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Low prevalence of meticillin-resistant *Staphylococcus aureus* carriage at hospital admission: implications for risk-factor-based vs universal screening

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SUMMARY

Background: There is debate over the optimal policy for detecting meticillin-resistant *Staphylococcus aureus* (MRSA) colonization at hospital admission. The emergence of community-associated (CA)-MRSA may compromise targeted screening strategies based on risk factors for healthcare-associated (HA)-MRSA.

Aim: To determine the prevalence of MRSA colonization at admission, and the genotype and molecular epidemiology of the strains involved.

Methods: A 12-month observational study was performed at a 1200-bed London tertiary referral hospital from 1 April 2008 to 1 March 2009. All available MRSA isolates were genotyped by *spa* and staphylococcal cassette chromosome *mec* (SCC*mec*) typing.

Findings: The overall MRSA colonization rate was 2.0% of 28,892 admissions (range 6.6% in critical care to 0.8% in obstetrics/gynaecology/neonatology). The overall frequency of previously unknown carriage of MRSA on admission was 1.4%. Most colonizing strains were epidemic HA-MRSA-15 and -16. However, heterogeneous CA strains accounted for 18% of recovered isolates, including 37.5% of MRSA from accident and emergency and 23.1% of MRSA from surgery. The CA-MRSA strain types had significantly different epidemiological associations from the HA-MRSA strains, so risk factors used for the identification of HA-MRSA may not detect CA-MRSA reliably.

Conclusion: The low rate of HA-MRSA in the UK increases the relative proportion due to CA-MRSA, for which conventional risk-factor-based screening strategies may be less effective. Cost–benefit analyses of universal MRSA admission screening will need to take account of this new epidemiology.

Introduction

Asymptomatic colonization with meticillin-susceptible or meticillin-resistant *Staphylococcus aureus* (MRSA) is a risk factor for subsequent infection.[1] The identification of MRSA carriers on admission can help to control the spread of MRSA in hospitals by facilitating targeted isolation and decolonization.[2,3] For many

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years, England and most other European countries have used a risk-based approach to MRSA screening.[3,4] However, the English Government has mandated that National Health Service (NHS) acute hospitals perform universal MRSA screening for all elective and emergency admissions since December 2010.[2] Several states in the USA have also mandated active MRSA surveillance cultures.[5] These legal directives have prompted considerable debate regarding the cost-effectiveness, ethics and practicalities of implementing universal screening programmes, with many experts maintaining that a targeted screening policy is most cost-effective.[2,4,5]

Risk factors for colonization with healthcare-associated (HA)-MRSA are well established.[1,3,6] However, the same is not true for community-associated (CA)-MRSA strains that have emerged worldwide over the past decade and can affect otherwise healthy individuals of all ages in community settings.[7,8] CA-MRSA have begun to transmit in hospitals, confounding epidemiological definitions and making a case for the definition and identification of CA-MRSA by their distinct genotypes.[9]

The study hospital introduced a universal MRSA screening policy in April 2008. All MRSA isolates identified during the first year of universal screening were collected to determine the prevalence and molecular epidemiology of MRSA colonization among patients admitted to an acute hospital.

Methods

Setting, MRSA screening policy and culture methods

Guy's and St. Thomas' NHS Foundation Trust comprises two hospitals in central London with about 1200 beds and approximately 120,000 admissions per annum, including day visits. From 1 April 2008, an admission MRSA screen was collected from all adult and paediatric elective surgical and medical patients during pre-admission clinics, and from all emergency cases within the first 48 h of admission. Repeated screens from the same patient were excluded. Cotton-tipped swabs (Sterilin Amies Transport, Sterilin Limited, Newport, UK) were used to sample nose, throat and perineal (groin in children) colonization sites. The three swabs were pooled and plated on to MRSA selective chromogenic agar (Brilliance™ MRSA, Oxoid, Basingstoke, UK). Swabs were also taken to detect rectal colonization in patients admitted to the adult intensive care unit (ICU) and high dependency unit and processed separately. Admission MRSA screens were taken at the same time from any clinical sites such as skin breaches and catheter urines.[10] Presumptive MRSA isolates were confirmed by standard methods, and tested for antimicrobial susceptibility by automated broth microdilution (Vitek 2, bioMérieux, Basingstoke, UK). During the study period, one MRSA isolate per patient was collected prospectively and stored on a nutrient agar slope at room temperature.

