

# Transmission and Microevolution of USA300 MRSA in U.S. Households: Evidence from Whole-Genome Sequencing

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**ABSTRACT** Methicillin-resistant *Staphylococcus aureus* (MRSA) USA300 is a successful *S. aureus* clone in the United States and a common cause of skin and soft tissue infections (SSTIs). We performed whole-genome sequencing (WGS) of 146 USA300 MRSA isolates from SSTIs and colonization cultures obtained from an investigation conducted from 2008 to 2010 in Chicago and Los Angeles households that included an index case with an *S. aureus* SSTI. Identifying unique single nucleotide polymorphisms (SNPs) and analyzing whole-genome phylogeny, we characterized isolates to understand transmission dynamics, genetic relatedness, and microevolution of USA300 MRSA within the households. We also compared the 146 USA300 MRSA isolates from our study with the previously published genome sequences of the USA300 MRSA isolates from San Diego ( $n = 35$ ) and New York City ( $n = 277$ ). We found little genetic variation within the USA300 MRSA household isolates from Los Angeles (mean number of SNPs  $\pm$  standard deviation,  $17.6 \pm 35$ ;  $\pi$  nucleotide diversity,  $3.1 \times 10^{-5}$ ) or from Chicago (mean number of SNPs  $\pm$  standard deviation,  $12 \pm 19$ ;  $\pi$  nucleotide diversity,  $3.1 \times 10^{-5}$ ). The isolates within a household clustered into closely related monophyletic groups, suggesting the introduction into and transmission within each household of a single common USA300 ancestral strain. From a Bayesian evolutionary reconstruction, we inferred that USA300 persisted within households for 2.33 to 8.35 years prior to sampling. We also noted that fluoroquinolone-resistant USA300 clones emerged around 1995 and were more widespread in Los Angeles and New York City than in Chicago. Our findings strongly suggest that unique USA300 MRSA isolates are transmitted within households that contain an individual with an SSTI. Decolonization of household members may be a critical component of prevention programs to control USA300 MRSA spread in the United States.

**IMPORTANCE** USA300, a virulent and easily transmissible strain of methicillin-resistant *Staphylococcus aureus* (MRSA), is the predominant community-associated MRSA clone in the United States. It most commonly causes skin infections but also causes necrotizing pneumonia and endocarditis. Strategies to limit the spread of MRSA in the community can only be effective if we understand the most common sources of transmission and the microevolutionary processes that provide a fitness advantage to MRSA. We performed a whole-genome sequence comparison of 146 USA300 MRSA isolates from Chicago and Los Angeles. We show that households represent a frequent site of transmission and a long-term reservoir of USA300 strains; individuals within households transmit the same USA300 strain among themselves. Our study also reveals that a large proportion of the USA300 isolates sequenced are resistant to fluoroquinolone antibiotics. The significance of this study is that if households serve as long-term reservoirs of USA300, household MRSA eradication programs may result in a uniquely effective control method.

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*Staphylococcus aureus* is the most common cause of human skin and soft tissue infections (SSTIs) and is also a common cause of osteomyelitis, endocarditis, and pneumonia (1). Methicillin-resistant *S. aureus* (MRSA) strains are resistant to all  $\beta$ -lactam antibiotics, with the exception of new cephalosporins, and have posed therapeutic challenges since their first description more than 50 years ago (2). In the 1990s, an epidemic of MRSA infections in the United States began outside health care facilities (3). With this shift in epidemiology, the majority of patients who seek

care for *S. aureus* SSTIs in United States emergency departments (4), jails (5), large medical centers (6), and community primary-care offices (7) are infected with MRSA.

By 2004, nearly all of the MRSA isolates from community-associated SSTIs in the United States (>97%) had a common pulsed-field gel electrophoresis (PFGE) type, known as USA300 (6, 8). In these strains, the Panton-Valentine leukocidin (PVL) toxin genes (*lukS-PV* and *lukF-PV*), the arginine catabolic mobile element (ACME), and staphylococcal cassette chromosome *mec*

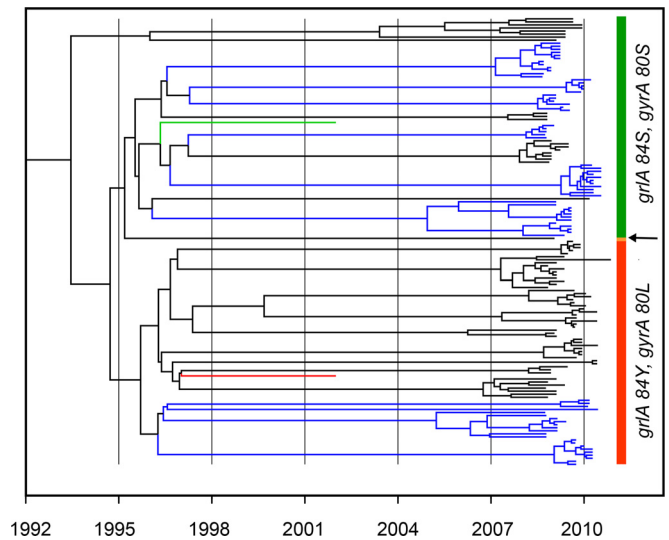
(SCC*mec*) type IV were almost uniformly present. In contrast, these characteristics were rarely found in health care-associated MRSA (HA-MRSA) strains (9). USA300 MRSA (referred to here as USA300), in addition to causing SSTIs, has emerged as a common cause of invasive infections (10). The success of USA300 in both community and health care settings has been attributed to overexpression of the global transcriptional regulator *agr* and *sae*, leading to increased expression of toxin genes, including PVL (11–13). Also in USA300, the presence of ACME likely enhances the survival of MRSA on the skin (14).

