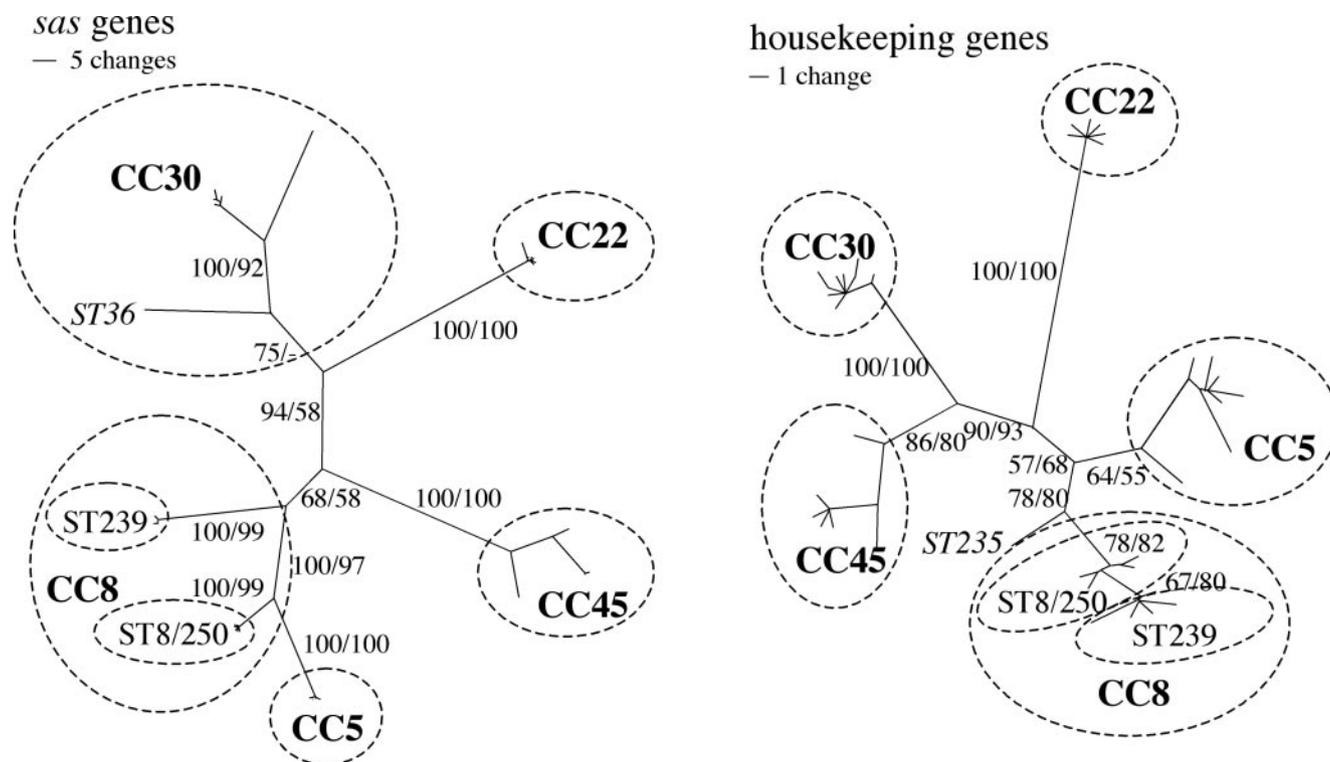


FIG. 1. Phylogenetic trees of STs based on *sas* and housekeeping genes. The trees were constructed with the NJ algorithm and were based on the absolute number of nucleotide differences between STs. The scale shows the relative amount of change along branches. The trees were also constructed by MP analyses. The numbers on the branches refer to the NJ or MP bootstrap percentages. The two isolates of ST36 and ST235 that grouped anomalously on the trees are in italics. The five major CCs are circled.

over that provided by the housekeeping genes and *SCCmec* type.