Identification and characterization of MRSA cases based on clinical and epidemiological factors

Culture results of all MRSA admission screens collected between 1 April 2008 and 31 March 2009 were recorded prospectively. Patient age, gender, record of previous visits to the study hospitals, previous history of MRSA, admitting specialty and underlying medical conditions were obtained from patient electronic medical records. CA-MRSA and HA-MRSA strain types were defined genotypically (see below). Regardless of the strain types involved, cases were classified as healthcare-associated if: (1) their MRSA-positive screen during the study period was collected less than 12 months after a previous inpatient stay, or (2) the patient had (a) previous

Table I
Prevalence of meticillin-resistant *Staphylococcus aureus*-positive admission screens by specialty

Specialty	Total	Positive	% positive	% of all positives
Surgery				
General surgery	2361	41	1.7	7.0
Urology	2250	38	1.7	6.5
Orthopaedics	1822	31	1.7	5.3
Ear, nose and throat/ oral surgery	1561	33	2.1	5.7
Cardiothoracic surgery	1317	21	1.6	3.6
Paediatric surgery	1225	14	1.1	2.4
Plastic surgery	1137	11	1.0	1.9
Vascular surgery	480	12	2.5	2.1
Breast surgery	387	3	0.8	0.5
Total surgery	**12,540**	**204**	**1.6**	**35.0**
Medicine				
General medicine	4632	142	3.1	24.4
Cardiology	2729	32	1.2	5.5
Paediatric medicine	1732	18	1.0	3.1
Haematology/oncology	1150	17	1.5	2.9
Renal medicine	972	19	2.0	3.3
Respiratory medicine	361	17	4.7	2.9
Elderly care	218	9	4.1	1.5
Gastroenterology	171	4	2.3	0.7
Ophthalmology	135	4	3.0	0.7
Rheumatology	129	4	3.1	0.7
Dermatology	85	7	8.2	1.2
Total medicine	**12,314**	**273**	**2.2**	**46.8**
Accident and emergency				
Adult accident and emergency	1280	38	3.0	6.5
Paediatric accident and emergency	72	1	1.4	0.2
Total accident and emergency	**1352**	**39**	**2.9**	**6.7**
Intensive care unit				
Adult intensive care unit	624	40	6.4	6.9
Paediatric intensive care unit	154	11	7.1	1.9
Total intensive care unit	**778**	**51**	**6.6**	**8.7**
Obstetrics/gynaecology/neonatology				
Obstetrics/ gynaecology	1433	16	1.1	2.7
Neonatology	475	0	0.0	0.0
Total obstetrics/ gynaecology/ neonatology	**1908**	**16**	**0.8**	**2.7**
Grand total	**28,892**	**583**	**2.0**	–

MRSA episodes, (b) regular day care (e.g. haematology and renal patients), (c) day surgery or (d) evidence of risk factors (e.g. long-term indwelling devices). All other cases were classified epidemiologically as community-associated.

It was not possible to investigate MRSA acquisition because no discharge screening was performed. However, submission of an MRSA-positive specimen from a clinical site in the 12 months after admission was used as a proxy measure of MRSA infection.

Genotypic definitions of HA- or CA-MRSA isolates

DNA was extracted from MRSA using the ChargeSwitch™ gDNA mini-bacteria kit (Invitrogen Ltd., Paisley, UK). Isolates were characterized by staphylococcal cassette chromosome *mec* (SCC*mec)* type, *spa* type and carriage of Panton-Valentine leukocidin (PVL)-encoding genes; *spa* types were grouped into related clonal clusters (CCs) using the based upon repeat patterns (BURP) algorithm with a calculated cost between members of six or less, as described previously.[11]

CA-MRSA typically possess SCC*mec* types IV or V.[8,12] However, in the study setting, the most common HA-MRSA clone, multi-locus sequence type CC22-IV (EMRSA-15), is SCC*mec* IV.[13] Therefore, a combination of *spa* type and SCC*mec* type was used to define HA- and CA-MRSA. CA-MRSA strains were defined as isolates that were SCC*mec* IV or V that were not in the cluster relating to EMRSA-15.[13] Isolates with non-typeable SCC*mec* regions were defined as CA-MRSA because they were considered to be unlikely to represent common hospital lineages.[13] Two strains from a recently described CC22 CA-MRSA lineage were *t005* and PVL positive,[14] so were defined as CA-MRSA types despite clustering with EMRSA-15. All other isolates were classified as HA-MRSA.

Statistical analysis

Univariate and multiple logistic regression analyses were used to investigate risk factors for MRSA colonization on admission, and for submitting an MRSA-positive clinical specimen in the 12 months after admission (SPSS Inc., Chicago, IL, USA). Variables that were significant on univariate analysis ($P < 0.05$) were included in the multiple logistic regression analysis. Univariate analysis was used to compare

Table II
Risk factors for meticillin-resistant *Staphylococcus aureus* (MRSA) colonization

