

SHORT REPORT

The impact of household transmission on duration of outpatient colonization with methicillin-resistant *Staphylococcus aureus*

E. LAUTENBACH^{1,2,3,4*}, P. TOLOMEO³, I. NACHAMKIN^{4,5}, B. HU^{3,5}
AND T. E. ZAOUTIS^{2,3,4,6}

¹ Division of Infectious Diseases, Department of Medicine; ² Department of Biostatistics and Epidemiology;

³ Center for Clinical Epidemiology and Biostatistics; ⁴ Center for Education and Research on Therapeutics;

⁵ Department of Pathology and Laboratory Medicine, University of Pennsylvania School of Medicine, Philadelphia, PA, USA

⁶ Division of Infectious Diseases, Department of Pediatrics, The Children's Hospital of Philadelphia, PA, USA

(Accepted 22 December 2009; first published online 29 January 2010)

SUMMARY

We identified eight consecutive patients who presented with a skin or soft tissue infection due to MRSA. Of seven household members of these cases, three were colonized with MRSA. The mean duration of MRSA colonization in index cases was 33 days (range 14–104), while mean duration of colonization in household cases was 54 days (range 12–95). There was a borderline significant association between having a concurrent colonized household member and a longer duration of colonization (mean 44 days vs. 26 days, $P=0\cdot08$).

Key words: Colonization, household, MRSA.

Infections due to methicillin-resistant *Staphylococcus aureus* (MRSA) have risen markedly over the past 20 years [1]. Although historically limited to healthcare settings, MRSA infections in the community [i.e. community-acquired MRSA (CA-MRSA)] have increased rapidly [2]. Efforts to control CA-MRSA have been challenging due to an incomplete understanding of the epidemiology of colonization with this organism. Focusing on CA-MRSA colonization is critical because the longer a patient remains colonized, the greater the likelihood of both developing a new CA-MRSA infection as well as transmitting the organism to others. Reports have described spread of MRSA in

households [3, 4]. However, no longitudinal studies of CA-MRSA colonization and transmission in the household setting have been performed. The goals of this study were to determine the duration of CA-MRSA colonization and explore the impact of household MRSA transmission on duration of colonization.

During a 2-week period in June 2008, we identified all consecutive adult patients who presented to a University of Pennsylvania Health System outpatient setting with a skin or soft tissue infection (SSTI) confirmed by culture to be due to MRSA. Eligible subjects were contacted via phone and asked whether they and all household members were willing to participate in the study. For those households in which all members agreed to participate, research staff visited the household within 1 week of the initial presentation of the SSTI in the household index case. Following enrolment, each subject in the household (i.e. the index case and all household members) underwent self-sampling

* Author for correspondence: Dr E. Lautenbach, University of Pennsylvania School of Medicine, Center for Clinical Epidemiology and Biostatistics, 825 Blockley Hall, 423 Guardian Drive, Philadelphia, PA 19104-6021, USA.
(Email: ebbing@mail.med.upenn.edu)

This paper was presented in part at the 19th Annual Meeting of the Society for Healthcare Epidemiology of America (SHEA), 19–22 March 2009, San Diego, CA, USA.

for MRSA colonization. It should be noted that self-sampling for MRSA is highly sensitive compared to sampling by a healthcare professional [5]. Every subject provided self-collected swabs from the following anatomic sites: nares, axillae, throat, groin, and perineum. These swabs were obtained every 2 weeks and sent to the study laboratory via express mail. Subjects were requested to submit swabs for a total of 3 months after the first swab was obtained (i.e. about 14 weeks total).

ChromAgar MRSA medium (BBL™ CHROMagar™ MRSA, BD Diagnostic Systems, USA) was used to plate swab samples [6]. The genetic relatedness of MRSA isolates was determined by molecular typing using pulsed-field gel electrophoresis (PFGE). Chromosomal DNA was digested with *Sma*I restriction profiles [7] with the results analysed using the Fingerprinting II Informatix Software version 3.0 (Bio-Rad, USA) and interpreted using established criteria [8]. *SCCmec* typing was performed using a PCR protocol previously described [9]. Presence of Pantón–Valentine leukocidin (PVL) was not assessed.

The actual end date of colonization was considered as the midpoint between the date of the last positive culture and the date of the first negative culture. If the last culture during the follow-up period was positive, this was considered the date of last positive culture. The unadjusted association between specific variables and duration of colonization was assessed using the Wilcoxon rank sum test. A two-tailed *P* value of <0.05 was considered significant. All statistical calculations were performed using Stata version 10 (StataCorp, USA).

This study was reviewed and approved by the University of Pennsylvania Institutional Review Board.