**Evolution within CC5 and CC8.** CC5 and CC8 represented the most diversified lineages of MRSA and contained the most pandemic clones (Fig. 2, left panel). The putative ancestors of these lineages were the STs that had the largest number of single-step variants (i.e., single-locus variants and single-nucleotide variants) and were represented by historically early MSSA isolates (5). Within CC5, we propose that all four *SCCmec* types were acquired once by ST5-MSSA ancestors (Fig. 2, left panel). Within CC8, we propose that three *SCCmec* types were acquired on multiple occasions (Fig. 2, left panel).

Of note, we propose that ST254-MRSA-I, represented by two isolates from the United Kingdom from 1962 and 1965, respectively, arose independently of the archaic clone (30) in the early days of MRSA emergence. It is simpler to assume that ST254-MRSA-I evolved from ST8-MSSA by acquiring *SCCmec* type I and point mutations in *aroE* and *sasF* rather than to assume that ST254-MRSA-I evolved from ST250-MRSA-I, which would require a back-mutation at *yqiL* and the point mutations in *aroE* and *sasF*. To our knowledge, there are no known isolates of ST254-MSSA, but this possibility is indicated by dashed lines in Fig. 2 (left panel).

The integration of pUB110 into the *SCCmec* locus (28) gave rise to the variant *SCCmec* types IA and IVA (Fig. 2, left panel). The lineage leading to the Irish-1 clone is marked by several uncharacterized modifications in the *SCCmec* locus.

ST8-MRSA-IV from Australia and Ireland have the *ccr* and *mec* genes characteristic of *SCCmec* type IV (27) but amplify only *mecA* in a multiplex PCR (28). Likewise, ST8-MRSA-II from the United Kingdom and Ireland, the Irish-1 clone, have the *ccr* and *mec* genes characteristic of *SCCmec* type II but either lack the *kdp* gene characteristic of *SCCmec* type II or have a multiplex PCR pattern identical to that of *SCCmec* type IV. Thus, the evolutionary pathways of this lineage remain unclear, as indicated by the dashed lines in Fig. 2 (left panel).

**A hypothesis for the origin of ST239.** It was noted that ST239 represents a distinct branch within CC8 (Fig. 1). This lineage includes numerous clones such as the epidemic methicillin-resistant *S. aureus* type 1 (EMRSA-1); EMRSA-4; EMRSA-7; EMRSA-9; EMRSA-11; and the Brazilian, Portuguese, and Vienna clones (7, 19, 23, 34). The proposed path leading from ST8 to ST239 involved the acquisition of *SCCmec* type III and alleles at *arcC*, *sasA*, *sasD*, *sasF*, *sasH*, and *spa* (Fig. 2A). Surprisingly, with the exception of *sasD4*, the derived alleles were exclusive to ST239 and ST30 and their descendants; *sasD4* also occurred in two isolates from CC22. These data suggest either that parallel evolution of multiple genes had occurred in unrelated lineages of *S. aureus* or that recombination had occurred. We favor the latter hypothesis for two reasons. First, the *sasD4* allele had two characteristic deletions of 18 and 42 nucleotides, respectively, which are unlikely to arise independently in different lineages. Second, the genes *arcC*, *sasF*, *sasA*, *sasH*, *spa*, and *sasD* are contiguous on the COL genome sequence and are centered around the

