significant day-to-day change in the trend, and after the intervention there was no significant change in the day-to-day trend. In phase 2, individual compliance ranged from 72% to 100% with a median compliance of 92%, and a mean compliance of 91%. Nearly half (47%) of the nurses had compliance rates \geq 95%. Compliance on room entry was 90% and on room exit 94%. There was no significant difference in compliance rates between work shifts. Using the alcohol sensor badges, we determined that there were 10 HHO per nurse-hour.

A post-study questionnaire was completed by 14 nurses. Twelve felt that the alcohol sensor badge improved their compliance, one felt it had no effect, and one felt that it did not improve compliance. Ten respondents felt that all healthcare workers should wear the badge.

Our study demonstrated easy use of an alcohol sensing badge, with rapid and significant improvement in hand hygiene compliance. Our results may underestimate the impact of this technology since performance was not reviewed by the nurse supervisor and no feedback was given. Moreover, we did not involve patients in the study. Patients could be instructed to observe the colour of the badge light before contact with the healthcare worker and request that he/she perform hand hygiene if the badge light is red, even though most patients are not comfortable asking caregivers to perform hand hygiene. We were also able to provide estimates of HHO per nursing hour. This is an underestimate since the badge only measures compliance on room entry and exit, and misses opportunities that may occur inside the patient room.

The limitations of the study are its brevity and its performance in one ward of a single medical centre. In addition, compliance could only be assessed when the nurse performed hand hygiene using an alcohol product. This limitation could be overcome by adding a marker to liquid soaps used with water. Lastly, the quasi-experimental study design lacks randomisation, and may be complicated by temporal confounders and regression to the mean. Segmented regression analysis was performed to minimise these effects. To our knowledge, these results represent the most complete performance data and the highest level of compliance reported. A solution to monitoring hand hygiene compliance may be within reach.

Conflict of interest statement

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References

- Klevens RM, Edwards JR, Richards Jr CL. Estimating health care-associated infections and deaths in U.S. hospitals. *Public Health Rep* 2002;2007(122):160–166.
- The Joint Commission. Measuring hand hygiene adherence: overcoming the challenges. Oakbrook Terrace, IL: The Joint Commission; 2009, p. xvii.
- Haas JP, Larson EL. Measurement of compliance with hand hygiene. J Hosp Infect 2007:66:6–14.
- Stevens MP, Hunter JD, Ober JF, Bearman G, Edmond MB. Watching them wash: description of a hand hygiene observation program. *Infect Control Hosp Epidemiol* 2010;31:198–199.
- Dubowski KM. Method for alcohol determination in biological liquids by sensing with a solid-state detector. Clin Chem 1976;22:863–867.
- Longtin Y, Sax H, Allegranzi B, Hugonnet S, Pittet D. Patients' beliefs and perceptions of their participation to increase healthcare worker compliance with hand hygiene. *Infect Control Hosp Epidemiol* 2009; 30:830–839.
- Lent V, Eckstein EC, Cameron AS, Budavich R, Eckstein BC, Donskey CJ. Evaluation
 of patient participation in a patient empowerment initiative to improve hand
 hygiene practices in a Veterans Affairs medical center. Am J Infect Control
 2009;37:117–120.

M.B. Edmond^{a,b,*}
A. Goodell^c
W. Zuelzer^d
K. Sanogo^b
K. Elam^a
G. Bearman^{a,b}

^aDivision of Infectious Diseases, Department of Internal Medicine, Virginia Commonwealth University Medical Center, Richmond, VA, USA

^bHospital Epidemiology Unit, Virginia Commonwealth University Medical Center, Richmond, VA, USA

^cDivision of Surgical Nursing, Virginia Commonwealth University Medical Center, Richmond, VA, USA

dDepartment of Orthopaedic Surgery, Virginia Commonwealth
University Medical Center, Richmond, VA, USA

* Corresponding author. Address: Department of Internal
Medicine, Virginia Commonwealth University Medical Center,
Box 980019, Richmond, VA 23298-0019, USA.
Tel.: +1 804 828 2121; fax: +1 804 828 2125.
E-mail address: medmond@vcu.edu (M.B. Edmond)

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New sequence types of *Legionella pneumophila* circulating in northern Italy and comparison with other regions of the world

Madam,

Legionnaires' disease is caused by *Legionella* spp., which are environmental Gram-negative bacteria that colonise and persist in moist environments, particularly water distribution systems. The mortality associated with hospital-acquired *Legionella* pneumonia is greater than mortality for community-acquired cases.¹

In a previous study we showed that use of sequence-based typing (SBT) may be useful in identifying the source of infection, demonstrating the link between clinical and environmental isolates.² In the present study, we used a new approach to the clinical and environmental surveillance of legionellosis in homes for the mentally disabled, which takes into account the needs of patients with mental retardation in varying degrees (mild to very serious, including diseases such as West, Lennox, fragile X, Dandy–Walker syndrome) and those who find routine diagnostic procedures difficult. For this reason, we compared the sequence type (ST) designed by SBT of four clinical and 12 environmental strains of *Legionella pneumophila* serogroup 1 (LP1), isolated from hospital facilities for the mentally disabled and an associated hospital.^{3,4} The strains were selected after a retrospective surveillance of 565 clinical records (2002–2009) and investigations of environmental routine and *ad hoc* water circuits.