Eight households comprising 15 subjects were enrolled in the study. Of the 15 subjects, 10 (67%) were female, eight were white, three were African American, and four were of unknown race. The median age of subjects was 46 years (range 21–76). There was one four-person household, four two-person households, and three one-person households. By definition, there were eight index cases (i.e. subjects who initially presented with a SSTI due to MRSA) who were all colonized with MRSA upon enrolment. In addition, of seven household members, three (43%) were found to be colonized with MRSA. Of the latter, one was positive at baseline (upon initial sampling) while another two became newly colonized after enrolment. No clinical MRSA infections were

identified during the study nor were any decolonization protocols offered to subjects.

The mean duration of follow-up in all subjects was 56 days (range 14–104). The mean duration of colonization in index cases was 33 days (range 14–104), while mean duration of colonization in household cases was 54 days (range 12–95). Of all 11 subjects who were colonized (eight index cases and three household members), three remained colonized at the end of follow-up. For index cases, there were no significant associations between baseline demographics and duration of MRSA colonization. However, there was a borderline significant association between having a concurrent colonized household member and a longer duration of colonization (mean 44 days vs. 26 days, *P*=0.08). Several PFGE types were detected, with the same type detected within a family. One of the types was identical to USA300 [10]. Both *SCCmecII* and *SCCmecIVa* MRSA isolates were identified although the *SCCmec* type was not associated with duration of colonization.

We found that MRSA colonization in the outpatient setting is often prolonged. Furthermore, nearly 50% of household members were also found to be colonized. This raises issues both for the impact of colonization of the index case on potential spread to household members, as well as the potential for spread from household members to the index case. Indeed, the borderline association between presence of an MRSA-colonized household member and prolonged MRSA colonization in the index case supports this concept. We also demonstrated the feasibility of longitudinal self-collection of swab samples for MRSA by study subjects. Overall, our results demonstrate the important role of household transmission in the epidemiology and propagation of CA-MRSA. Future efforts to curb the spread and impact of CA-MRSA must be based on a thorough understanding of the longitudinal dynamics of MRSA colonization within households.

ACKNOWLEDGEMENTS

This work was supported by a Commonwealth Universal Research Enhancement (CURE) grant from the Pennsylvania Department of Health (E.L.), a National Institutes of Health (NIH) grant K24AI080942 (E.L.) and by grant no. U18HS016946 from the Agency for Healthcare Research and Quality. The content is solely the responsibility of the authors and does not necessarily represent the official

views of the Agency for Healthcare Research and Quality.

DECLARATION OF INTEREST

Dr Lautenbach has received research support from Merck, Ortho-McNeil, Cubist and AstraZeneca.

REFERENCES

1. **National Nosocomial Infections Surveillance (NNIS) System Report.** Data summary from January 1992 through June 2004, issued October 2004. *American Journal of Infection Control* 2004; **32**: 470–485.
2. **Herold BC, et al.** Community-acquired methicillin-resistant *Staphylococcus aureus* in children with no identified predisposing risk. *Journal of the American Medical Association* 1998; **279**: 593–598.
3. **Wagenvoort JH, et al.** Risk of re-introduction of methicillin-resistant *Staphylococcus aureus* into the hospital by intrafamilial spread from and to healthcare workers. *Journal of Hospital Infection* 2005; **59**: 67–68.
4. **Huang YC, et al.** Nasal carriage of methicillin-resistant *Staphylococcus aureus* in household contacts of children with community-acquired diseases in Taiwan. *Pediatric Infectious Diseases Journal* 2007; **26**: 1066–1068.
5. **Lautenbach E, et al.** Surveillance cultures for detection of methicillin-resistant *Staphylococcus aureus*: Diagnostic yield of anatomic sites and comparison of provider- and patient-collected samples. *Infection Control and Hospital Epidemiology* 2009; **30**: 380–382.
6. **Han Z, et al.** Evaluation of mannitol salt agar, CHROMagar™ Staph aureus and CHROMagar™ MRSA for detection of methicillin-resistant *Staphylococcus aureus* from nasal swab specimens. *Journal of Medical Microbiology* 2007; **56**: 43–46.
7. **Peacock SJ, et al.** Comparison of multilocus sequence typing and pulsed-field gel electrophoresis as tools for typing *Staphylococcus aureus* isolates in a micro-epidemiological setting. *Journal of Clinical Microbiology* 2002; **40**: 3764–3770.
8. **Tenover FC, et al.** Interpreting chromosomal DNA restriction patterns produced by pulsed-field gel electrophoresis: criteria for bacterial strain typing. *Journal of Clinical Microbiology* 1995; **33**: 2233–2239.
9. **Zhang K, et al.** Novel multiplex PCR assay for characterization and concomitant subtyping of staphylococcal cassette chromosome mec types I to V in methicillin-resistant *Staphylococcus aureus*. *Journal of Clinical Microbiology* 2005; **43**: 5026–5033.
10. **McDougal LK, et al.** Pulsed-field gel electrophoresis typing of oxacillin-resistant *Staphylococcus aureus* isolates from the United States: establishing a national database. *Journal of Clinical Microbiology* 2003; **41**: 5113–5120.