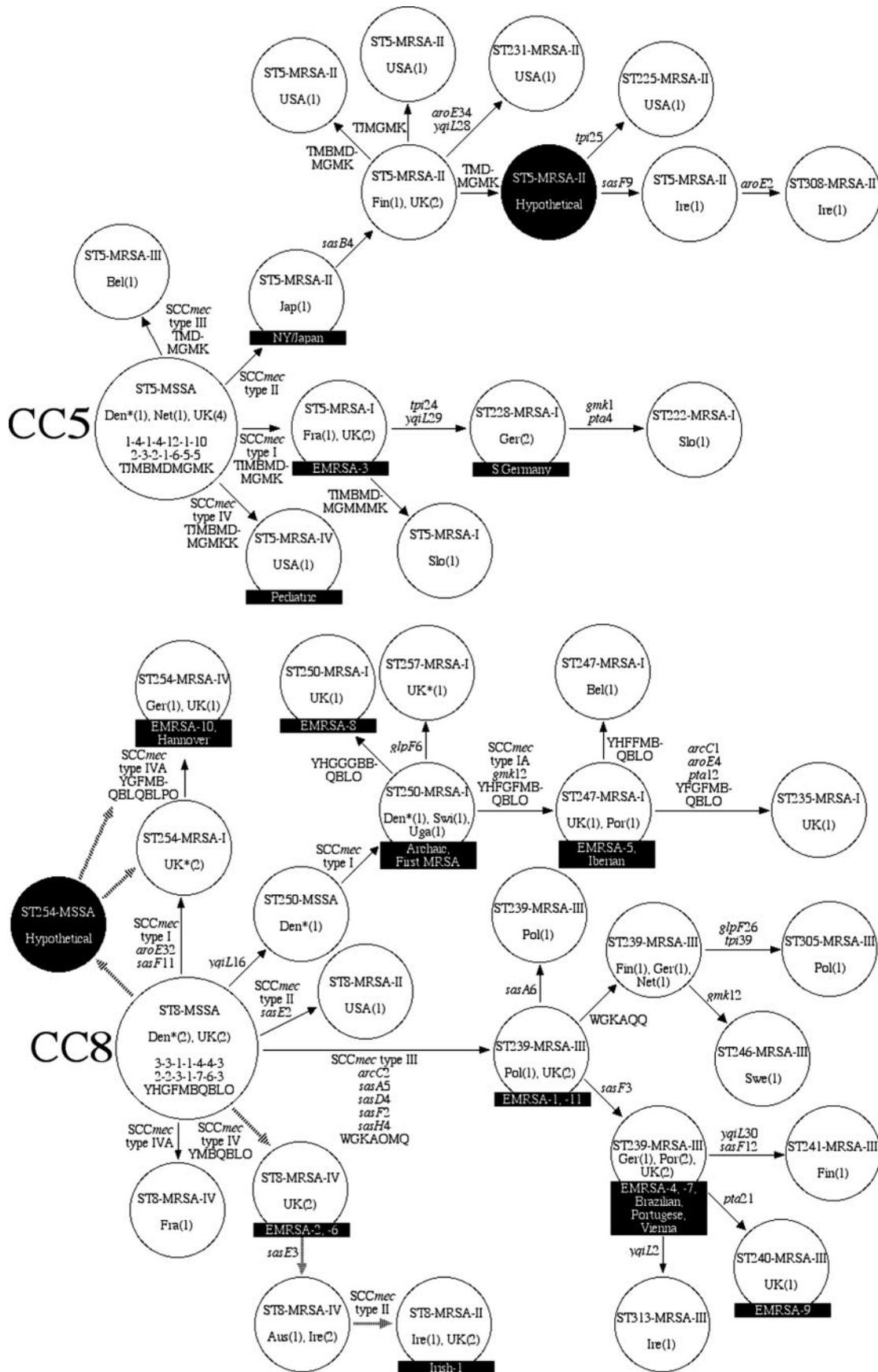


FIG. 2

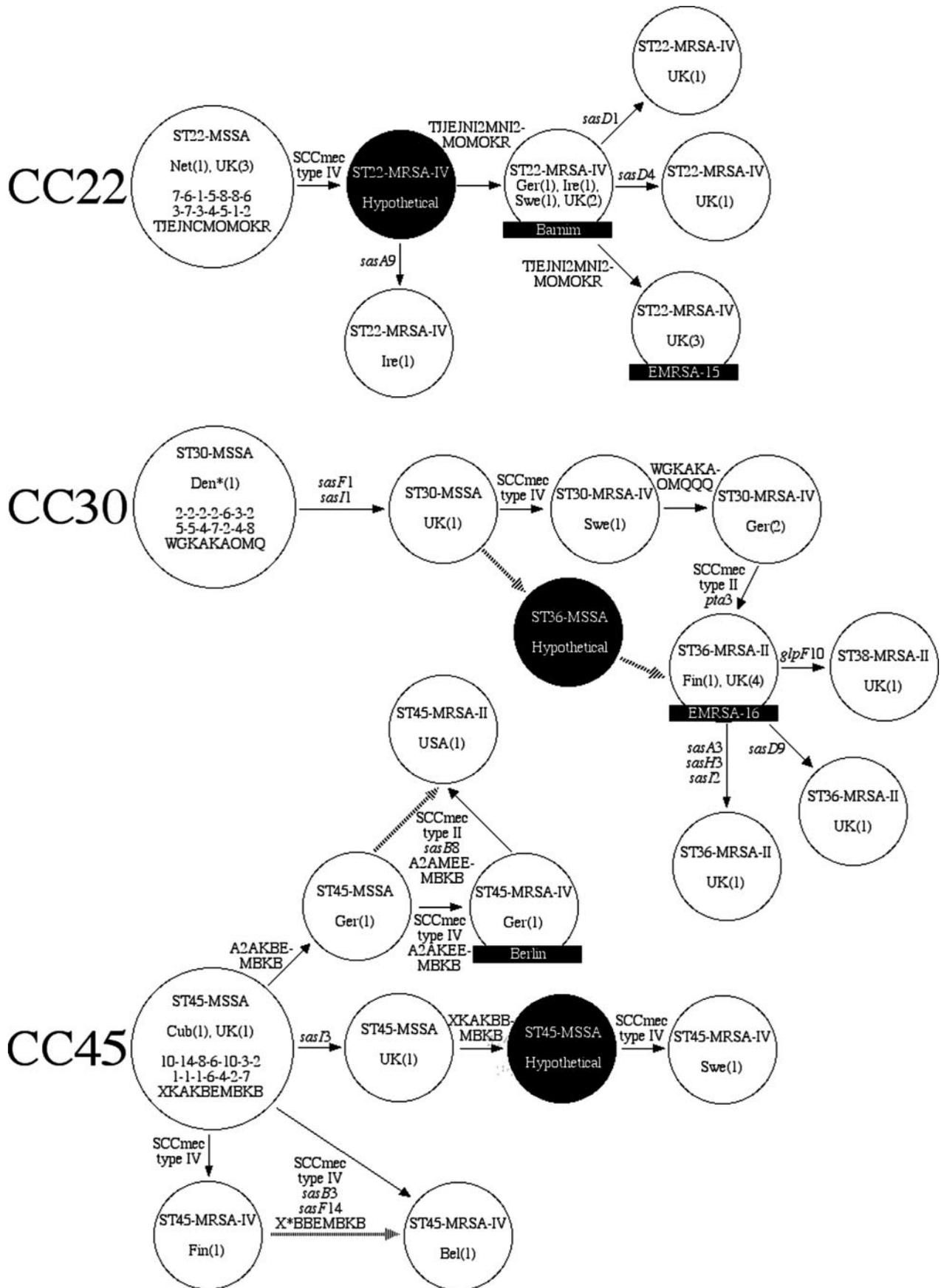


FIG. 2—Continued.

TABLE 4. Characteristics of SCCmec

SCCmec type	Size of element (kb)	No. of inferred acquisitions by:		No. of variants
		MSSA clones	MRSA clones	
I	34	3		2
II	52	2	3	5
III	67	2		7
IV	21–24	9	1	3

origin of replication. We propose that ST239 arose from a single recombination event that involved the exchange of >200 kb of contiguous DNA between ST30 and ST8. The donor of SCCmec type III remains unknown; the only clone to carry this element besides the clones in the ST239 branch was a single isolate from ST5 (Fig. 2, left panel).

**Evolution within CC22, CC30, and CC45.** CC22, CC30, and CC45 represent less diversified lineages of MRSA strains mostly isolated from Europe (Fig. 2, right panel). The putative ancestors for CC22 and CC45 were the STs that had the largest number of single-step variants. No historically early MSSA isolates were available for these lineages. The putative ancestor for CC30 was more difficult to assign. ST30 had one less single-step variant than ST36 but was represented by an historically early MSSA isolate (5) and shared *sas* alleles with ST39, presumably an old clone within CC30 that has also evolved several single-step variants (10). Thus, our evolutionary model for CC30 is based on the assumption that ST30 should be considered ancestral.

