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-armor 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.

References

1. Choi YJ, Jang WJ, Kim JH, Ryu JS, Lee SH, Park KH, et al. Spotted fever group and typhus group rickettsioses in humans, South Korea. Emerg Infect Dis. 2005;11:237–44. http://dx.doi.org/10.3201/eid1102.040603
2. Jin HS, Chu C, Han DY. Spatial distribution analysis of scrub typhus in Korea. Osong Public Health Res Perspect. 2013;4:4–15. http://dx.doi.org/10.1016/j.phrp.2012.12.007
3. O'Guinn ML, Klein TA, Lee JS, Richards AL, Kim HC, Ha SJ, et al. Serological surveillance of scrub typhus, murine typhus, and leptospirosis in small mammals captured at Firing Points 10 and 60, Gyeonggi Province, Republic of Korea, 2001–2005. Vector Borne Zoonotic Dis. 2010;10:125–33. http://dx.doi.org/10.1089/vbz.2008.0123
4. Ko S, Kim HC, Yang YC, Chong ST, Richards AL, Sames WJ, et al. Detection of *Rickettsia felis* and *Rickettsia typhi* and seasonal prevalence of fleas collected from small mammals at Gyeonggi Province in the Republic of Korea. Vector Borne Zoonotic Dis. 2011;11:1243–51. http://dx.doi.org/10.1089/vbz.2010.0261
5. Shin SH, Seo HJ, Choi YJ, Choi MK, Kim HC, Klein TA, et al. Detection of *Rickettsia monacensis* from *Ixodes nipponensis* collected from rodents in Gyeonggi and Gangwon Provinces, Republic of Korea. Exp Appl Acarol. 2013;61:337–47. http://dx.doi.org/10.1007/s10493-013-9699-1
6. Rubertone MV, Brundage JF. The Defense Medical Surveillance System and the Department of Defense serum repository: glimpses of the future of public health surveillance. Am J Public Health. 2002;92:1900–4. http://dx.doi.org/10.2105/AJPH.92.12.1900
7. Richards AL, Soeatmandji DW, Widodo MA, Sardjono TW, Yanuwiadi B, Hernowati TE, et al. Seroepidemiological evidence for murine and scrub typhus in Malang, Indonesia. Am J Trop Med Hyg. 1997;57:91–5.
8. Graf PC, Chretien JP, Ung L, Gaydos JC, Richards AL. Prevalence of seropositivity to spotted fever group rickettsiae and *Anaplasma phagocytophilum* in a large, demographically diverse US sample. Clin Infect Dis. 2008;46:70–7. http://dx.doi.org/10.1086/524018
9. Richards AL, Malone JD, Sheris S, Weddle JR, Rossi CA, Ksiazek TG, et al. Arboviral and rickettsial infections among combat troops during Operation Desert Shield/Storm. J Infect Dis. 1993;168:1080–1. http://dx.doi.org/10.1093/infdis/168.4.1080
10. Jiang J, Marienau KJ, May LA, Beecham HJ, Wilkinson R, Ching W-M, et al. Laboratory diagnosis of two scrub typhus outbreaks at Camp Fuji, Japan in 2000 and 2001 by enzyme-linked immunosorbent assay, rapid flow assay, and Western blot assay using outer membrane 56 kDa recombinant proteins. Am J Trop Med Hyg. 2003;69:60–6.

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

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)