A critical reservoir of USA300, as for all *S. aureus* strains, is asymptomatic colonization of the human body. Studies have been performed among household contacts of patients with *S. aureus* infections to assess the frequency of asymptomatic colonization (15, 16). *S. aureus* colonization of more than one individual in the household of a patient already infected has been identified, but until recently, studies have either not assessed the genetic relatedness of strains or have used sequence-based techniques with limited discriminatory power (17).

Whole-genome sequencing (WGS) has come into general use in bacterial epidemiological studies as it offers the ultimate level of sensitivity in the genetic discrimination of closely related strains and the identification of genetic markers associated with virulence and antibiotic resistance (18–20). We set out to determine if WGS could identify single nucleotide polymorphisms (SNPs) among USA300 isolates that would cluster by household or city of origin. Using a large number of isolates collected in two different geographic regions, we provide strong evidence that USA300 spreads within households and persists for a period of several years. Furthermore, we show that a large number of the USA300 isolates, predominantly from California, had acquired mutations associated with fluoroquinolone resistance, whereas the prevalence of resistance remained low in Chicago. This study reveals the micro-evolutionary processes that are shaping the USA300 epidemic.

## RESULTS

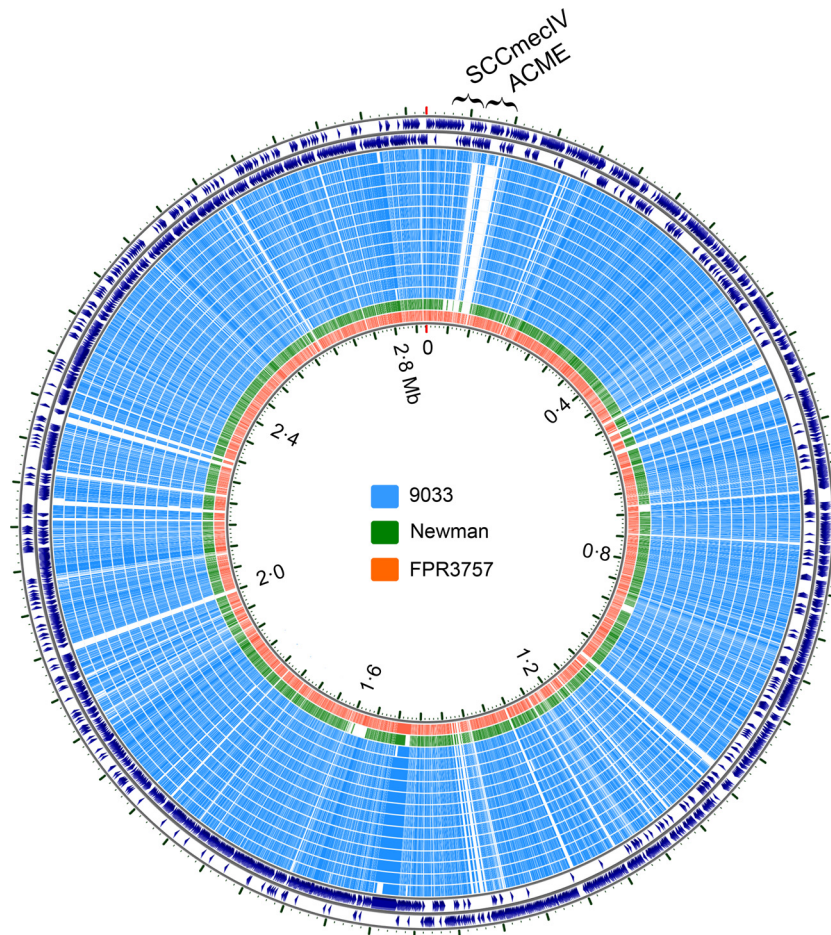
**Long-term persistence of USA300 MRSA in households.** We sequenced 146 USA300 isolates to an  $\sim 200\times$  median depth of coverage per strain. The strains were reconfirmed as belonging to sequence type 8 (ST8) from the WGS data by using the Short Read Sequence Typing (SRST) tool (21). The 2,203,292-bp core nucleotide sequence (of the 2.9-Mb genome) common to all USA300 isolates extracted from the progressiveMauve alignment was used for a Bayesian coalescent analysis implemented in BEAST (Bayesian evolutionary analysis by sampling trees) to derive estimated dates for the common ancestries of the strains. Using a strict molecular clock and a Bayesian skyline coalescent model, we estimated an average mutation rate of  $1.25 \times 10^{-6}$  (95% confidence interval,  $1.02 \times 10^{-6}$  to  $1.52 \times 10^{-6}$ ) mutations per site per year, similar to that reported previously in USA300 and other *S. aureus* genetic types (17, 22–25). Uhlemann et al. reported a mutation rate of  $1.22 \times 10^{-6}$  (95% confidence interval,  $6.04 \times 10^{-7}$  to  $1.86 \times 10^{-6}$ ) mutations per site per year in the USA300 isolates analyzed from the New York City (17). Similarly, a mean nucleotide substitution rate of  $2.0 \times 10^{-6}$  (95% confidence interval,  $1.2 \times 10^{-6}$  to  $2.9 \times 10^{-6}$ ) per site per year in ST225 *S. aureus* strains of Central Europe was estimated (22). The average estimate of the time to the most recent common ancestor (TMRCA) of the USA300 isolates indicates a divergence at around 1993, consistent with observations of the start of the epidemic of community-



