



Review article

Non-hospital environment contamination with *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus*: proportion meta-analysis and features of antibiotic resistance and molecular genetics



Jialing Lin, Dongxin Lin, Ping Xu, Ting Zhang, Qianting Ou, Chan Bai, Zhenjiang Yao*

Department of Epidemiology and Health Statistics, Guangdong Pharmaceutical University, Guangzhou 510310, China

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ABSTRACT

Background: *Staphylococcus aureus* (*S. aureus*), including methicillin-resistant *Staphylococcus aureus* (MRSA), survives in dry conditions and can persist for long periods on surfaces touched by humans. Studies that estimate the proportions and characteristics of *S. aureus* and MRSA contamination in non-hospital environments are lacking. Therefore, we conducted a proportion meta-analysis and reviewed the features of antibiotic resistance and molecular genetics.

Methods: Articles published between January 2005 and December 2015 that studied proportions of *S. aureus* and MRSA contamination in non-hospital environments were retrieved from the Medline database, Ovid database and Science Direct database. All statistics were analyzed by STATA 14.1.

Results: Twenty-nine articles were included. The overall proportions of *S. aureus* and MRSA contamination were 41.1% (95%CI 29–54%) and 8.6% (95%CI 5–13%), respectively. The proportion of MRSA contamination increased over time. From the articles, the proportion of Pantone-Valentine Leukocidin (PVL) genes among MRSA isolates was 54.5%, and the proportion of the *qac* gene was 100.0%. Distribution of the multilocus sequence type (MLST) and pulsed-field gel electrophoresis (PFGE) of MRSA indicated that MRSA strains were from both hospitals and communities.

Conclusion: The overall proportions of *S. aureus* and MRSA contamination in non-hospital environments were high. The outcomes of antibiotic resistance and high proportions of PVL genes indicated that the antibiotic resistance of *S. aureus* and MRSA were notable. According to the different distributions of MLST and SCC_{mec} of MRSA, we can infer that cross-circulation is within hospitals, communities, and livestock. The results also show that the risk from the MRSA strains was cross-transmitted among the population. High proportions of the *qac* gene of MRSA might indicate that current disinfection of MRSA has not been achieved, and it might be better to further identify the efficiency of the sterilization processes in a non-hospital environment so that relevant departments can take measures to improve disinfection of MRSA in non-hospital environments.

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* Corresponding author.

E-mail address: zhijiao2001@yahoo.com (Z. Yao).

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1. Introduction

Staphylococcus aureus (*S. aureus*) is an important pathogenic bacteria both in hospitals and communities (Chen et al., 2015; Khanal et al., 2015) and can cause various life-threatening infections, including necrotizing pneumonia and subcutaneous abscesses (Montagnani et al., 2013; Nazareth et al., 2012). Moreover, *S. aureus* is part of the normal flora and can be found in the anterior nares, skin, axilla, perineum, and pharynx. Due to overuse of antibiotics in clinical treatment, the antibiotic resistance of *S. aureus* has increased and methicillin-resistant *S. aureus* (MRSA) has emerged since 1961 (Eriksen, 1961).

In the United States, the proportion of methicillin resistance in *S. aureus* strains approached almost 60% in 2003, with an average resistance rate of approximately 50% over the period from 1998 to 2002 (NNIS, 2004). In Europe, the proportion of methicillin resistance in *S. aureus* strains isolated from infected patients increased from 21% in 2002–2023% in 2005 and then decreased to 19% in 2008. Between 2002 and 2005, the annual increase was 7.6%, followed by an average annual decrease of 4.8% (de Kraker et al., 2013). In China, the proportion of methicillin resistance in *S. aureus* strains decreased over the period from 2009 to 2014, but it was still high all over the world (Gesualdo et al., 2013; Ziakas et al., 2014). This has not only limited the choices of clinical antibiotics but also has increased the rate of infection and prolonged hospitalization (Yaw et al., 2014).

S. aureus, including MRSA, survives in dry conditions and can persist for long periods on surfaces touched by humans (Stepanovic et al., 2008). *S. aureus* and MRSA can be transmitted from person to person, from fomites to humans, and from air to humans (Huang et al., 2006; Zuckerman et al., 2009). Moreover, people colonized or infected with MRSA shed this bacteria into their environments and contaminate surfaces at concentrations sufficient for survival for extended periods of time. This process allows this bacteria to transmit to skin, clothing, and other fomites (Otter et al., 2011).

At present, most studies focus on the risk of transmission of *S. aureus* and MRSA in hospitals and patients in hospitals. Some studies on the proportions of *S. aureus* and MRSA contamination in non-hospital environments, including samples that have been collected from transportation (Lutz et al., 2014; Stepanovic et al., 2008), schools (Brooke et al., 2009; Mbogori et al., 2013), communities (Roberts et al., 2011a, 2011b), parks (Zhou and Wang, 2013), fire stations (Roberts and No, 2014), libraries (Roberts et al., 2011a, 2011b), and marine beaches (Fogarty et al., 2015; Soge et al., 2009). However, studies that reviewed the proportions of *S. aureus*

and MRSA contamination from non-hospital environments along with antibiotic resistance and molecular genetics are lacking. Moreover, in recent years, some studies have found that *S. aureus* and MRSA infections in communities have increased (Baud et al., 2014; Falcone and Venditti, 2012). The role of the environment in transmitting *S. aureus* and MRSA in the population has also been increasingly emphasized (Boyce et al., 1997; Boyce, 2007).

Therefore, in the present work, we performed a systematic review of previous studies to estimate proportions of *S. aureus* and MRSA contamination in non-hospital environments by utilizing a meta-analysis and reviewing the features of antibiotic resistance and molecular genetics, which might provide scientific guidance for prevention of diseases from *S. aureus* and MRSA in non-hospital environments.

2. Methods

2.1. Literature databases

This systematic review was conducted following Preferred Reporting Items for Systematic Reviews and Meta-Analyses guidelines (Moher et al., 2009). Major electronic databases were systematically searched, including the Medline database, Ovid database, and Science Direct database. Key words used for searching were: “MRSA” OR “methicillin resistant *Staphylococcus aureus*” OR “methicillin resistant *Staphylococcus aureus*” OR “*Staphylococcus aureus*” OR “*S. aureus*” AND “environment.” All the articles for studies published between January 2005 and December 2015 were included. References for all included articles and for additional studies were scanned. No language restrictions were applied.

2.2. Inclusion and exclusion criteria

Studies included in this systematic review met all the following criteria: (a) the study design was cross-sectional, (b) samples were from non-hospital environments, and (c) the study provided total number and proportions of identified *S. aureus* and/or MRSA contamination. Studies excluded according to one of the following criteria: (a) the study was based on mixed human-environment sampling without specific data on non-hospital environmental samples or reported epidemiological data on outbreaks, (b) the study was a microbiological study, (c) the study was a duplicate report, or (d) the study was a reviews letter, editorial article or meta-analysis.

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