

Nasal Carriage of Epidemic Methicillin-Resistant *Staphylococcus aureus* 15 (EMRSA-15) Clone Observed in Three Chicago-Area Long-Term Care Facilities

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The spread of pandemic methicillin-resistant *Staphylococcus aureus* (MRSA) clones such as USA300 and EMRSA-15 is a global health concern. As a part of a surveillance study of three long-term care facilities in the Greater Chicago area, phenotypic and molecular characterization of nasal MRSA isolates was performed. We report a cluster of pandemic EMRSA-15, an MRSA clone rarely reported from the United States, detected during this study.

The global spread of methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the most serious public health challenges worldwide. MRSA-related hospitalizations have increased by an estimated 118% between 1999 and 2005 (1) and continue to rise at many U.S. academic hospitals (2). Long-term care facility (LTCF) residents are at high risk for MRSA carriage (3). Rates of MRSA infection may increase faster in nursing home residents than in hospital inpatients (4), possibly due to unique associated risk factors, such as greater social interaction and multiple interactions with health care workers, including repeated hospital admissions (5). Recent evidence suggests that infection control strategies in the LTCF, such as identification of MRSA carriage and prevention of disease, could have a long-term positive impact on regional MRSA control (6). Infection control policies are often guided by, and benefit from, knowledge of the local MRSA epidemiology, especially identification of the reservoirs of epidemic clones in the population or of major changes in the existing MRSA clones (7). We report the detection of epidemic MRSA-15 (EMRSA-15), a clone that is widespread in the United Kingdom and 15 countries worldwide, in LTCF residents (8), which has hitherto been reported to account for only a very small number of surveillance isolates across the United States (9).

The isolates included in this study were part of an active MRSA surveillance program to reduce colonization at three Chicago area LTCFs, between March 2011 and November 2012. Identification of nasal MRSA carriage was done using Cepheid Xpert MRSA (Cepheid, Sunnyvale, CA) according to the manufacturer's instructions. A positive result was confirmed by growth on selective agar, BBL CHROMagar II (BD Diagnostics, Sparks, MD), and a positive Staphaurex agglutination test (Remel, Lenexa, KS). Testing of antimicrobial susceptibility to ciprofloxacin, trimethoprim-sulfamethoxazole, gentamicin, minocycline, and clindamycin was performed by disk diffusion on Mueller-Hinton agar (BD Diagnostics) and interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines (10). Isolates were typed by pulsed-field gel electrophoresis (PFGE) using Smal as previously described (11, 12). The patterns were identified on BioNumerics version 6.6 (Applied Maths Inc., Austin, TX) using a dendrogram generated by the unweighted-pair group method with arithmetic mean based on Dice coefficients, where optimization and band position tolerance were set at 0.8 and 1.5%, respec-

tively. A similarity coefficient of 80% was selected to define the patterns (9, 12). Assignment of pulsotype was correlated by comparison to published literature (13, 14). All MRSA isolates were tested for genes encoding high-level mupirocin resistance (*mupA*) and the Panton-Valentine leukocidin (PVL) toxin as previously described (15, 16). The isolates included in this study also underwent *spa* typing (17). This study was approved by the Institutional Review Board of NorthShore University HealthSystem.

Among the 803 MRSA isolates identified, 22 (2.7%) isolates from 14 patients were recognized as belonging to the EMRSA-15 pulsotype (18). These isolates could be divided into three major PFGE patterns, with one pattern being predominant (Fig. 1). All except one isolate (*spa* type unknown) belonged to *spa* types included in the ST22 group, a characteristic of EMRSA-15 isolates (Ridom SpaServer database; <http://www3.ridom.de/spa-server/>). All isolates were uniformly resistant to ciprofloxacin but susceptible to trimethoprim-sulfamethoxazole and minocycline. One isolate was resistant to clindamycin, and one had intermediate susceptibility to gentamicin. One isolate tested positive for the PVL gene, and *mupA* was not detected in any of the isolates (Fig. 1). The susceptibility observed matches the EMRSA-15 susceptibility pattern: susceptible to trimethoprim-sulfamethoxazole and gentamicin but resistant to ciprofloxacin (7). Evidence in the literature suggests that ciprofloxacin resistance confers a survival advantage to EMRSA-15 and could be a factor enabling it to supplant other existing clones (19, 20). Whole-genome sequencing studies show that ciprofloxacin resistance is a recently acquired genetic trait in EMRSA-15, which has led to the separation of clade ST22A2 (19). The emergence of this clade has been traced to shortly after the introduction of fluoroquinolones into clinical medicine in the United Kingdom (19). It appears therefore that