**FIG 1** Maximum clade credibility tree resulting from BEAST analysis of the core genome alignment of 146 USA300 isolates from Los Angeles and Chicago. Bayesian analysis was run under a strict molecular clock and with an HKY model of nucleotide substitution assuming a Bayesian skyline demographic model. Blue branches are isolates from Chicago households, and black ones are from Los Angeles households. The green and red branches, respectively, are the USA300 TCH1516 and FPR3757 reference strains. The fluoroquinolone-susceptible (with *grlA* 84S and *gyrA* 80S) and -resistant (with *grlA* 84Y and *gyrA* 80L) clades are indicated by vertical green and red bars, respectively. The arrow indicates a single strain with the *grlA* 84F *gyrA* 80L genotype.

associated MRSA (CA-MRSA) infections caused by this strain type in the United States (26). In addition, our analysis revealed that the fluoroquinolone-resistant strains emerged in the mid-1990s (Fig. 1). The BEAST analysis demonstrated a range of mean TMRCA based on the final date of isolation of bacteria in 2010 from households of 2.33 years (household 9131) to 8.35 years (household 8113) (see Table S1 in the supplemental material). However, the 95% confidence intervals for these dates fail to overlap only for the two isolates at the maximum and minimum ends of the scale. We also constructed a well-supported root-to-tip regression plot of the date of isolation of these strains and increased genetic diversity by using Path-O-Gen (correlation coefficient, 0.351;  $r^2 = 0.123$ ) (see Fig. S1 in the supplemental material). The root-to-tip regression analysis suggested a rate estimate ( $1.21 \times 10^{-6}$  per site per year) and TMRCA of the USA300 isolates very similar to those obtained in the Bayesian coalescent analysis.

**Continuous reshaping of the USA300 pangenome.** We investigated the pangenome composition of the 146 USA300 draft sequenced strains and 49 completely sequenced genomes of *S. aureus* available in the National Center for Biotechnology Information (NCBI) refSeq database (see Table S2 in the supplemental material). Unsupervised hierarchical clustering based on patterns of the presence or absence of gene families (27) grouped all of the USA300 strains in the same clade (see Fig. S2 in the supplemental material). Twelve strains from Chicago household 9033 were missing the ACME cassette (Fig. 2). The position of the ACME-negative strains in the phylogeny suggested the deletion of a preexisting island. Interestingly, the index infection isolate of this household (strain 120381) is from a phylogenetically distinct ACME-positive lineage. This genotype was not subsequently detected in household 9033 at 3 or 6 months. Our study design



**FIG 2** BLAST map showing ACME deletion in the USA300 isolates from Chicago household 9033. The map was generated by the CCT, which uses all-versus-all BLAST and arranges the genomes compared according to their homology with reference genomes (the reference genome here is TCH1516, which is shown in the outermost two rings). Each ring is a genome (isolate), as indicated. As shown, one isolate in household 9033 (the outermost blue ring) was ACME positive, while the remaining isolates had this element deleted. Strain Newman also lacks ACME (shown as the green ring). FPR3757 was included here as another ACME-positive USA300 reference strain.

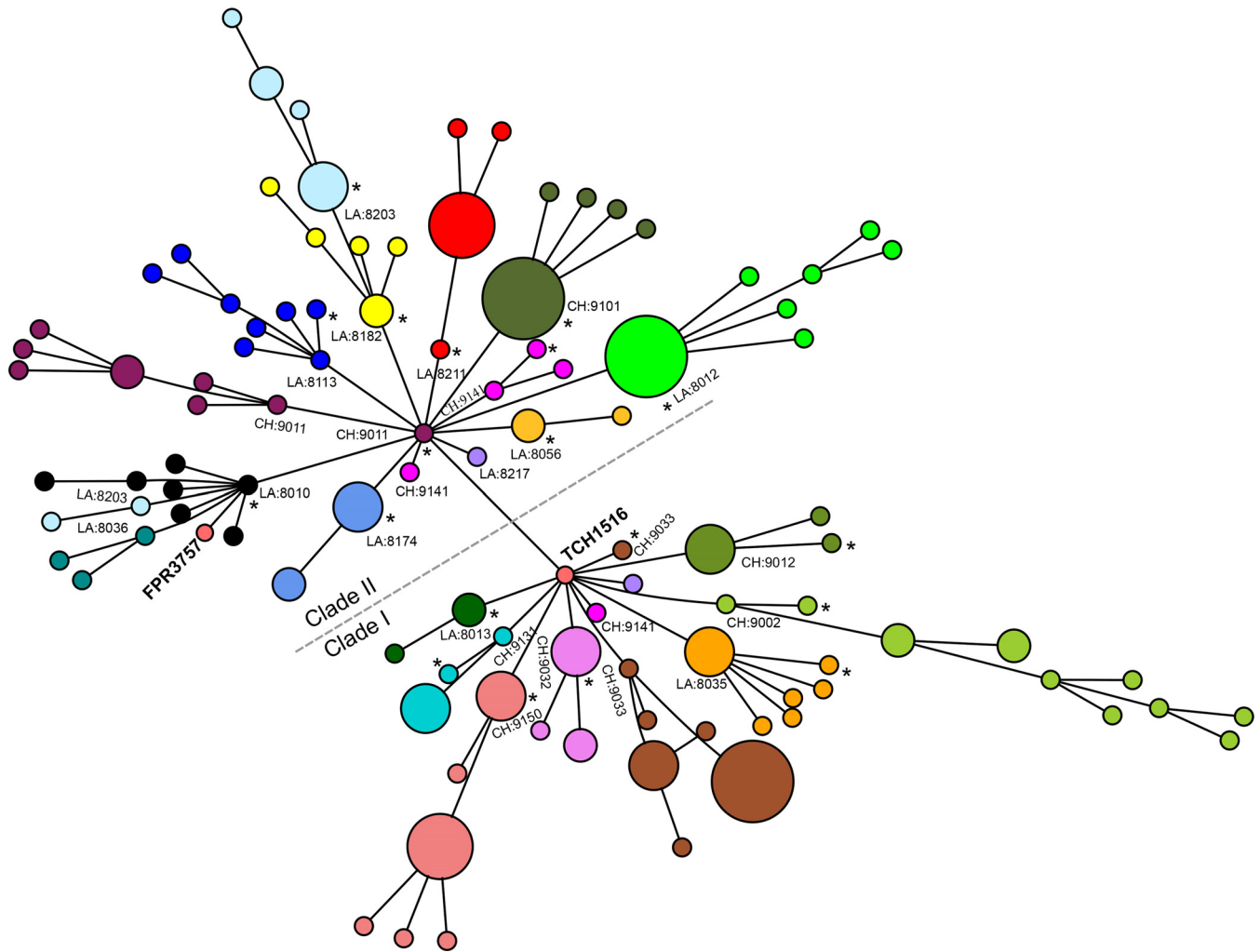
precluded an analysis of the loss or gain of PVL genes because the presence of the PVL genes was a criterion for isolate inclusion in this study.

