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Short report

Sequence type 72 community-associated meticillin-resistant *Staphylococcus aureus* emerged as a predominant clone of nasal colonization in newly admitted patients[☆]

S.Y. Park^{a,†}, D.R. Chung^{a,b,c,*}, J.R. Yoo^{a,‡}, J.Y. Baek^b, S.H. Kim^b, Y.E. Ha^a, C.-I. Kang^a, K.R. Peck^a, N.Y. Lee^d, J.-H. Song^{a,b}

^a Division of Infectious Diseases, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, South Korea

^b Asia Pacific Foundation for Infectious Diseases (APFID), Seoul, South Korea

^c Infection Control Office, Samsung Medical Center, Seoul, South Korea

^d Department of Laboratory Medicine and Genetics, Samsung Medical Center, Seoul, South Korea

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SUMMARY

Current knowledge of community-associated (CA) meticillin-resistant *Staphylococcus aureus* (MRSA) carriage in hospitalized patients is incomplete. Genotypic characteristics of 637 nasal MRSA isolates from newly admitted patients in South Korea were investigated. Sequence type (ST) 72 accounted for 52.1%, 46.3%, and 52.8% of the isolates during the periods of 2007–2008, 2009–2010, and 2013–2014, respectively. Instead of classic MRSA clones responsible for healthcare-associated infections, including ST5 and ST239, MRSA with community genotype ST72 was the predominant strain in newly admitted patients regardless of age and home province of the patients. Active strategies are needed to prevent healthcare-associated infection by CA-MRSA.

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* Corresponding author. Address: Division of Infectious Diseases, Samsung Medical Center, Sungkyunkwan University School of Medicine, Irwon-ro 81, Gangnam-gu, Seoul 135-710, South Korea. Tel.: +82 2 3410 0323; fax: +82 2 3410 0064.

E-mail address: iddrchung@gmail.com (D.R. Chung).

[†] Current address: Division of Infectious Disease, Kangdong Sacred Heart Hospital, Hallym University College of Medicine, South Korea.

[‡] Current address: Division of Infectious Disease, Jeju National University School of Medicine, Jeju, South Korea.

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Introduction

Staphylococcus aureus is a leading human pathogen, and antimicrobial resistance of this organism has been a significant therapeutic challenge. Meticillin-resistant *S. aureus* (MRSA) is highly prevalent in hospitals in most countries worldwide. Emergence and spread of community-associated MRSA (CA-MRSA) during the past decades has made the situation more serious.^{1,2} *S. aureus* infections are usually preceded by colonization, and the most frequent body site of colonization is the