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
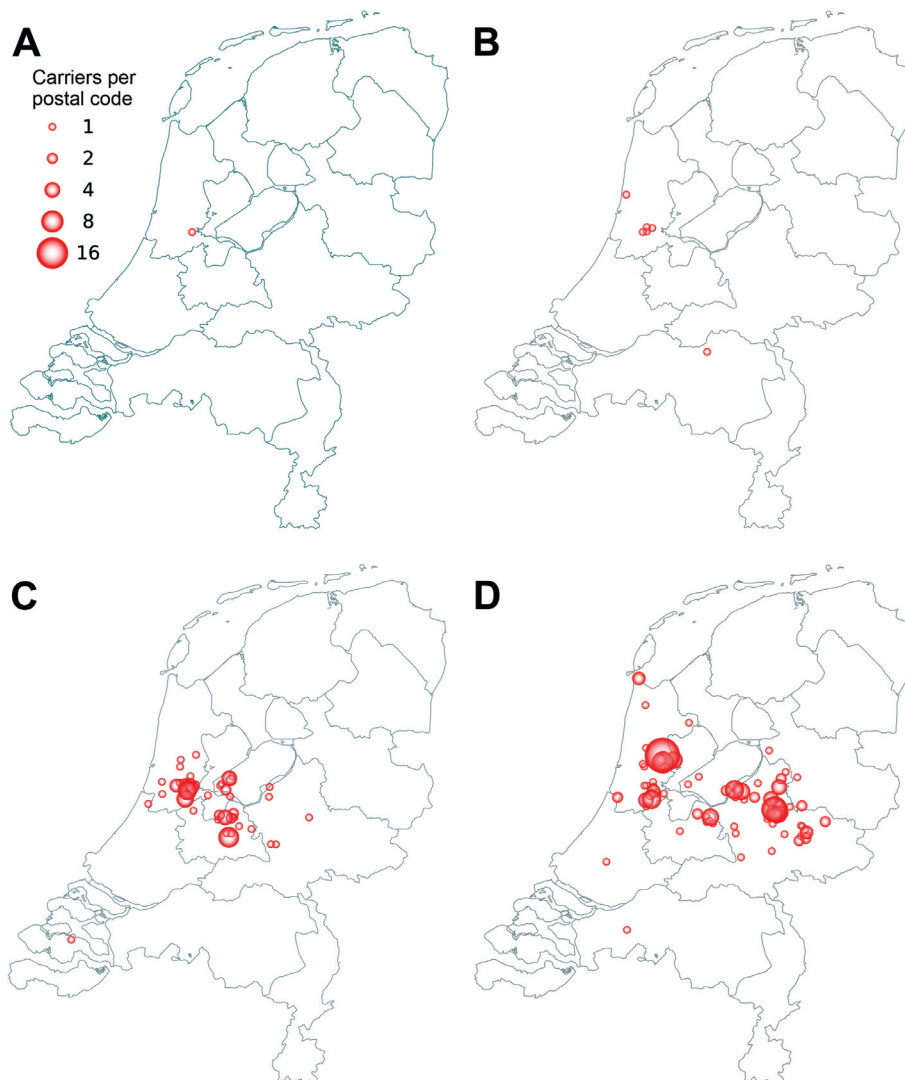

Figure. Spread of methicillin-resistant Staphylococcus aureus spa t1081 in the Netherlands, 2007–2013. A) 2007; B) 2009; C) 2011; D) 2013. Source: National Institute for Public Heath and the Environment (RIVM).

HK2008 (97.32% and 97.61% identity, respectively). NL2011 and NL2013 showed slightly decreasing similarity to HK2005 (96.86% and 96.59% identity, respectively) and HK2008 (96.97% and 96.69% identity, respectively). Staphylococcal cassette chromosome *mec* type V sequences in our isolates were more closely related to each other than to the closest reference sequence (GenBank accession no. AB505629), which originated from a CC398 isolate.

Phenotypic resistance to tetracycline and ciprofloxacin is common in t1081 and is often combined with gentamicin and macrolide resistance. *tet*K, a gene coding resistance to tetracycline that is located on the staphylococcal cassette chromosome *mec* element, was detected in reads of all sequenced isolates. The macrolide resistance gene *erm*C on plasmid pKH19 (GenBank accession no. NC_010685.1) was detected in HK2008, NL2011, and NL2013. Resistance to gentamicin (*aac*A/*aph*D genes) was detected in all isolates. A recent report on epidemic MRSA strain 15 based on many whole-genome sequenced strains highlights antimicrobial drug use as an evolutionary driving force (*8*). The *tet*K gene might benefit t1081 in LTCFs in the Netherlands, in which doxycycline is used more frequently than in hospitals (Neth-Map-MARAN 2014; http://www.swab.nl/nethmap).

None of our isolates was positive for Panton-Valentine leukocidin, and all isolates had the collagen-binding adhesion gene. In methicillin-sensitive *S. aureus*, this gene has been associated with carriage (*9*). The apparent high transmissibility of t1081 remains to be explained.