There was evidence that USA300 clones, when persisting in households, continued to acquire extraneous DNA by horizontal gene transfer (HGT) and recombination. A few isolates acquired new genes on phages (e.g., isolate 119700 in household 8012) compared with others within the same household. This event could only have occurred after the strain entered the household, and thus, the DNA must have originated from coresident *Staphylococcus* species (28) on the colonized human host. Likewise, there are at least two SNP patterns that are best explained by an exchange of short segments of DNA through homologous recombination with a non-USA300 *S. aureus* isolate. In strain 119720, from household 8182 in Los Angeles, there are five SNPs in a short intergenic region (coordinates 1996070 to 1996129 bp of the TCH1516 genome) that match the ancestral *S. aureus* genome rather than the typical USA300 genome. This suggests that a homologous recombination event may have taken place prior to the introduction of USA300 into household 8182.

**Clustering of USA300 within households.** To investigate the clustering of strains within households, we constructed a mini-

imum spanning tree (MST) based on an alignment matrix of 1,629 core protein clusters (1,335,849 bp) of USA300 as determined by OrthoMCL. Similar to BEAST phylogeny, strains in the MST were split into two clades (Fig. 3). Also, 18 of 21 households contained USA300 isolates clustered into closely related monophyletic groups, which suggested the introduction into each household of a single USA300 ancestor strain. The index infection isolate haplotype was the connection of the household-specific branch to the majority of the strains in the MST (12 out of 21 households,  $P = 1.0$ , Fisher's exact test). This suggests that in many households the index cases' infection isolates were not responsible for the introduction of USA300 into these households; instead, the infecting isolate was derived from isolates that were already present in the household.

In addition, households could generally be connected to the root of the phylogenetic tree without passing through another household. This finding supports the hypothesis that, for the samples in this study, transmission occurred primarily within the households after a single introduction and does not support the alternative explanation that there were frequent or repeated introductions of USA300 from another reservoir outside the household. Overall, the levels of genetic diversity within the Los Angeles



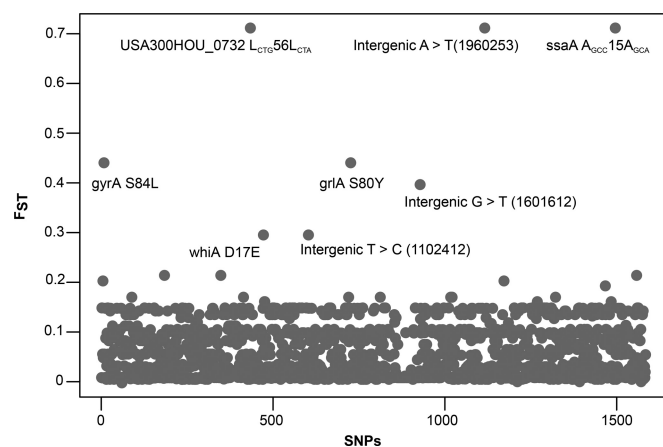
**FIG 3** Minimum spanning tree showing genetic relationships among all household USA300 isolates. Each circle represents an individual genotype based on a 1,335,849-bp core gene alignment, and each color represents a different household. The size of the circle is proportional to the number of isolates with the genotype indicated. The household numbers are prefixed with CH (for Chicago) or LA (for Los Angeles). The index infection isolate in the household is indicated by an asterisk. The clades of USA300 strains with and without the *grlA* 80Y and *gyrA* 84L mutations are labeled clades I and II, respectively. As shown, the isolates from Los Angeles household 8203 split into two clusters but still remained in larger clade II. The isolates from Chicago household 9141 separated into two different clades with the presence or absence of *grlA* and *gyrA* mutations.

and Chicago isolates were similar, with medians of six (mean and standard deviation of  $17.6 \pm 35$  [range, 0 to 199]) and five (mean and standard deviation of  $12 \pm 19$  [range, 0 to 102]) SNPs per household, respectively (see Fig. S3 and Table S1 in the supplemental material). The nucleotide diversity ( $\pi$ , the average number of nucleotide differences per site between two sequences) was also the same ( $\pi = 3.1 \times 10^{-5}$ ) in both Los Angeles and Chicago isolates and was similar to the diversity reported for *S. aureus* isolates of the ST225 genetic background from Central Europe (22). The theta ( $\theta$ ) diversities of Chicago and Los Angeles isolates, respectively, were estimated to be  $5.4 \times 10^{-5}$  and  $7.1 \times 10^{-5}$ . A core protein alignment-based maximum-likelihood (ML) phylogeny resulted in similar clustering of the isolates within the households studied (see Fig. S4 in the supplemental material).

