titer to TGR, SFGR, or STGO, the age range was 19–49 (median 25) years, and job specialties were infantrymen (63.5%), fighting vehicle infantrymen (16.4%), indirect fire infantrymen (14.2%), and heavy anti-hero weapons infantrymen (5.9%).

These results indicate that many US military personnel were exposed to rickettsiae and orientiae before their deployment to South Korea (Figure), perhaps because of previous deployments around the world or because of exposure to rickettsial agents at home (8–10). However, 206 (2.2%) of the men became infected with either a typhus group (n = 10) or spotted fever group (n = 181) rickettsia or a scrub typhus group orientia (n = 15) during their deployment to South Korea.

More SFGR infections occurred than TGR and STGO infections, although the pathogens for the latter infections (R. typhi and O. tsutsugamushi) are considered endemic to South Korea and are believed to affect the public and military health more than SFGR (3). The SFGR infections might correlate with recent observations of highly prevalent rickettsia-infected tick and R. felis–infected flea populations seen in South Korea (4,5). No evidence of co-infection was found in the men assessed during the deployment. These results suggest a risk for rickettsial disease, including scrub typhus and especially spotted fever, among US military personnel stationed in or visiting South Korea.

This study was supported by the Armed Forces Health Surveillance Center (Global Emerging Infections Surveillance and Response System) work unit #0000188M.0931.001.A0074.

The views expressed herein are those of the authors and do not necessarily reflect the official policy or position of the Department of the Navy, Department of Defense, or the US Government. Copyright protection for this work is not available under Title 17 U.S.C. §105 and Title 17 U.S.C. §101.

Address for correspondence: Allen L. Richards, Viral and Rickettsial Diseases Department, Naval Medical Research Center, 503 Robert Grant Ave, Silver Spring, MD 20910-7500, USA; email: Allen.L.Richards.civ@mail.mil

References


MRSA spa t1081, a Highly Transmissible Strain Endemic to Hong Kong, China, in the Netherlands

Paul Gruteke, Pak-Leung Ho, Anja Haenen, Wai-U Lo, Chi-Ho Lin, Albert J. de Neeling

Author affiliations: Onze Lieve Vrouwe Gasthuis, Amsterdam, the Netherlands (P. Gruteke); Amsterdam Health Service, Amsterdam (P. Gruteke); University of Hong Kong, Hong Kong, China (P.-L. Ho, W.-U. Lo, C.-H. Lin); National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands (A. Haenen, A.J. de Neeling)

DOI: http://dx.doi.org/10.3201/eid2106.141597

To the Editor: Control of methicillin-resistant Staphylococcus aureus (MRSA) is an international public health priority. The Netherlands is among countries in Europe that have a low prevalence of MRSA among humans, largely because of a national search and destroy policy (1). The overall prevalence in long-term care facilities (LTCFs) is low (2). However, this policy is challenged by an increase
in MRSA *S. aureus* protein A (*spa*) t1081, which specifically affects LTCFs. MRSA with the same *spa* type is endemic to Hong Kong, China, and affects hospitals and LTCFs (3–5). This finding prompted us to jointly explore epidemiologic and strain-related factors.

The low prevalence of MRSA enables the National Institute for Public Health and the Environment (Bilthoven, the Netherlands) to type all first MRSA isolates referred from clinical laboratories in the Netherlands. In 2007, *spa* typing replaced pulsed-field gel electrophoresis typing. The annual number of referred isolates ranged from 1,570 in 2008 to 2,439 in 2013, excluding livestock-associated strains. Numbers of MRSA *spa* t1081 isolates were low during 2007–2009 but increased to 127 isolates in 2011 and 218 isolates in 2013.

The search and destroy policy in the Netherlands requires that detection of MRSA infection is followed by screening of neighboring patients and personnel in successive circles until no new colonizations are found. Most reported t1081 isolates represent colonization. In 2013, there were 30 infection isolates, 19 unknown isolates, and 169 colonization isolates.

Severe illness caused by t1081 is rarely reported, and eradication therapy is usually successful. In LTCFs, MRSA t1081 was more prevalent, accounting for 27% (65/242) and 24% (72/299) of all MRSA isolates from LTCFs in 2011 and 2013 respectively. LTCF clusters were often small, but some became large. The t1081 strain was probably introduced into Amsterdam and subsequently spread eastward (Figure).

We sequenced 5 t1081 isolates, 3 from The Netherlands (NL2007, NL2011, and NL2013) and 2 from Hong Kong (HK2005 and HK2008), by using whole-genome sequencing (Illumina, San Diego, CA, USA). Sequence data showed the CC45/agr IV-MRSA V type (3,6). A total of 91.39% of reads of NL2007 aligned with the published CC45/USA600 sequence (7); NL2007 was more similar to HK2005 and


Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 21, No. 6, June 2015 1075
The spread of MRSA can be inferred. Link between insufficient skill levels in specific LTCFs and eryngly stringent admission criteria. Skill levels of personnel have more illnesses than a decade ago because of increasing drug use as an evolutionary driving force. The latest initiative to control multidrug-resistant organisms, including MRSA in LTCFs, is included in an existing program for rapid outbreak reporting and support for hospitals by the National Institute for Public Health and the Environment. This initiative is expected to begin early in 2015 and should facilitate control of MRSA in LTCFs.

This study was supported by grants from the Health and Medical Research Fund (formerly Research Fund for the Control of Infectious Diseases) of the Food and Health Bureau of the Government of the Hong Kong Special Administrative Region.

References


Address for correspondence: Paul Gruteke, Medisch Microbiologisch Laboratorium, Onze Lieve Vrouwe Gasthuis, Oosterpark 9, PO Box 95500, 1090 HM Amsterdam, the Netherlands; email: p.gruteke@olvg.nl