	MRSA negative ($N = 28,309$)		MRSA positive ($N = 583$)			Unadjusted OR (95% CI)	Univariate *P*	Adjusted OR (95% CI)	Multiple regression *P*
	Count	(% of all negatives)	Count	(% positive)	(% of all positives)				
Demographics									
Mean age (standard deviation)/years	50 (25)		58 (24)			1.01 (1.01–1.02)	**<0.001**	1.01 (1.01–1.01)	**<0.001**
Median age (range)/years	52 (0–109)		64 (0–97)						
Gender (female)	13,068	(46.2)	225	(1.7)	(43.7)	0.9 (0.8–1.1)	0.246	–	–
Epidemiological data									
Previous hospitalization	3676	(13.0)	136	(3.6)	(23.3)	–	**<0.001**	–	–
Overnight hospital stay in the past 12 months	2028	(7.2)	96	(4.5)	(16.5)	2.6 (2.1–3.3)	**<0.001**	1.8 (1.4–2.3)	**<0.001**
Day hospital visit in the past 12 months	1648	(5.8)	40	(2.4)	(6.9)	1.3 (1.0–1.9)	0.082	1.0 (0.7–1.4)	0.931
Previous positive for MRSA	582	(2.1)	176	(23.2)	(30.2)	20.6 (16.9–25.0)	**<0.001**	16.8 (13.7–20.5)	**<0.001**
Pre-admission screen	8870	(31.3)	130	(1.4)	(22.3)	0.6 (0.5–0.8)	**<0.001**	0.9 (0.7–1.2)	0.530
Admitted from a care home or hostel	276	(1.0)	20	(6.8)	(3.4)	–	**<0.001**		
Admission from care home	254	(0.9)	18	(6.6)	(3.1)	3.5 (2.2–5.7)	**<0.001**	1.9 (1.1–3.2)	**0.020**
Admission from homeless hostel	22	(0.1)	2	(8.3)	(0.3)	4.5 (1.1–19.3)	**0.041**	5.5 (0.9–19.2)	**0.022**
Specialty							**<0.001**		
Surgery	12,336	(43.6)	204	(1.6)	(35.0)	0.6 (0.4–0.8)	**0.001**	0.8 (0.5–1.1)	0.187
Medicine	12,041	(42.5)	273	(2.2)	(46.8)	0.8 (0.5–1.1)	0.12	0.9 (0.6–1.3)	0.516
Obstetrics/gynaecology/neonatology	1892	(6.7)	16	(0.8)	(2.7)	0.3 (0.2–0.5)	**<0.001**	0.5 (0.3–0.9)	**0.032**
Accident and emergency	1313	(4.6)	39	(2.9)	(6.7)	Reference group		Reference group	
Intensive care unit	727	(2.6)	51	(6.6)	(8.7)	2.4 (1.5–3.6)	**<0.001**	2.8 (1.8–4.4)	**<0.001**
Total	**28,309**	**(100.0)**	**583**	**(2.0)**	**(100.0)**				

OR, odds ratio; CI, confidence interval.

the epidemiological associations of HA- and CA-MRSA strain types.

Results

In total, 583 (2.0%) of 28,892 admission screens were MRSA positive during the study period. Four hundred and seven (1.4%) of 27,727 patients without a history of MRSA had a positive admission screen. The highest prevalence of MRSA colonization was found in patients admitted to the ICU (6.6%), and the lowest prevalence was found in patients admitted to obstetrics/gynaecology/neonatology (0.8%) and paediatrics (1.2%); the prevalence of MRSA colonization was lower in surgical than medical specialties (1.6% vs 2.2%) (Table I).

Four percent of screens included non-standard sites: 1.6% were from incomplete nose, throat and perineum sets; 2.2% included rectal screens (standard in the ICU) and 0.3% included clinical sites. Compared with standard screening sets, MRSA-positive screens were more likely from clinical sites [$P < 0.001$, odds ratio (OR) 31.2, 95% confidence interval (CI) 20.6–47.3] and rectal screens ($P < 0.001$, OR 5.2, 95% CI 3.9–6.9).

Significant associations with an MRSA-positive admission screen after adjusting for other factors were increasing age (OR 1.01, 95% CI 1.01–1.01; each year was associated with a 1% increase in the risk of carrying MRSA), having a history of MRSA (OR 16.8, 95% CI 13.7–20.5), admission to the ICU (OR 2.8, 95% CI 1.8–4.4), admission from a care home (OR 1.9, 95% CI 1.1–3.2) or hostel (OR 5.5, 95% CI 0.9–19.2), and overnight hospital stay in the 12 months prior to the screen (OR 1.8, 95% CI 1.4–2.3). Admission to obstetrics/gynaecology/neonatology was associated with a negative screen (OR 0.5, 95% CI 0.3–0.9) (Table II). Risk factors associated with previously unknown MRSA carriage were similar (Table III).

Significant associations with an MRSA-positive clinical specimen in the 12 months after admission after adjusting for other factors were increasing age (OR 1.01, 95% CI 1.00–1.02; each year was associated with a 1% increase in the risk of carrying MRSA), an MRSA-positive admission screen (OR 48.7, 95% CI 35.4–66.9), having a history of MRSA (OR 4.8, 95% CI 3.4–6.9) and admission to the ICU (OR 4.5, 95% CI 2.0–10.1) (Table IV).

Four hundred and eighty-four (83%) of 583 MRSA admission isolates were recovered from storage. HA-MRSA strain types accounted for 82.4% of the recovered MRSA. The majority (80.2%) of the HA-MRSA isolates were in a cluster relating to ST22-IV (phage type EMRSA-15),[8] with *t032* (49.1% of all HA-MRSA) predominating. A further 15.2% were in a cluster relating to ST36-II (EMRSA-16) and other HA-MRSA clones.