**Evolution of fluoroquinolone-resistant USA300.** To identify genetic changes driving the clustering of strains within the two larger clades, we estimated genome-wide Weir and Cockerham's  $F_{ST}$  (genetic differentiation) between the bacterial populations

identified in Los Angeles and Chicago. We found eight SNPs (three nonsynonymous, two synonymous, and three intergenic) that were highly differentiated between Chicago and Los Angeles isolates (Fig. 4). Two of the three nonsynonymous SNPs within the gyrase A (*gyrA* S84L) and topoisomerase IV (*grlA* S80Y) genes were associated with fluoroquinolone resistance in *S. aureus* (17, 29) and several other bacterial species (30–32). The third nonsynonymous SNP was in a poorly characterized gene called *whiA* (*whiA* D17E) located close to the essential *walkR* cell wall two-component signal transduction system.

Phenotypic ciprofloxacin resistance segregated with the presence of the *gyrA* and *grlA* SNPs. All of the isolates from the households in clade II harbored the mutations *gyrA* S84L and *grlA* S80Y, conferring fluoroquinolone resistance, whereas those in clade I were fluoroquinolone susceptible (Fig. 1 and 3; Table 1). With the exception of one household (no. 9141), fluoroquinolone resistance also clustered by household; all of the isolates within a household were either susceptible or resistant. The four



**FIG 4** Weir and Cockerham  $F_{ST}$  at 1,595 SNP positions identified in 146 USA300 MRSA isolates analyzed in this study. Each dot represents an SNP, and those with elevated  $F_{ST}$  values are indicated ( $F_{ST}$  across all SNPs, 0.15). Numbers in parentheses are genomic coordinates corresponding to the TCH1516 reference genome.

fluoroquinolone-resistant strains in household 9141 segregated with clade II, while only one susceptible strain segregated with clade I (Fig. 3). In an example of parallel evolution, the same two mutations were observed in EMRSA-15, an epidemic health care-associated ST22 strain that emerged in the United Kingdom in the 1980s (25). Fluoroquinolone resistance has also been associated with the rapid intercontinental spread of another Gram-positive pathogen, *Clostridium difficile* (32).

**Fluoroquinolone resistance in USA300 is not geographically constrained.** A high-resolution ML phylogeny based on core genome alignment of 460 USA300 strains from San Diego (23), Los

Angeles (this study), Chicago (this study), and New York City (17) was constructed in REALPHY (33). As shown in Fig. 5, the isolates with and without fluoroquinolone resistance-conferring mutations *gyrA* S84L and *grlA* S80Y were grouped into two clades (Fig. 5). Fluoroquinolone-resistant USA300 strains, however, were more widespread in San Diego (28/35, 80.0%), Los Angeles (59/70, 84.2%), and New York (186/277, 67.1%) than in Chicago (23/75, 30.6%) ( $P < 0.0001$  for each comparison).

## DISCUSSION

Utilizing WGS of USA300 isolates from households in two cities, Chicago and Los Angeles, we have demonstrated that households serve as major sites of MRSA transmission. A recent study by Uhlemann et al. observed similar results in household isolates from New York City (17). With time, strains in the households that we studied acquired a small number of point mutations and DNA from HGT from other bacteria (likely *Staphylococcus* species or other close relatives of *S. aureus*). It would be useful in the context of USA300 epidemiology to consider whether the virulence potential of strains decreases over time in a small human population. We found no genome-wide patterns of nucleotide substitution or HGT to distinguish strains colonizing individuals from those causing infections, unlike in other studies (23, 34). There were few SNPs in Los Angeles and Chicago household isolates, similar to findings in earlier studies, suggesting a recent clonal expansion and diversification of USA300 clones (17, 23, 35). We also observed that the USA300 isolates from different regions of the United States belonged to the same clade of the whole-genome ML phylogenetic tree, suggesting frequent migration of strains between geographical regions.

Importantly, we showed in this study that USA300 clonal lineages persisted within households for about 2 to 8 years before a

**TABLE 1** Ciprofloxacin susceptibility profiles of the Los Angeles and Chicago USA300 household MRSA isolates and SNPs in their *grlA* and *gyrA* genes

Household	Region	$n^a$	Ciprofloxacin susceptibility <sup>b</sup> (MIC [ $\mu$ g/ml])	<i>grlA</i> position 80 nucleotide	<i>gyrA</i> position 84 nucleotide
8010	Los Angeles	7	R (>4.0)	Y	L
8012	Los Angeles	11	R (>4.0)	Y	L
8013	Los Angeles	3	S (1.0)	S	S
8035	Los Angeles	8	S (1.0)	S	S
8036	Los Angeles	3	R (>4.0)	Y	L
8056	Los Angeles	3	R (>4.0)	Y	L
8113	Los Angeles	8	R (>4.0)	Y	L
8174	Los Angeles	5	R (>4.0)	Y	L
8182	Los Angeles	6	R (>4.0)	Y	L
8203	Los Angeles	9	R (>4.0)	Y	L
8211	Los Angeles	7	R (>4.0)	Y	L
8217	Los Angeles	1	ND <sup>c</sup>	Y	L
9002	Chicago	12	S (0.5)	S	S
9011	Chicago	9	R (>4.0)	Y	L
9012	Chicago	5	S (0.5)	S	S
9032	Chicago	6	S (0.5)	S	S
9033 <sup>d</sup>	Chicago	13	S (0.5)	S	S
9101	Chicago	9	R (>4.0)	Y	L
9131	Chicago	5	S (1.0)	S	S
9141 <sup>e</sup>	Chicago	5	R (>4.0)	Y	L
9150	Chicago	11	S (0.5)	S	S

