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# Meticillin-resistant *Staphylococcus aureus* in elderly residents of care homes: colonization rates and molecular epidemiology☆

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SUMMARY

***Background:*** Meticillin-resistant *Staphylococcus aureus* (MRSA) is a significant cause of mortality and morbidity in healthcare and community settings; however, there is a paucity of large-scale, longitudinal studies monitoring the occurrence of MRSA in the care home setting.
***Aim:*** To determine the molecular epidemiology of MRSA colonizing elderly residents of care homes.
***Methods:*** Residents in 65 care homes in Leeds, UK, were screened for MRSA nasal colonization in four consecutive years (2006–2009). Isolates were characterized using antibiotic susceptibility testing, detection of the Panton–Valentine leucocidin (PVL) locus, accessory gene regulator allotyping, characterization of the staphylococcal cassette chromosome *mec* element, *spa*-typing and pulsed-field gel electrophoresis.
***Findings:*** MRSA was recovered from 888 nasal swabs of 2492 residents and prevalence was similar (19–22%) throughout the study. Resistance to ≥3 antibiotic classes was common (34%), but resistance to only β-lactam agents was rare (3%); no PVL-positive isolates were identified. Most isolates were related to healthcare-associated epidemic-MRSA type 15 (EMRSA-15, ST22-IV); such isolates decreased in prevalence during the study (86–72%; $P < 0.0001$, $\chi^2$-test). The remainder belonged to five different multi-locus sequence type clonal complexes (CC). Most notably, CC59 strains increased in prevalence (10–25%; $P < 0.0001$, $\chi^2$-test) and were associated with high-level mupirocin resistance.
***Conclusions:*** The molecular epidemiology of MRSA in care homes is complex and dynamic. There was a high, consistent prevalence of MRSA nasal colonization, dominated by healthcare-associated strains. Vigilance is recommended; however, as high-level mupirocin resistance was associated with a single clonal group (CC59) that significantly increased in prevalence during the study.


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## Introduction

Meticillin-resistant *Staphylococcus aureus* (MRSA) has traditionally been associated with hospitals and other healthcare institutions (known as healthcare-associated MRSA, or HA-MRSA). Following the establishment of mandatory reporting and hospital infection 'targets' in England, there have been marked reductions in MRSA bacteraemia incidence; however, less is known about the epidemiology of MRSA in other healthcare settings, such as care homes.[1–3]

Care home residents are a group at risk of MRSA colonization. Recent studies report MRSA colonization rates of up to 20% in care home residents, likely reflecting endemic MRSA in hospitals. Factors such as sedentary lifestyle, the need for invasive devices, the presence of chronic wounds such as pressure sores or ulcers, dependence on healthcare workers, and previous hospitalization have been associated with a risk of acquiring MRSA.[4–11]

The present study took place in one primary care trust (PCT) (Leeds), which is served by a large, single acute-care institution, Leeds Teaching Hospitals NHS Trust (LTHT). This work forms part of a larger project that investigated the effectiveness of improving infection prevention knowledge and practice on MRSA colonization of elderly residents in care homes, the results of which have been reported elsewhere.[12] The objective of the present study was to determine the molecular epidemiology of MRSA colonizing a large sample of elderly residents of care homes in Leeds PCT over a four-year period (2006–2009).

## Methods

### Participation

In the UK, a care home is defined as 'any home that provides accommodation, together with nursing or personal care, for any person who is, or has been, ill or is disabled or infirm'.[13] Care homes with 20 or more beds registered in the City of Leeds were eligible to take part in the study. Homes that provided care for people with mental, physical or learning disabilities were excluded. The study received approval from the East Leeds Research Ethics Committee.

Ninety of the 186 registered care homes met the study criteria and were invited to participate. Each participating care home was given a unique identifying number and was anonymized to laboratory staff. Eligibility to participate in the study was based on mental capacity. Residents were judged to be eligible to participate by care home staff. In the first instance, written consent was obtained, followed by verbal consent if the resident agreed to participate in subsequent surveys. No specific infection prevention interventions were initiated on the identification of a resident who was found to be colonized with MRSA.

### Study design

Nasal swabs were used to sample the anterior nares of consenting residents during four periods: 16 November 2006 to 13 December 2006 (Survey 1); 1 October 2007 to 12 November 2007 (Survey 2); 1 May 2008 to 26 June 2008 (Survey 3); and 5 January to 12 February 2009 (Survey 4).

### Microbiological methods

Each nasal swab (Amies' Transport swabs, Barloworld Scientific, Stone, UK) was used to inoculate a single chromogenic agar plate (MRSA *Select*™; Bio-Rad, Marnes la Coquette, France), which was incubated for 18–24 h at 37 °C. Dark pink colonies were considered to be presumptive MRSA.

Presumptive MRSA colonies were confirmed as *S. aureus* by DNase agar testing and a positive agglutination reaction using the Pastorex™ Staph plus kit (Bio-Rad). Meticillin resistance was confirmed by breakpoint susceptibility testing using Iso-Sensitest agar (Oxoid, Basingstoke, UK) supplemented with 4, 8 and 12 mg/L meticillin, respectively (Medical Wire and Equipment Co. Ltd, Corsham, UK) or 4 mg/L cefoxitin (Mast Diagnostics, Bootle, UK). Meticillin-susceptible *S. aureus* strain NCTC 6571 and MRSA strain NCTC 10442 were used as control organisms.

### Characterization of isolates

The susceptibility of all isolates to six antibiotic classes (ciprofloxacin, erythromycin, fusidic acid, mupirocin, tetracycline and trimethoprim) was determined using the British Society for Antimicrobial Chemotherapy standardized disc susceptibility testing method.[14]

Genomic DNA was extracted using the Wizard® Genomic DNA Purification kit according to the manufacturer's instructions (Promega UK Ltd, Southampton, UK). Published methods were used for detection of the PVL locus (*luk*S–*luk*F) and accessory gene regulator (*agr*) allotyping.[15,16] Multiplex polymerase chain reaction schemes were used to characterize the staphylococcal cassette chromosome *mec* (SCC*mec*) elements.[17,18]

### Pulsed-field gel electrophoresis

Restriction endonuclease digestion of bacterial whole-cell DNA with *Sma*I followed by pulsed-field gel electrophoresis (PFGE) was used to assess epidemiological relatedness of the MRSA isolates using a standardized protocol.[19] The resultant profiles were compared using BioNumerics software (Applied Maths NV, Sint-Martens-Latem, Belgium). Isolates were considered to be indistinguishable, related or different according to guidelines recommended by Tenover *et al.*[20] Multi-locus sequence type clonal complexes (MLST CC) were predicted for the PFGE clusters using the results of *spa*-typing, *agr* and SCC*mec* typing.

### Spa-typing

Thirty-six isolates were selected for *spa*-typing; each isolate had a unique PFGE pattern that was unrelated to EMRSA-15. *Spa*-typing was performed using the method of Harmsen *et al.* and *spa*-types assigned using Ridom StaphType software (Ridom GmbH, Würzburg, Germany).[21]

## Results

### Prevalence of MRSA colonization

Sixty-five of the 90 (72%) eligible care homes participated in all four surveys. In total, 4327 swabs were collected from 2492 residents (1210, 1067, 1023 and 1027, in Surveys 1, 2, 3 and 4,