Table III
Risk factors for meticillin-resistant *Staphylococcus aureus* (MRSA) colonization excluding previously positive patients

	MRSA negative ($N = 27,727$)		MRSA positive ($N = 407$)			Unadjusted OR (95% CI)	Univariate *P*	Adjusted OR (95% CI)	Multiple regression *P*
	Count	(% of all negatives)	Count	(% positive)	(% of all positives)				
Demographics									
Mean age (standard deviation /years	49 (25)		57 (25)			1.01 (1.01–1.02)	**<0.001**	1.01 (1.01–1.01)	**<0.001**
Median age (range)/years	52 (0–109)		63 (0–97)						
Gender (female)	12,805	(46.2)	188	(1.4)	(46.2)	1.0 (0.8–1.2)	1.000	–	–
Epidemiological data									
Previous hospitalization	3517	(12.7)	82	(2.3)	(20.1)	–	**<0.001**	–	–
Overnight hospital stay in the past 12 months	1940	(7.0)	57	(2.8)	(14.0)	1.8 (1.1–3.0)	**0.011**	1.9 (1.4–2.6)	**<0.001**
Day hospital visit in the past 12 months	1577	(5.7)	25	(1.6)	(6.1)	0.8 (0.6–1.3)	0.427	1.2 (0.8–1.7)	0.489
Pre-admission screen	8760	(31.6)	90	(1.0)	(22.1)	0.6 (0.5–0.8)	**<0.001**	0.8 (0.6–1.0)	0.053
Admitted from a care home or hostel	256	(0.9)	15	(5.5)	(3.7)	–	**<0.001**		
Admission from care home	234	(0.8)	13	(5.3)	(3.2)	3.9 (2.2–6.9)	**<0.001**	3.0 (1.7–5.3)	**<0.001**
Admission from homeless hostel	23	(0.1)	2	(8.0)	(0.5)	6.3 (1.5–27.2)	**0.012**	5.6 (1.3–24.1)	**0.022**
Specialty							**<0.001**		
Surgery	12,139	(43.8)	151	(1.2)	(37.1)	0.7 (0.4–1.0)	0.058	0.8 (0.5–1.1)	0.187
Medicine	11,739	(42.3)	182	(1.5)	(44.7)	0.8 (0.5–1.3)	0.363	0.8 (0.5–1.3)	0.461
Obstetrics/gynaecology/ neonatology	1879	(6.8)	13	(0.7)	(3.2)	0.4 (0.2–0.7)	**0.004**	0.5 (0.3–1.0)	0.065
Accident and emergency	1268	(4.6)	24	(1.9)	(5.9)	Reference group		Reference group	
Intensive care unit	702	(2.5)	37	(5.0)	(9.1)	2.8 (1.6–4.7)	**<0.001**	3.0 (1.8–5.2)	**<0.001**
Total	**27,727**	**(100.0)**	**407**	**(1.4)**	**(100.0)**				

OR, odds ratio; CI, confidence interval.

Table IV
Risk factors for a positive meticillin-resistant *Staphylococcus aureus* (MRSA) clinical specimen in the 12 months after hospital admission

	No clinical specimen ($N = 28,660$)		Clinical specimen ($N = 232$)			Unadjusted OR (95% CI)	Univariate *P*	Adjusted OR (95% CI)	Multiple regression *P*
	Count	(% of all negatives)	Count	(% positive)	(% of all positives)				
Demographics									
Mean age (standard deviation)/years	50 (25)		61 (24)			1.02 (1.01–1.03)	**<0.001**	1.01 (1.00–1.02)	**<0.001**
Median age (range)/years	52 (0–109)		64 (0–93)						
Gender (female)	13,224	(46.1)	99	(0.7)	(42.7)	1.2 (0.9–1.5)	0.292	–	–
Epidemiological data									
MRSA admission screen positive	444	(1.5)	139	(23.8)	(59.9)	95.0 (71.9–125.5)	**<0.001**	48.7 (35.4–66.9)	**<0.001**
Previous hospitalization	5433	(13.1)	50	(0.9)	(21.5)	–	**<0.001**	–	–
Overnight hospital stay in the past 12 months	2091	(7.3)	33	(1.5)	(14.2)	2.2 (1.5–3.1)	**<0.001**	1.0 (0.6–1.5)	0.873
Day hospital visit in the past 12 months	1671	(5.8)	17	(1.0)	(7.3)	1.4 (0.8–2.3)	0.195	1.1 (0.6–1.9)	0.822
Previous positive for MRSA	670	(2.3)	88	(11.6)	(37.9)	25.5 (19.3–33.6)	**<0.001**	4.8 (3.4–6.9)	**<0.001**
Pre-admission screen	8951	(31.2)	49	(0.5)	(21.1)	0.6 (0.4–0.8)	**<0.001**	0.8 (0.5–1.1)	0.166
Admitted from a care home or hostel	288	(1.0)	8	(2.7)	(3.4)	–	**0.001**		
Admission from care home	264	(0.9)	8	(2.9)	(3.4)	3.8 (1.9–7.8)	**<0.001**	1.7 (0.7–4.0)	0.237
Admission from homeless hostel	24	(0.1)	0	(0.0)	(0.0)	–	0.998	–	0.998
Specialty							**<0.001**		
Surgery	12,451	(43.4)	89	(0.7)	(38.4)	0.9 (0.5–1.6)	0.668	1.7 (0.8–3.6)	0.187
Medicine	12,215	(42.6)	99	(0.8)	(42.7)	1.0 (0.5–1.8)	0.970	1.2 (0.6–2.5)	0.546
Obstetrics/gynaecology/neonatology	1904	(6.6)	4	(0.2)	(1.7)	0.3 (0.1–0.8)	**0.020**	0.8 (0.2–2.6)	0.657
Accident and emergency	1341	(4.7)	11	(0.8)	(4.7)	Reference group		Reference group	
Intensive care unit	749	(2.6)	29	(3.7)	(12.5)	4.7 (2.3–9.5)	**<0.001**	4.5 (2.0–10.1)	**<0.001**
Total	**28,660**	**(100.0)**	**232**	**(0.8)**	**(100.0)**				