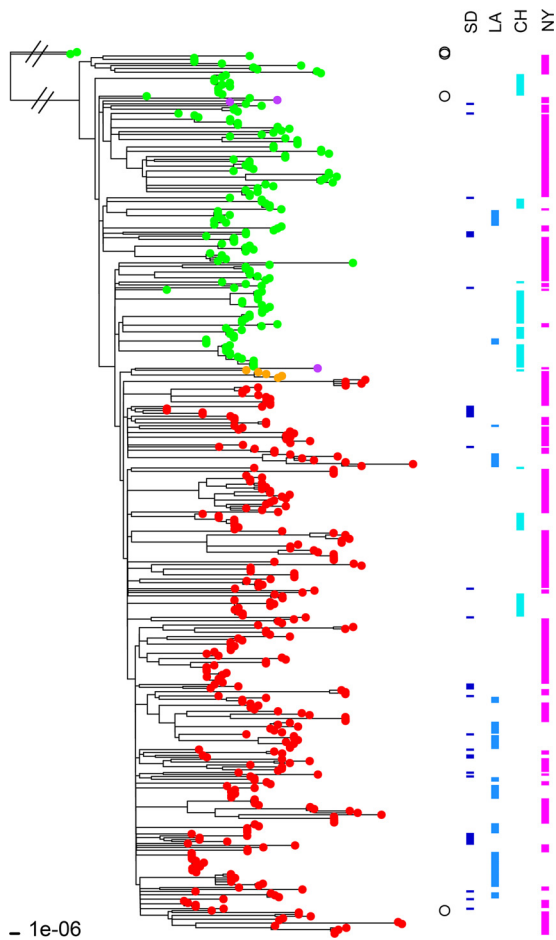
<sup>a</sup> Number of isolates sequenced in the household.

<sup>b</sup> R, resistant; S, susceptible.

<sup>c</sup> ND, MIC not determined.

<sup>d</sup> One isolate (120381) in household 9033 had *grlA* 80F and *gyrA* 84L SNPs and was ciprofloxacin sensitive.

<sup>e</sup> One isolate (119813) in household 9141 did not have these SNPs.



**FIG 5** ML tree of 460 USA300 MRSA isolates along with two non-USA300 strains (Newman and COL) included as outgroups. The ML tree was constructed with the 2,104,213-bp core sequence alignment of these isolate genomes in REALPHY. The fluoroquinolone-susceptible isolates (i.e., with no mutations in the *grlA* and *gyrA* genes) are indicated by green branch tips, whereas fluoroquinolone-resistant strains (i.e., with the *grlA* 80Y and *gyrA* 84L mutations) are indicated by red branch tips. Five fluoroquinolone-resistant isolates had a different set of mutations (*grlA* 80F and *gyrA* 84L) and are indicated by orange branch tips. Three isolates indicated by purple tips had only one mutation in the *grlA* gene (80F). The two non-USA300 strains, Newman (*grlA* 80S and *gyrA* 84S) and COL (*grlA* 80S and *gyrA* 84S), and two USA300 reference strains, TCH1516 (*grlA* 80S and *gyrA* 84S) and FPR3757 (*grlA* 80Y and *gyrA* 84L), are indicated by open circles to the right of the tree. USA300 strains TCH1516 and FPR3757 segregated with their fluoroquinolone-susceptible and -resistant clades, respectively. Isolates from San Diego (SD), Los Angeles (LA), Chicago (CH), and New York City (NY) are indicated by the bars on the right.

symptomatic patient was admitted to a hospital and continued for at least another year afterward. This could be caused by a combination of long-term asymptomatic human carriage (36) and/or frequent reinfections from other household members, pets, or fomites. We need to understand how MRSA persists (the reasons may be different in different households) to design decolonization strategies and public health programs aimed at controlling the spread of USA300. Interventions may need to address all of the symptomatically infected and asymptotically colonized individuals in a household.

We found that households were common sites of USA300

transmission and that once USA300 was introduced, within-household transmission was more common than repeated reintroduction of this *S. aureus* genetic background. While other reservoirs of USA300 such as health care settings, jails, gyms, schools, and other public institutions may be sites of transmission and sources of isolates of this genetic background in U.S. households, the WGS data in our study provided the resolution to support the hypothesis that within-household transmission creates the conditions for a long-term reservoir and for CA-MRSA persistence. Our results are supported by the findings of other studies (34, 37).

The presence of ACME has been postulated to contribute to the success of the USA300 clone (14). ACME contains the *arc* operon thought to be important for arginine catabolism, enhancing survival in acidic environments on the skin. In USA300, ACME includes *speG*, which encodes spermidine acetyltransferase, which decreases the toxicity of spermidine, which is secreted as a defense molecule on mammalian skin. The recent addition of *speG* to ACME is thought to have been an important factor in the emergence of the USA300 epidemic in the late 1990s (14). In our study, as in other studies of USA300 (17, 23, 35), ACME was not universally present, and we found that isolates lacking ACME were still able to spread in a household and colonize people stably. The importance of ACME in the fitness of USA300 thus requires further study.

