Journal of Infection and Public Health (2015) **8**, 90—97

http://www.elsevier.com/locate/jiph

Molecular epidemiology of nasal isolates of methicillin-resistant *Staphylococcus aureus* from Jordan

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Received 5 March 2014; received in revised form 9 April 2014; accepted 24 May 2014

KEYWORDS
MRSA;
Healthcare workers;
Healthy individuals;
SCC*mec*IVa

Summary Asymptomatic carriage of methicillin-resistant *Staphylococcus aureus* (MRSA) can predispose the host to a wide range of infections. To inform public health strategies, this study sought to determine the prevalence and the phenotypic and genotypic characteristics of MRSA from nasal swabs of health care workers (HCWs) and other healthy individuals in Jordan. Overall, 716 nasal swabs were collected from 297 HCWs, 141 adults and 278 children in the community. MRSA was recovered from 56 (7.8%) nasal swabs, which represented carriage rates of 10.1%, 4.3% and 7.2% among HCWs, adults and children, respectively. The MRSA isolates were resistant to oxacillin (100%), erythromycin (42.8%), tetracycline (37.5%), clindamycin (5.3%), fucidin (5.3%), and ciprofloxacin (3.5%). A total of 17 different *spa* types belonging to eight different clonal complexes (CCs) were identified. All isolates were *mecA* positive, and *mecC*-MRSA was not detected. Analysis of the staphylococcal cassette chromosome *mec* (SCC*mec*) elements revealed that the majority (54; 96.4%) of the samples harbored the smaller type IV and V elements (the most common were SCC*mec* IVa or IVc, and there were two each of the IVg and V elements), and two were nontypable. The genes for Panton-Valentine leukocidin (*luk-PV*) were detected in 5.4% of the study isolates. A *tst*-positive, CC22-MRSA-SCC*mec*IVa clone (*spa* type t223) was identified as the dominant MRSA lineage among the nasal carriage isolates from both HCWs and other individuals (adults and children) in the community.

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http://dx.doi.org/10.1016/j.jiph.2014.05.007

These findings provide important information for public health personnel for the formulation of effective infection prevention and control strategies. Studies to further our understanding of the distribution, pathogenicity, transmissibility and fitness of this lineage would be prudent.

Introduction

Methicillin-resistant *Staphylococcus aureus* (MRSA) has long been recognized as a major nosocomial pathogen that is associated with severe morbidity and mortality [1]. Worldwide, MRSA infections and outbreaks have become an increasing problem not only in healthcare but also in community settings [2]. Studies from various countries have sought to establish the nasal carriage rate of MRSA in the community. The figures vary widely across the different locations and populations that have been surveyed. Published data show the nasal carriage rates of MRSA in Europe and the USA range from <0.1% to 2.5%, and rates up to 10.5% have been reported in Africa [3—8]. In countries in the Middle East (including Saudi Arabia, Kuwait, Lebanon and Palestine), 0—13.2% MRSA nasal carriage rates have been observed [9—14]. Studies in Jordan suggest high MRSA carriage rates of 7.5—19% among healthy individuals [15,16]. An additional concern is that a 3-year study (2003—2005) reported an MRSA rate of 56% among invasive isolates of *S. aureus* from multiple medical centers in Jordan [17]. Another study from Jordan [18] indicated that of the 232 *S. aureus* isolates recovered from diverse clinical samples (abscesses, wounds, skin infections, blood and nasal swabs), 62% were MRSA.

An understanding of the molecular epidemiology of MRSA is crucial for the formulation and implementation of appropriate infection prevention and control measures [19,20]. Despite the high MRSA rates, few reports have been published on the molecular epidemiology of MRSA in Jordan [16,21,22]. To our knowledge, a detailed analysis of the nasal strains of MRSA that occur in healthcare and community settings in Jordan has not been published. The objectives of the current study were to establish the prevalence and phenotypic and genotypic characteristics of MRSA from nasal swabs from HCWs and other healthy individuals (adults and children) in southern Jordan.

Material and methods

Study design and sample collection

The sample size of the current study was calculated using Kish's formula for cross-sectional studies [23] based on MRSA prevalences of 5.8%, 7.5% and 13% [15,21,24] in HCWs, adults and children, respectively, in Jordan. The minimum sample sizes required were 84 samples from HCWs, 107 samples from adults and 174 samples from children. The randomly collected samples examined in this study (297, 141 and 278 from HCWs, adults and children, respectively) exceeded these figures.

Between May 2011 and April 2012, non-duplicate nasal swabs were collected from the study population. Written informed consent and a questionnaire about general information and specific risk factors for MRSA carriage were obtained from each participant or, in the cases of the children, their parents or guardians. The ethics and scientific committee of the faculty of Medicine, Mu'tah University approved this study. All HCWs (medical doctors, nurses, technicians, domestic and administrative staff) were screened while working in the nursery, maternity, pediatric, medical, surgery and intensive care wards of Alkarak governmental hospital in Jordan. No MRSA outbreaks were apparent during the sampling period. All other adults and children were randomly selected from Alkarak province (population of 249,100 inhabitants in 2012). Nasal swabs were immersed in nutrient broth (Oxoid, Cambridge, UK) containing 5% NaCl and incubated for 3 h at 37 °C. Each broth was subcultured on mannitol salt agar (Oxoid, Cambridge, UK) and incubated at 35 °C for 24—72 h. Presumptive identifications of *S. aureus* were based on colony morphology, Gram staining, and positive catalase and slide agglutination reactions (bioMérieux, Marcy l'Etoile, France). The MRSA isolates were identified by disk diffusion using