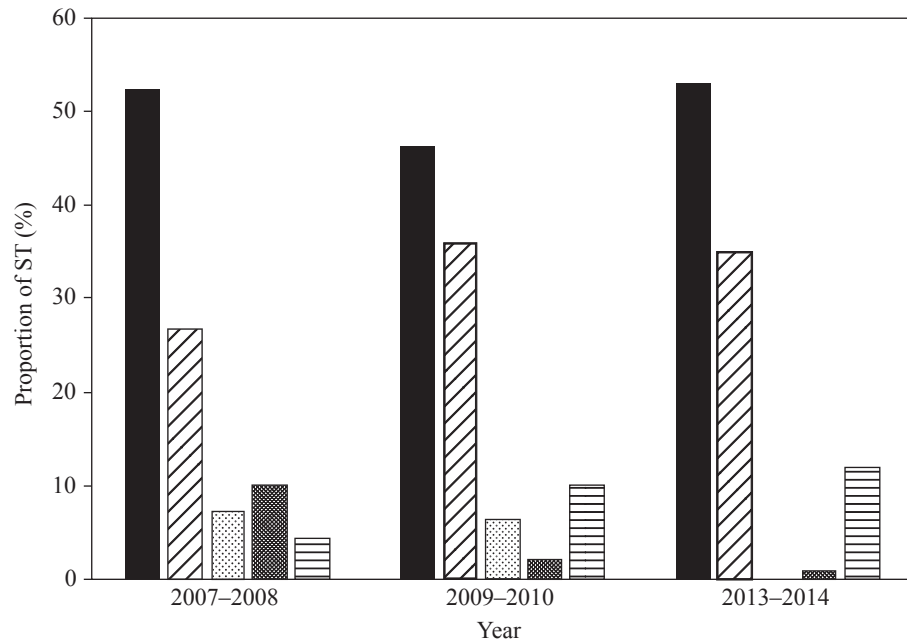


Figure 1. Temporal distribution of the major sequence types (ST) of nasal meticillin-resistant *Staphylococcus aureus* isolates in newly admitted patients during 2007–2014. ■ ST72 ▨ ST5 ▩ ST239 ▨ ST1 □ Others

anterior nares.³ Approximately one-third of healthy adults have been reported to carry *S. aureus* nasally, which has been shown to be highly associated with subsequent infection.⁴ Despite increasing prevalence of CA-MRSA infection, current understanding of CA-MRSA carrier status at admission and its role in healthcare-associated infection are not clear. In this study, we investigated the genotypic characteristics of nasal MRSA strains isolated from newly admitted patients in South Korea.

Methods

Bacterial strains included 637 non-duplicate MRSA nasal isolates collected from newly admitted patients at Samsung Medical Center (Seoul, South Korea), a university-affiliated tertiary care hospital with 1979 patient beds, during the periods of 2007–2010 and 2013–2014 according to the active surveillance policy of the hospital and were stocked in the Asian Bacterial Bank (Seoul, South Korea). For 2014, bacterial isolates and data from January to March were included. This study was approved by the Institutional Review Board of Samsung Medical Center. MRSA nasal screening for admitting patients was performed according to the infection control policy in our institution. The indications for screening included patients referred from other hospitals or chronic care facilities, patients scheduled for operations in the departments of orthopedic surgery, neurosurgery, thoracic surgery and general surgery, and patients receiving dialysis. The numbers of non-duplicate patients screened for MRSA nasal carriage at admission were 8779, 12,005, and 4193 during the periods of 2007–2008, 2009–2010, and 2013–2014, respectively. Only isolates from newly admitted patients were selected for this study. Conventional culture methods were used for screening and confirmation of nasal carrier status of MRSA. Only the first MRSA isolate from each patient was included. Staphylococcal

protein A (*spa*) typing was performed as previously described and the *spa* type was determined using Ridom SpaServer (<http://spaserver2.ridom.de/spatypes.shtml>). Multilocus sequence typing (MLST) was carried out using polymerase chain reaction amplification and sequencing of seven housekeeping genes (*arcC*, *aroE*, *glpF*, *gmk*, *pta*, *tpi*, and *yqiL*), as previously described.⁵ The allelic profiles and sequence types (STs) were assigned according to the MLST web site (<http://saurus.mlst.net/>). All statistical analyses were performed with Stata version 11.2 (StataCorp., College Station, TX, USA). All tests of significance were two-tailed, and $P < 0.05$ was considered statistically significant. Categorical variables were compared between different time periods using the χ^2 -test.

Results

MRSA nasal carriage rates of the admitted patients screened during the periods 2007–2008, 2009–2010, and 2013–2014 were 8.1%, 8.0% and 9.8%, respectively. Among those isolates, 637 non-duplicate isolates from newly admitted patients were selected and tested. A total of 29 different sequence types and 37 *spa* types were identified among nasal MRSA isolates. ST72 was the most frequent sequence type (52.1%, 46.3%, and 52.8%, respectively) of the isolates during the periods of 2007–2008, 2009–2010, and 2013–2014 (Figure 1). ST5 was the second most frequent sequence type (26.7%, 35.6%, and 34.7%, respectively). ST239 was identified in 7.1% and 6.3% of the isolates during the periods of 2007–2008 and 2009–2010, but was not found among the isolates in 2013–2014. ST1, the fourth most frequent sequence type (10.0%) during 2007–2008, decreased to 2.0% and 0.7%, respectively, during the periods of 2009–2010 and 2013–2014. Changes in the distribution of the nasal MRSA sequence type during the three periods were statistically significant ($P < 0.001$).

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