A phylogeny of 460 strains from Los Angeles, Chicago, San Diego, and New York City revealed that USA300 strains form two clades according to their fluoroquinolone resistance phenotypes (with or without *gyrA* 84L plus *grlA* 80Y/F mutations). These findings echo other recent North American studies (17, 38). We cannot ascertain at this stage whether clade II is replacing the older fluoroquinolone-sensitive lineage or what the significance of the higher frequency of fluoroquinolone resistance in Los Angeles than in Chicago is. Unlike ST22 (EMRSA-15) (25), another clade that has acquired and frequently exhibits fluoroquinolone resistance and is primarily HA-MRSA, USA300 is primarily CA-MRSA (all of the strains in this study were epidemiologically characterized as CA-MRSA). Cheng et al. showed that fluoroquinolone use might increase the rate of nasal colonization by MRSA (39). The fluoroquinolone-resistant strains may have been selected for by antibiotic treatment for other conditions. This raises the question of what the selection pressures are that allow long-term maintenance of the *gyrA/grlA* mutations within households. Presumably, there is little fitness cost to the mutations and/or regular antibiotic exposure is occurring.

We believe the next step to answering the questions raised in this work is a longitudinal evaluation of the USA300 isolates within households to examine the patterns of person-to-person transmission, the persistence of fluoroquinolone resistance, and whether mutations, over time, lead to enhanced human colonization or to enhancement of the potential of a USA300 strain to cause an infection.

## MATERIALS AND METHODS

**Household survey and strain collection.** In our household contact study, 350 evaluable index patients with SSTIs were enrolled between August 2008 and June 2010 at the University of Chicago Medical Center ( $n = 177$ ) or at the Harbor-UCLA Medical Center ( $n = 173$ ). Details of this study have been described previously (16). Each member of the household of each consenting index patient was visited on three occasions, <21 days after the treatment of the SSTI (baseline) and 3 and 6 months after the baseline visit. At each visit, the index patient and each household contact

were tested for *S. aureus* colonization by culturing samples from the nares, the oropharynx, and the inguinal region. All of the *S. aureus* isolates obtained from the index SSTI (the index infection isolate) and from colonization cultures from index patients and household contacts from all three household visits underwent genotyping by multilocus sequence typing (MLST), SCCmec typing, and assessment for the presence of PVL genes. Isolates were considered to be USA300 if they were of ST8 and carried SCCmec type IV and the PVL genes (16), as shown in a previous validation study (40). Susceptibility to ciprofloxacin was tested by the broth microdilution method as recommended by the Clinical and Laboratory Standards Institute (41).

Among 1,162 persons enrolled (350 index patients and 812 household members), *S. aureus* colonized 40% (137/350) of the index patients and 50% (405/812) of their household contacts at one or more sites. Factors independently associated ( $P < 0.05$ ) with the index infection isolate strain type being present colonizing a household contact were recent skin infection in the contact, recent cephalixin use, and USA300 genetic background of the index infection isolate (see Table S3 in the supplemental material) (16). USA300 was the predominant *S. aureus* type identified among the infecting (53%) and colonizing (29%) isolates. We randomly selected 21 households, 12 from Los Angeles and 9 from Chicago (a total of 146 isolates) for WGS that met the following criteria. (i) The index infection isolate was USA300, and (ii) at least two household members (one of whom could be the index patient) were colonized with USA300 at one or more body sites at the baseline visit (see Table S3 in the supplemental material). Additional information on recruitment has been previously published (16).

**WGS, SNP calling, genome assembly, and annotation.** DNA was extracted from each isolate with the Qiagen genome preparation kit according to the manufacturer's protocol. Sequencing libraries were prepared with 1 to 2  $\mu$ g of DNA by following the standard Illumina protocols and chemistry and paired-end sequencing was performed on the Illumina HiSeq 2000 platform (Illumina Inc., San Diego, CA), generating 100-bp sequence reads. The MLST genetic background of the isolates was reconfirmed from the WGS data by using the SRST tool (21). To minimize errors and artifacts in the downstream analyses, sequence reads were preprocessed with PRINSEQ (version 0.20.3) (42). The preprocessing of the reads involved two sequential steps. In the first step, we simply discarded any reads with two or more N's or a mean Phred quality score of  $< 20$ . In the second step, bases with low Phred quality scores ( $\leq 19$ ) were trimmed from the 3' end, and if the length of the trimmed reads fell below 70 bp, they were removed from further analysis. The resulting high-quality reads were aligned against the *S. aureus* USA300 TCH1516 reference genome (GenBank accession number NC\_010079; 2,872,915-bp length) with the Burrows-Wheeler Aligner (version 0.7.2) with a mismatch penalty of 3 and a gap open penalty of 5 (43). The programs SAMtools and Picard Tools were used to format and reformat the intermediate-alignment files, and variant SNPs and insertions-deletions (indels) were identified with the Genome Analysis Toolkit UnifiedGenotyper (44, 45). We considered only those variant positions that were covered by at least 10 reads, and 90% or more sequence reads supported mutation (an allele different from the TCH1516 reference genome). We also excluded the variants if they were in the homopolymer tract regions or were ambiguous in or missing from any of the isolates.

Velvet (version 1.2.06) was used for *de novo* genome assembly (46). The assembled contigs larger than 200 bp were ordered and converted into a single pseudocontig with Abacas (47) and finally annotated with the bacterial genome annotation tool Prokka (48).