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Isolate No.	Molecular Characteristics				Antimicrobial Susceptibility				
	Pulsotype	<i>Spa</i> type†	MUP	PVL	CIP	TMSZ	GENT	MINO	CLND
1	A	t032	N	N	R	S	S	S	S
2	A	t032	N	N	R	S	S	S	S
3	A	t032	N	N	R	S	S	S	S
4	A	t032	N	N	R	S	S	S	S
5	A	t032	N	N	R	S	S	S	S
6	A	t032	N	N	R	S	S	S	S
7	A	t032	N	N	R	S	S	S	S
8	A	t032	N	N	R	S	S	S	S
9	A	t032	N	N	R	S	S	S	S
10	A1	t032	N	N	R	S	S	S	S
11	A1A	UK**	N	N	R	S	S	S	S
12	B	t022	N	N	R	S	S	S	S
13	B	t022	N	N	R	S	S	S	R
14	C	t005*	N	P	R	S	I	S	S
Cont.1	USA100	t002	-	-	-	-	-	-	-
Cont.2	USA300	t008	-	-	-	-	-	-	-

FIG 1 Molecular characterization and antibiogram of isolates showing EMRSA-15 pulsotype. The PFGE dendrogram compares fingerprint patterns of the related isolates from 14 patients. Columns marked “MUP” and “PVL” indicate the results for genetic tests performed to detect the *mupA* and PVL genes, respectively. CIP, ciprofloxacin; TMSZ, trimethoprim-sulfamethoxazole; GENT, gentamicin; MINO, minocycline; CLIND, clindamycin; N, negative; P, positive; S, susceptible; R, resistant; I, intermediate; †, all isolates belong to *spa* types included in the cluster ST22, a recognized cluster for EMRSA-15; **, this isolate has a unique pulsotype, although it is closely related to pulsotype A; the *spa* sequence was unique and not listed in the Ridom SpaServer database; *, this isolate had a distinct PFGE profile and belongs to *spa* type t005; it is also the only isolate positive for the PVL gene; of note, *spa* type t005 has been reported to be PVL positive (29).

the EMRSA-15 isolates observed in this study are comparable to the ones described in Europe (7, 19, 20).

The epidemiology of MRSA is unique in being able to spread in pandemic waves with successful global dissemination of certain MRSA clones, such as USA300 between Australia (21) and Europe (22), which is of significant concern to health care professionals around the world. The mechanisms leading to the relative success of these pandemic clones in being able to effectively displace other existing ones remain poorly understood. Epidemic MRSA or EMRSA-15 is one such clone; emerging in the United Kingdom in the 1990s, it has not only successfully spread in hospitals within the United Kingdom but also repeatedly replaced other established MRSA strains locally in several different countries in Europe, Australia, and Asia (19). In recent years, EMRSA-15 and EMRSA-16 strains combined have accounted for 93 to 95% of MRSA bacteremias in the United Kingdom, with EMRSA-15 alone accounting for greater than 60% of infections (23, 24). Recent surveillance studies in the United States, however, found EMRSA-15 to account for only 0.5% of MRSA isolated from the blood (1 of 194 isolates) and 0.3% of MRSA isolated from the nares (1 of 299) in the United States (25). Earlier U.S. national surveillance reported an EMRSA-15 prevalence of 0.2% among 1,984 invasive isolates (9). We identified 22 EMRSA-15 isolates from 14 patients in three nursing homes that share patients with some 40 acute care facilities in the region. Further, 12 of these 14 patients were residents of one nursing home, and their nasal surveillance isolates accounted for 5.8% of all MRSA isolates identified at that facility. In fact, to the best of our knowledge this rep-

resents the largest identified cluster of EMRSA-15 isolates observed in the United States, which is of concern since EMRSA-15 has been shown to replace previously predominant MRSA strains in Germany, Spain, Portugal, and Singapore (26–28). Further studies are required to monitor the rates of colonization by EMRSA-15 in these LTCFs and other hospitals in the area to determine whether this is an isolated event or an indication of the introduction of a new pandemic clone.

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