Within CC22, we propose that SCCmec type IV was acquired once (Fig. 2, right panel). Within CC30, we propose that both SCCmec types II and IV were acquired once (Fig. 2, right panel). To our knowledge, there are no known isolates of ST36-MSSA, but this possibility is indicated by dashed lines in Fig. 2 (right panel). Within CC45, we propose that SCCmec type IV was acquired four times and that SCCmec type II was acquired once (Fig. 2, right panel). Alternative evolutionary hypotheses within CC45 are indicated by dashed lines in Fig. 2 (right panel).

**Patterns of acquisition and variation of SCCmec.** Our evolutionary models indicate that a minimum of 20 acquisitions of SCCmec have occurred in *S. aureus*. There were 16 acquisitions of SCCmec by an MSSA clone and 4 putative reacquisitions of SCCmec by an MRSA clone (Table 4). There were 10 acquisitions of SCCmec type IV and 10 acquisitions of the other SCCmec types (Table 4). Nearly half (9 of 20) of all acquisitions involved an MSSA clone that acquired SCCmec type IV.

SCCmec variants IA and IVA have been characterized by others (28) and were included in our evolutionary models. We note that there were two conflicts in the classification of SCCmec types based on the *ccr* and *mec* gene (16, 27) and multiplex PCR (28) analyses. These cases involved isolates of SCCmec types II and IV and types II and III, which differed in the *ccr* and *mec* analyses but which had identical multiplex patterns (data not shown). We observed a total of 17 variants of SCCmec (Table 4). The largest SCCmec types, types II and III, presented the most STs. As further work is necessary to characterize the new variants, we have not included them in our evolutionary models.

## DISCUSSION

For a decade it has been recognized that methicillin resistance has emerged multiple times within *S. aureus* (11, 26), but the frequency of resistance acquisition and any underlying historical patterns have remained unknown. Our previous work (9) has shown that MRSA has arisen on multiple occasions within successful MSSA lineages, but we were unable to resolve the full evolutionary history of MRSA since multiple acquisitions of the same SCCmec type by a single ST could not be discerned. In this work, we augmented the standard multilocus sequence typing scheme with an additional set of highly variable *sas* genes which allowed us to resolve a more complete evolutionary history of MRSA.

We propose several novel hypotheses for the emergence of MRSA. First, we propose that two MRSA clones (ST247, ST257) emerged from the first MRSA clone (ST250) by stepwise evolution and that one MRSA clone (ST254) emerged independently within 4 to 5 years of the first reported isolation of MRSA. These data make a case for multiple emergences of MRSA early in its history. Second, we propose that ST239 was created by the exchange of >200 kb of contiguous DNA between ST30 and ST8. This hypothesis is supported by partial sequencing of an additional 26 genes (D. A. Robinson and M. C. Enright, submitted for publication). ST239 and its descendants represent a phylogenetically distinct and clinically important branch within CC8. de Lencastre and colleagues (29) have reported that clones of ST239 are among the most prevalent in Portuguese hospitals and were recently found to be highly prevalent in hospitals in China and Taiwan (6). Third, we propose that CC22, CC30, and CC45 represent major lineages of MRSA that account for 8 of 20 SCCmec acquisitions. CC45, in particular, has not been widely recognized as a major lineage of MRSA, but we found that isolates of CC45

FIG. 2. Proposed evolutionary models for the emergence of MRSA in CC5 and CC8 (left panel) and CC22, CC30, and CC45 (right panel). The models were based on MP analyses of the combined *sas* and housekeeping genes. The SCCmec type and the *spa* type were added to the models by assuming the fewest additional changes to the trees. Only those branches on which MRSA isolates have emerged are shown. Large circles represent ancestral clones. Smaller circles represent descendant clones. Arrows indicate the directions and relative amounts of change between isolates. Names and countries of isolation are given for all clones. The numbers in parentheses after the country names represent the numbers of clones. Full genotypes are given for the ancestors with their housekeeping gene alleles at *arcC-aroE-glpF-gmk-pta-tpi-yqiL* (top line), *sas* gene alleles at *sasA-sasB-sasD-sasE-sasF-sasH-sasI* (middle line), and *spa* repeats (bottom line). Previously named clones are indicated in black boxes. Dotted lines represent alternative evolutionary hypotheses. Isolates from the 1950s and 1960s are indicated by asterisks next to the country of isolation; all other isolates are from the 1980s and 1990s. The country abbreviations are as follows: Aus, Australia; Bel, Belgium; Cub, Cuba; Den, Denmark; Fin, Finland; Fra, France; Ger, Germany; Ire, Ireland; Jap, Japan; Net, Netherlands; Pol, Poland; Por, Portugal; Slo, Slovenia; Swe, Sweden; UK, United Kingdom; USA, United States.