OR, odds ratio; CI, confidence interval.

CA-MRSA strain types accounted for 85 (17.6%) of the recovered isolates. Thus, assuming the same frequency of CA-MRSA strain types in the isolates that were not recovered, the prevalence of CA-MRSA strain types was 0.3%. CA-MRSA represented a substantial proportion of MRSA identified in certain specialties; for example, CA-MRSA strains accounted for 37.5% of MRSA from accident and emergency, 23.1% from surgery and 21.4% from obstetrics/gynaecology/neonatology. CA-MRSA isolates were more diverse than the HA-MRSA isolates: *t127* (ST1, PVL negative) and *t044* (ST80, PVL positive), both from *spa* CC5, accounted for 25.8% and 3.5% of the CA-MRSA strain types, respectively; 20.0% were *spa* CC3 (ST8) (41.2% of which were PVL positive) and a further 22.4% were either singleton lineages or had *spa* types that were too short to analyse by BURP clustering.

Compared with HA-MRSA, CA-MRSA strains were associated with younger patients (OR 0.98, 95% CI 0.97–0.99; each year younger was associated with a 2% increase in the chance of carrying CA-MRSA), were less likely to be classified epidemiologically as healthcare-associated (OR 0.5, 95% CI 0.3–0.8), were less likely in medical specialties (OR 0.5, 95% CI 0.3–0.8) and the ICU (OR 0.2, 95% CI 0.1–0.8), were resistant to fewer classes of antimicrobial agents although more likely to be resistant to tetracycline (OR 3.5, 95% CI 1.7–7.3) and fusidic acid (OR 5.7, 95% CI 3.3–9.7), were more likely to be PVL positive (OR 1.3, 95% CI 1.2–1.4) and were more diverse (Table V). A high proportion (62.3%) of patients with CA-MRSA strain types were classified epidemiologically as healthcare-associated, and there was no significant difference in the likelihood of previous hospital contact in patients with HA- or CA-MRSA strains (Table V).

Discussion

Only 2% of all patients presenting to a London acute hospital and 1.4% of patients without a history of MRSA were

Table V
Comparison of the characteristics of patients with healthcare-associated and community-associated meticillin-resistant *Staphylococcus aureus* (HA- and CA-MRSA) strain types