The present t1081 outbreak has elicited a debate on the policy in the Netherlands. Some elder-care physicians question benefits and costs of this policy for a strain that is weakly pathogenic. Residents in whom MRSA carriage cannot be eradicated face prolonged measures that some physicians say are unethical. Conversely, hospital infection control professionals emphasize that if MRSA can be controlled in hospitals, why not in LTCFs? The search and destroy policy in the Netherlands faced a major challenge in 2001 (*10*). Uncontrolled dissemination of MRSA had occurred throughout a large hospital in Rotterdam among patients and staff, as well as in neighboring institutions. This outbreak was eventually controlled (*10*). The Rotterdam area, which is southwest of Amsterdam, has not been affected by the current t1081 outbreak.

Concurrent with this professional debate, a public debate is ongoing on the quality of care in LTCFs. Residents have more illnesses than a decade ago because of increasingly stringent admission criteria. Skill levels of personnel have not kept pace in several LTCFs, as noted by the Health Care Inspectorate. Although virtually all LTCFs are publicly funded, quality differences are substantial. This situation is no longer acceptable, according to public opinion. A link between insufficient skill levels in specific LTCFs and spread of MRSA can be inferred.

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.

References

1. Bode LG, Wertheim HF, Kluytmans JA, Bogaers-Hofman D, Vandenbroucke-Grauls CM, Roosendaal R, et al. Sustained low prevalence of meticillin-resistant *Staphylococcus aureus* upon admission to hospital in the Netherlands. J Hosp Infect. 2011;79:198–201. http://dx.doi.org/10.1016/j.jhin.2011.05.009
2. Greenland K, Rijnders MI, Mulders M, Haenen A, Spalburg E, van de Kassteele J, et al. Low prevalence of methicillin-resistant *Staphylococcus aureus* in Dutch nursing homes. J Am Geriatr Soc. 2011;59:768–9. http://dx.doi.org/10.1111/j.1532-5415.2011.03325.x
3. Ho PL, Lai EL, Chow KH, Chow LS, Yuen KY, Yung RW. Molecular epidemiology of methicillin-resistant *Staphylococcus aureus* in residential care homes for the elderly in Hong Kong. Diagn Microbiol Infect Dis. 2008;61:135–42. http://dx.doi.org/10.1016/j.diagmicrobio.2007.12.017
4. Cheng VC, Chan JF, Lau EH, Yam WC, Ho SK, Yau MC, et al. Studying the transmission dynamics of meticillin-resistant *Staphylococcus aureus* in Hong Kong using spa typing. J Hosp Infect. 2011;79:206–10. http://dx.doi.org/10.1016/j.jhin.2011.03.024
5. Cheng VC, Tai JW, Wong ZS, Chen JH, Pan KB, Hai Y, et al. Transmission of methicillin-resistant *Staphylococcus aureus* in the long term care facilities in Hong Kong. BMC Infect Dis. 2013;13:205. http://dx.doi.org/10.1186/1471-2334-13-205
6. Monecke S, Coombs G, Shore AC, Coleman DC, Akpaka P, Borg M, et al. A field guide to pandemic, epidemic and sporadic clones of methicillin-resistant *Staphylococcus aureus*. PLoS ONE. 2011;6:e17936. http://dx.doi.org/10.1371/journal.pone.0017936
7. Stegger M, Driebe EM, Roe C, Lemmer D, Bowers JR, Engelthaler DM, et al. Genome Sequence of *Staphylococcus aureus* strain CA-347, a USA600 methicillin-resistant isolate. Genome Announc. 2013;1:e00517–13.
8. Holden MT, Hsu LY, Kurt K, Weinert LA, Mather AE, Harris SR, et al. A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant *Staphylococcus aureus* pandemic. Genome Res. 2013;23:653–64. http://dx.doi.org/10.1101/gr.147710.112
9. Rasmussen G, Monecke S, Ehricht R, Soderquist B. Prevalence of clonal complexes and virulence genes among commensal and invasive *Staphylococcus aureus* isolates in Sweden. PLoS ONE. 2013;8:e77477. http://dx.doi.org/10.1371/journal.pone.0077477
10. van Trijp MJ, Melles DC, Hendriks WD, Parlevliet GA, Gommans M, Ott A. Successful control of widespread methicillin-resistant *Staphylococcus aureus* colonization and infection in a large teaching hospital in the Netherlands. Infect Control Hosp Epidemiol. 2007;28:970–5. http://dx.doi.org/10.1086/519210

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