were geographically distributed in both the Eastern and the Western Hemispheres and that the lineage has acquired *SCCmec* four or five times.

We provide the first estimate of the number of times that *SCCmec* has been acquired by *S. aureus* in nature. In most cases, *SCCmec* is retained as the lineages evolve. Our data suggest that the spontaneous excision of *SCCmec* does not occur frequently from an evolutionary perspective. We propose that on four occasions *SCCmec* was reacquired by an MRSA clone. The proposed evolutionary events leading to the Irish-1 clone within CC8 are unclear. However, the proposed evolutionary events leading to the Hannover clone within CC8 and the EMRSA-16 clone within CC30 are clearer, and there are no known MSSA intermediates to support an alternative evolutionary path. The proposed acquisition of *SCCmec* type II by an *SCCmec* type IV clone within CC45 can be interpreted differently and requires testing. A mechanism for reacquisition of *SCCmec* could involve the loss of one *SCCmec* type followed by acquisition of another *SCCmec* type within a short time period. Although experiments have shown that the recombinase genes encoded by *SCCmec*, *ccrA*, and *ccrB* are sufficient to transfer the element from a multicopy plasmid into the chromosome in a site-specific and orientation-specific manner (18), the precise mechanism by which *SCCmec* is transferred in nature is not known. We note that our estimate provides a lower bound of the actual number of acquisitions that have occurred in nature. The estimate will undoubtedly increase as more isolates from patients with community-acquired disease and more isolates from a wider geographic area are studied.

The observation that the largest *SCCmec* elements, types II and III, had the most structural variants, as detected by PCR, might be explained by the fact that these elements carry more copies of transposable elements, such as *IS431* and *Tn554* (16). The activities of these transposable elements might play a role in remodeling the structure of *SCCmec* and, thus, lead to a greater number of structural variants. The observation that the smallest *SCCmec* element, type IV, had been acquired most often might be explained by a size dependence on the efficiency of DNA transfer. Smaller *SCCmec* elements may simply transfer more efficiently than larger *SCCmec* elements.

Alternatively, *SCCmec* type IV may have been acquired and subsequently retained in *S. aureus* most often because it has been the selectively favored element of methicillin resistance. Hiramatsu and colleagues (22, 27) suggest that *SCCmec* type IV may have a lower cost on fitness because it carries only the structural and regulatory genes for methicillin resistance and the recombinase genes for movement of the element. In contrast, *SCCmec* types I to III can carry additional genes, such as those encoding resistance to non- $\beta$ -lactam antibiotics and heavy metals (16). The combination of smaller size and lower cost on fitness may make *SCCmec* type IV the selectively favored element for transfer among all *S. aureus* isolates.

*SCCmec* type IV was first discovered in recent studies that examined isolates of community-acquired MRSA (1, 22). Several new clones that carry *SCCmec* type IV have also been identified from samples from patients with community-acquired MRSA (27). Our results, based on inferences from evolutionary models, show that *SCCmec* type IV is also the most frequently acquired element within the five major lineages responsible for most hospital-acquired MRSA infec-

tions. While the prevalence of disease caused by clones that carry *SCCmec* types I to III at present may be higher than that caused by clones that carry *SCCmec* type IV, the more frequent acquisition of *SCCmec* type IV has markedly increased the genetic diversity of MRSA and suggests that the prevalence of disease caused by clones that carry this element will increase.

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