	HA-MRSA ($N = 399$)		CA-MRSA ($N = 85$)		OR (95% CI)	*P*
	N	(%)	*N*	(%)		
Demographics						
Mean age (standard deviation)/years	61.2 (22.5)		46.5 (25.1)		0.98 (0.97–0.99)	**<0.001**
Median age (range)/years	66 (0–97)		50 (0–94)			
Gender (female)	173	(43.4)	40	(47.1)	1.2 (0.7–1.9)	0.533
Epidemiological data						
Previous hospitalization	100	(25.1)	15.0	(17.6)	–	0.318
Overnight hospital stay in the past 12 months	73	(18.3)	10	(11.8)	0.7 (0.2–2.4)	0.139
Day hospital visit in the past 12 months	27	(6.8)	5	(5.9)	1.2 (0.5–3.4)	0.642
Previous positive for MRSA	128	(32.1)	20	(23.5)	0.6 (0.4–1.1)	0.122
Pre-admission screen	89	(22.3)	25	(29.4)	1.4 (0.9–2.4)	0.163
Admitted from a care home or hostel	11	(2.8)	3	(3.5)	–	0.872
Admission from care home	10	(2.5)	3	(3.5)	1.4 (0.4–5.3)	0.601
Admission from homeless hostel	1	(0.2)	0	(0.0)	–	1.000
Healthcare-associated (epidemiologically defined)	311	(77.9)	53	(62.3)	0.5 (0.3–0.8)	**0.003**
Specialty						
Surgery	130	(32.6)	39	(45.9)	Reference	
Medicine	196	(49.1)	28	(32.9)	0.5 (0.3–0.8)	**0.006**
Accident and emergency	20	(5.0)	12	(14.1)	2.0 (0.9–4.4)	0.090
Intensive care unit	42	(10.5)	3	(3.5)	0.2 (0.1–0.8)	**0.022**
Obstetrics/gynaecology/neonatology	11	(2.8)	3	(3.5)	0.9 (0.2–3.4)	0.888
Antimicrobial resistance						
Ciprofloxacin	380	(95.2)	28	(32.9)	0.02 (0.01–0.05)	**<0.001**
Erythromycin	272	(68.2)	29	(34.1)	0.2 (0.1–0.4)	**<0.001**
Fusidic acid	42	(10.5)	34	(40.0)	5.7 (3.3–9.7)	**<0.001**
Gentamicin	67	(16.8)	7	(8.2)	0.4 (0.2–1.0)	**0.047**
Tetracycline	21	(5.3)	14	(16.5)	3.5 (1.7–7.3)	**0.001**
Trimethoprim	62	(15.5)	18	(21.2)	1.5 (0.8–2.6)	0.206
Mupirocin	13	(3.3)	3	(3.5)	1.1 (0.3–3.9)	0.899
Number of non-beta lactam resistance classes						
Resistant to no non-beta lactam classes	9	(2.3)	18	(21.2)	11.6 (5.0–27.0)	**<0.001**
Resistant to <2 non-beta lactam classes	102	(25.6)	41	(48.2)	2.7 (1.7–4.4)	**<0.001**
PVL						
PVL	0	(0.0)	19	(22.3)	1.3 (1.2–1.4)	**<0.001**
SCC*mec* type						
I	1	(0.2)	0	(0.0)	–	–
II	56	(14.0)	0	(0.0)	–	–
III	10	(2.5)	0	(0.0)	–	–
IV	312	(78.2)	63	(74.1)	–	–
V	0	(0.0)	9	(10.6)	–	–
Non-typeable	20	(5.0)	13	(15.3)	–	–
***spa* diversity**						
Unique *spa* types	78	(19.5)	35	(41.2)	–	**<0.001**
Common *spa* types (inferred MLST CC)						
spa CC1 (CC22)	320	(80.2)	2	(2.3)		
t032	*196*	*(49.1)*	–	–		
t022	*19*	*(4.8)*	–	–		
spa CC2 (CC30)	62	(15.5)	7	(8.2)		
t018	*37*	*(9.3)*	*0*	*(0.0)*		
t012	*9*	*(2.3)*	*2*	*(2.3)*		
spa CC3	5	(1.3)	12	(14.1)		
spa CC4 (CC8)	12	(3.0)	17	(20.0)		
t190	*10*	*(2.5)*	–	*(0.0)*		

(*continued on next page*)

Table V (*continued*)

	HA-MRSA ($N = 399$)		CA-MRSA ($N = 85$)		OR (95% CI)	*P*
	N	(%)	*N*	(%)		
t008	*1*	*(0.2)*	*11*	*(12.9)*		
spa CC5	0	(0.0)	28	(32.9)		
t127	–	–	*22*	*(25.9)*		
t044	–	–	*3*	*(3.5)*		
Other	0	(0.0)	19	(22.3)		

PVL, Panton-Valentine leukocidin; SCC*mec*, staphylococcal cassette chromosome *mec*; MLST, multi-locus sequence type; CC, clonal clusters; OR, odds ratio; CI, confidence interval.

colonized with MRSA. Risk factors for MRSA carriage were similar to those reported in other studies.[1,3,6,15] Patients who had an MRSA-positive admission screen or a history of MRSA were considerably more likely to submit an MRSA-positive clinical specimen during the 12 months after their admission, in line with other studies.[1,15] Ninety-three (40%) patients who submitted a positive clinical specimen in the 12 months after admission had a negative admission screen, so it is likely that a proportion of these patients represent nosocomial acquisition.[15]

Of the MRSA isolates tested, 82% were HA-MRSA strain types and 18% were CA-MRSA strain types. CA-MRSA strains were disproportionately represented among certain specialties, accounting for more than 20% of the recovered MRSA identified in surgical patients (mainly pre-admission screens) and 38% of those from accident and emergency; both groups present mainly from the community, with less prior hospital exposure. The CA-MRSA strain types had different epidemiological associations from the HA-MRSA strains, so risk factors used for the identification of HA-MRSA may not detect CA-MRSA reliably. However, no significant difference in the proportion of HA-MRSA and CA-MRSA strain types from patients with prior hospital admission or previous MRSA episodes was identified, reflecting the continuing breakdown of purely epidemiological definitions of CA-MRSA.[9]