**Orthologous gene clustering, pangenome analysis, and core genome phylogeny.** The predicted proteins from each isolate were categorized into orthologous clusters by OrthoMCL (with the option  $-E$  value for BLAST alignments set at  $1e-05$  and  $-C$  set at 75%) as implemented in GET\_HOMOLOGUES (27, 49, 50). The pangenome matrix (presence and absence of genes/proteins) produced from the OrthoMCL step was used for hierarchical gene clustering analysis with the R heatmap2 func-

tion (51). Deletions of ACME or any other large region of the genome were examined and visualized with the CGView comparison tool (CCT) (52), which uses all-versus-all BLAST to compare the genomes and presents the homology as a circular map. The 1,629 core protein clusters identified in 148 USA300 isolates (proteins present in all 148 isolates), which included the two reference strains TCH1516 and FPR3757, by OrthoMCL were individually aligned with Muscle (53), edited in trimAl (54) to eliminate positions containing gaps and poorly aligned regions, and finally concatenated to generate a single alignment (445,283 amino acids) of the core protein clusters. The nucleotide sequence alignments corresponding to each core protein cluster were retrieved with PAL2NAL (55) and concatenated to create a nucleotide alignment matrix (1,335,849 bp) of core gene clusters.

Phylogenetic analysis with the above core protein and core gene alignment matrixes was performed to investigate genetic relationships among household strains by two different methods. An MST based on the alignment matrix of core gene clusters was generated in a Bioconductor library Rgraphviz (version 2.6.0) (56). ML trees based on the core gene and core protein alignment matrixes were constructed in RAxML (version 7.0.4) (57) under GTRGAMMA and HIVWF substitution models, respectively. The best-fit nucleotide and amino acid substitution models, respectively, were determined with jModelTest (v.0.1.1) (58, 59) and ProtTest (60) on the basis of the Akaike information criterion score and the number of estimated parameters. The node support of the ML tree was assessed by the nonparametric bootstrapping method with 200 replicates.

**Estimation of  $F_{ST}$ .** To identify the SNP loci highly differentiated between Los Angeles and Chicago USA300 MRSA isolates, the Weir and Cockerham genetic statistics ( $F_{ST}$ ) (61) across all 1,585 SNP loci identified in USA300 isolates with reference to the TCH1516 USA300 genome (obtained at the SNP calling step as described above) was estimated with the diveRsity R package (version 1.7.6) (62).

**Estimation of substitution rate and duration of presence within households.** The rate of substitution within the USA300 genome and age of infection within each household were estimated with BEAST, version 2.0.2 (63). For this analysis, we aligned 146 USA300 draft genomes produced in this study along with two completed genomes of USA300 strains TCH1516 and FPR3757 with the progressiveMauve algorithm of Mauve (64). The core alignment blocks longer than 500 bp, shared by all of the genomes (locally collinear blocks) were concatenated to produce a 2,203,292-bp alignment matrix. An ML tree was constructed with this alignment under the GTRGAMMA substitution model in RAxML as described above. Linear regression analysis was performed to assess the relationship between root-to-tip branch length and the date of isolation of the isolates in Path-O-Gen (<http://tree.bio.ed.ac.uk/software/pathogen/>). Three independent runs of BEAST, each with 300 million Markov chain Monte Carlo (MCMC) generations, sampling at every 10,000 generations were performed with the following settings: a strict molecular clock, the HKY model of nucleotide substitution, and a Bayesian skyline coalescent, as used by Uhlemann et al. (17) and Nübel et al. (22). The date of isolation of the USA300 strains for this analysis were specified in day, month, and year. The log files resulting from all three runs were analyzed to assess convergence by checking the effective sample sizes (ESSs) of different parameters in Tracer (version 1.5). After confirming that all three runs had converged on the same posterior distribution in the MCMC run with almost identical marginal density distributions and all of the parameters had an ESS of  $> 200$ , they were combined in LogCombiner (version 2.0.2), discarding the first 25% of the MCMC generations as a burn-in phase. A single maximum clade credibility tree was summarized in TreeAnnotator (version 2.0.9) and visualized in FigTree (version 1.4.0). We also conducted another BEAST run by using a strict molecular clock, the HKY nucleotide substitution model, and a constant size coalescent to rule out the impact of demographic models on our estimates (see Table S1 in the supplemental material).

**Phylogenetic structures of all available USA300 genomes.** In order to investigate the high-resolution phylogenetic structures of all of the avail-

able USA300 isolates sequenced to date, we reanalyzed 146 strains sequenced in this study along with 312 previously published sequences of USA300 isolates from San Diego, CA ( $n = 35$ ) (23), and New York, NY ( $n = 277$ ) (17). In addition, we included the completed genomes of USA300 strains TCH1516 and FPR3757. An ML phylogeny of these 460 USA300 isolates was constructed on the basis of their core genome alignment (2,104,213 bp) with PhyML as implemented in REALPHY (33).

**Nucleotide sequence accession numbers.** The raw sequence reads analyzed in this study have been deposited in the NCBI Sequence Read Archive database under accession number SRP039020. The GenBank accession numbers of all of the completed *S. aureus* genomes used in this study are listed in Table S2 in the supplemental material.

## SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <http://mbio.asm.org/lookup/suppl/doi:10.1128/mBio.00054-15/-/DCSupplemental>.

- Table S1, DOC file, 0.1 MB.
- Table S2, DOC file, 0.2 MB.
- Table S3, DOC file, 0.2 MB.
- Figure S1, PDF file, 0.03 MB.
- Figure S2, PDF file, 0.5 MB.
- Figure S3, PDF file, 0.02 MB.
- Figure S4, PDF file, 0.1 MB.

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