The finding of a 2% overall rate of colonization is comparable with hospitals performing universal screening in England between 2006 and 2009[16] and Scotland in 2010.[17] Rates from six Scottish hospitals performing universal screening in 2008–2009 were somewhat higher at 3.9%.[15] These rates are considerably lower than the rates reported from screening targeted specialities, including 6.7% of medical and surgical patients in the study hospital in 2006–2007,[18] 8.6% of emergency admissions to another London hospital in 2004–2005,[19] and 5.1% of Swiss surgical patients in 2005–2006.[20]

The present low rate of MRSA colonization at admission in England and Scotland may be the result of several factors. Firstly, universal screening includes a high proportion of patients at low risk of MRSA colonization and therefore inevitably reduces measured colonization rates compared with targeted screening. Secondly, as a result of national infection control improvement programmes, the rate of MRSA infection and transmission in hospitals in England and Scotland has fallen considerably in the last few years.[21,22] This has probably resulted in a smaller number of new patient carriers being discharged, and consequently a lower rate of 'revolving door' carriers being re-admitted.[23] Indeed, in a recent study from Scotland evaluating the impact of the introduction of universal screening, the rate of MRSA colonization fell from 5.5% at the start of the study to 3.5% at the end of the study.[15] It is likely that this change in MRSA epidemiology is happening throughout the UK, and the cost–benefit analyses used previously to justify universal and economic analyses based on a higher rate of colonization (6–7%) will need to be reviewed.[24,25] With a low overall admission prevalence of MRSA, it may be cost-beneficial to use targeted rather than universal screening if this could identify a significant proportion of carriers.[2,3] However, if, as seems likely, the prevalence of CA-MRSA strain types increases, targeted screening policies may require modification to accommodate the novel epidemiology of CA-MRSA strains. For example, in some parts of the USA, CA-MRSA now account for the majority of MRSA identified on hospital admission, so risk factors used to identify patients for targeted screening would require modification in these settings.[9,26,27]

The strengths of this study include the large number of patients admitted, molecular typing on most of the strains involved, and clinical information on all patients. Limitations include possible underestimation of true CA-MRSA prevalence because these strains can colonize non-standard sites.[28] Screens from clinical sites were included, but these were collected at the discretion of clinical staff. Not all MRSA isolates were saved by the clinical laboratory, which may have underestimated the prevalence of certain genotypes. Relatively few CA-MRSA strains were identified, so the epidemiological associations of CA-MRSA strain types are less certain than for HA-MRSA strain types. Detailed epidemiological and demographic data were lacking for the MRSA-negative patients, such as antimicrobial use, ethnicity, socio-economic factors and health status, which would be required to make a thorough investigation of risk factors.

At present, it is not clear what proportion of patients carrying MRSA at admission needs to be identified to prevent onward transmission. There is some evidence that both targeted screening and universal screening detect a sufficient amount of MRSA colonization to reduce transmission.[2,3] The situation is made more difficult by the changing epidemiology of MRSA in the UK. Overall MRSA colonization rates at admission are now low at approximately 2%. HA-MRSA colonization rates are low and apparently falling, and CA-MRSA rates are very low (approximately 0.3%) but represent a substantial proportion of MRSA in some specialties and may be increasing. Previous cost–benefit analyses of MRSA admission screening should be reviewed in light of the low overall colonization rate revealed by this study, and new screening and control strategies may need to be developed for the likely increasing prevalence of CA-MRSA.

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Conflict of interest statement

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References

1. Lowy FD. *Staphylococcus aureus* infections. *N Engl J Med* 1998;**339**:520—532.
2. Dancer SJ. Considering the introduction of universal MRSA screening. *J Hosp Infect* 2008;**69**:315—320.
3. Coia JE, Duckworth GJ, Edwards DI, *et al*. Guidelines for the control and prevention of meticillin-resistant *Staphylococcus aureus* (MRSA) in healthcare facilities. *J Hosp Infect* 2006;**63**:1—44.
4. Cookson B, Bonten MJ, Mackenzie FM, Skov RL, Verbrugh HA, Tacconelli E. Meticillin-resistant *Staphylococcus aureus* (MRSA): screening and decolonisation. *Int J Antimicrob Agents* 2011;**37**:195—201.
5. Weber SG, Huang SS, Oriola S, *et al*. Legislative mandates for use of active surveillance cultures to screen for methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant enterococci: position statement from the Joint SHEA and APIC Task Force. *Am J Infect Control* 2007;**35**:73—85.
6. Harbarth S, Sax H, Fankhauser-Rodriguez C, Schrenzel J, Agostinho A, Pittet D. Evaluating the probability of previously unknown carriage of MRSA at hospital admission. *Am J Med* 2006;**119**:275. e15—23.
7. Zetola N, Francis JS, Nuermberger EL, Bishai WR. Community-acquired meticillin-resistant *Staphylococcus aureus*: an emerging threat. *Lancet Infect Dis* 2005;**5**:275—286.
8. Otter JA, French GL. Molecular epidemiology of community-associated meticillin-resistant *Staphylococcus aureus* in Europe. *Lancet Infect Dis* 2010;**10**:227—239.
9. Otter JA, French GL. Community-associated meticillin-resistant *Staphylococcus aureus*: the case for a genotypic definition. *J Hosp Infect* 2012;**81**:143—148.
10. Batra R, Eziefula AC, Wyncoll D, Edgeworth J. Throat and rectal swabs may have an important role in MRSA screening of critically ill patients. *Intensive Care Med* 2008;**34**:1703—1706.
11. Otter JA, French GL. The emergence of community-associated methicillin-resistant *Staphylococcus aureus* at a London teaching hospital, 2000—2006. *Clin Microbiol Infect* 2008;**14**:670—676.
12. Milheirico C, Oliveira DC, de Lencastre H. Update to the multiplex PCR strategy for assignment of *mec* element types in *Staphylococcus aureus*. *Antimicrob Agents Chemother* 2007;**51**:3374—3377.
13. Otter JA, French GL. Utility of antimicrobial susceptibility-based algorithms for the presumptive identification of genotypically-defined community-associated methicillin-resistant *Staphylococcus aureus* at a London teaching hospital. *Eur J Clin Microbiol Infect Dis* 2011;**30**:459—463.
14. Boakes E, Kearns AM, Ganner M, *et al*. Molecular diversity within clonal complex 22 methicillin-resistant *Staphylococcus aureus* encoding Panton-Valentine leukocidin in England and Wales. *Clin Microbiol Infect* 2011;**17**:140—145.
15. Reilly JS, Stewart S, Christie P, *et al*. Universal screening for meticillin-resistant *Staphylococcus aureus* in acute care: risk factors and outcome from a multicentre study. *J Hosp Infect* 2012;**80**:31—35.
16. Collins J, Raza M, Ford M, Hall L, Brydon S, Gould FK. Review of a three-year meticillin-resistant *Staphylococcus aureus* screening programme. *J Hosp Infect* 2011;**78**:81—85.
17. van Velzen EV, Reilly JS, Kavanagh K, *et al*. A retrospective cohort study into acquisition of MRSA and associated risk factors after implementation of universal screening in Scottish hospitals. *Infect Control Hosp Epidemiol* 2011;**32**:889—896.
18. Jeyaratnam D, Whitty CJ, Phillips K, *et al*. Impact of rapid screening tests on acquisition of meticillin resistant *Staphylococcus aureus*: cluster randomised crossover trial. *BMJ* 2008; **336**:927—930.
19. Gopal Rao G, Michalczyk P, Nayeem N, Walker G, Wigmore L. Prevalence and risk factors for meticillin-resistant *Staphylococcus aureus* in adult emergency admissions — a case for screening all patients? *J Hosp Infect* 2007;**66**:15—21.
20. Harbarth S, Fankhauser C, Schrenzel J, *et al*. Universal screening for methicillin-resistant *Staphylococcus aureus* at hospital admission and nosocomial infection in surgical patients. *JAMA* 2008;**299**:1149—1157.
21. Edgeworth JD. Has decolonization played a central role in the decline in UK methicillin-resistant *Staphylococcus aureus* transmission? A focus on evidence from intensive care. *J Antimicrob Chemother* 2011;**66**(Suppl. 2):ii41—ii47.
22. *Health Protection Scotland, National Services Scotland, NHS Scotland MRSA Screening Pathfinder Programme; Final Report. Executive Summary* 2011. Health Protection Scotland [Report].
23. Cooper BS, Medley GF, Stone SP, *et al*. Methicillin-resistant *Staphylococcus aureus* in hospitals and the community: stealth dynamics and control catastrophes. *Proc Natl Acad Sci USA* 2004;**101**:10223—10228.
24. Jacqui Reilly, Sally Stewart, Traiani Stari, *et al*. *Health Protection Scotland, National Services Scotland, NHS Scotland MRSA Screening; Update Report on Pathfinder project* 2011. Health Protection Scotland [Report].
25. Robotham JV, Graves N, Cookson BD, *et al*. Screening, isolation, and decolonisation strategies in the control of meticillin resistant *Staphylococcus aureus* in intensive care units: cost effectiveness evaluation. *BMJ* 2011;**343**:d5694.
26. Popovich KJ, Weinstein RA, Hota B. Are community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) strains replacing traditional nosocomial MRSA strains? *Clin Infect Dis* 2008;**46**:787—794.
27. Otter JA, French GL. Community-associated meticillin-resistant *Staphylococcus aureus* strains as a cause of healthcare-associated infection. *J Hosp Infect* 2011;**79**:189—193.
28. Yang ES, Tan J, Eells S, Rieg G, Tagudar G, Miller LG. Body site colonization in patients with community-associated methicillin-resistant *Staphylococcus aureus* and other types of *S. aureus* skin infections. *Clin Microbiol Infect* 2009;**16**: 425—431.