The criteria for inclusion in the study of the strains for analysis were:

 Isolated from clinical cases detected [as defined by the European Working Group for Legionella Infections (EWGLI), with

- isolation from organic material] and environmental strains associated with them after an epidemiological investigation.
- Environmental strains, isolated in connection with suspected cases of legionellosis (i.e. high antibody levels but without isolation of clinical strain or urinary antigen).
- Environmental strains from departments with patients at particular risk and a significant number of episodes of nosocomial pneumonia with unknown aetiology (these patients are readily covered with antibiotic therapy for early symptoms, often making it impossible to do an aetiological diagnosis).

It was possible to correlate two clinical strains with the corresponding environment, which were collected from showers that had exposed the patients (ST685: 2, 10, 18, 10, 1, 1, 9; ST16: 2, 10, 18, 10, 2, 1, 9) and two clinical strains present in the same structure (ST1: 1, 4, 3, 1, 1, 1, 1).

The other environmental strains were isolated from showers in the department where there were confirmed or suspected clinical cases. All the strains (seven) from the first structure had ST188 (2, 6, 17, 6, 13, 3, 11); two from the second structure had ST34 (3, 13, 1, 25, 14, 9, 6); and the last from the third structure, which was colonised in a single point from LP1, had ST694 (6, 1, 22, 30, 6, 10, 11).

From this analysis, it appears that the distribution of environmental strains is homogeneous, with only one ST per structure, unlike the hospital which had at least three strains simultaneously, with different STs.

The results were compared with the EWGLI international database (Figure 1): the four STs (1, 16, 34, 188), which in our study

belong to strains isolated in wards with confirmed or suspected clinical cases, were already known in the literature. Their presence was confirmed among clinical and nosocomial cases, especially for ST1, the most frequent and most widely distributed worldwide.

Two STs were new to the database: ST685 and ST694. The allelic profile 685 was not found in the EWGLI database, but its pathogenicity has been demonstrated by the concomitant isolation from a symptomatic patient. Unlike ST694, this was isolated only from environmental samples (with 1800 cfu/L of LP1, but only in one point) and was not included in the database or other published data source. As there have never been cases of legionellosis detected or suspected in the structure and as elderly patients are considered at risk of infection, we can assume that the profile in question is rarer or less virulent than the other genotypes.

The problem of underreporting of cases was also evident in this study. There were considerable difficulties in obtaining clinical strains (patients are subjected only to urinary antigen) and in aetiological diagnosis (letting patients with mental retardation undergo routine testing is often more difficult). Great help can be provided from the intersection of clinical and environmental data, from genotyping of isolated strains, and comparing these with international data to determine the frequency of known (clinical and/or nosocomial) clones.

In agreement with European data a significant proportion (13/16) of bacterial isolates belonging to clones is already known to be for nosocomial clinical cases.^{5–7} As other studies have shown, we confirm that the collection and analysis of routine environmental strains may be an important strategy in preventing outbreaks of legionellosis.⁸

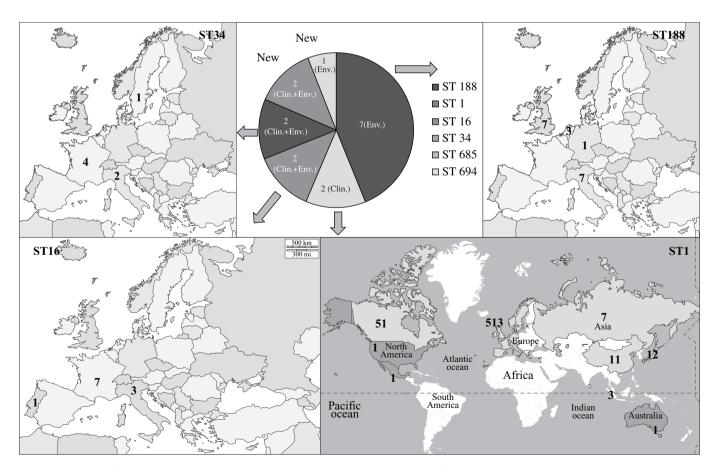


Figure 1. Occurrence of sequence types (STs) analysed in this study and comparison with other regions of the world (EWGLI database). Clin., clinical; Env., environmental.

Conflict of interest statement

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References

- Edelstein PH. Legionnaires' disease: history and clinical findings. In: Heuner K, Swanson M, editors. Legionella – molecular microbiology. Norfolk, UK: Caister Academic Press; 2008. p. 1–2.
- Galli MG, Bianchi A, Raimondi A, Tesauro M, Consonni M. Use of three molecular methods for investigations of Legionnaires' disease in a hospital in Milan. J Hosp Infect 2008;69:403–405.
- Gaia V, Fry NK, Afshar B, et al. Consensus sequence-based scheme for epidemiological typing of clinical and environmental isolates of Legionella pneumophila. [Clin Microbiol 2005;43:2047–2052.
- Ratzow S, Gaia V, Helbig JH, Fry NK, Luck PC. The addition of the acylneuraminate cytidylyl transferase gene (neuA) increases the discriminatory ability of the consensus-based typing scheme for *Legionella pneumophila* serogroup 1. *I Clin Microbiol* 2007:45:1965–1968.
- Borchardt J, Helbig JH, Luck PC. Occurrence and distribution of sequence types among Legionella pneumophila strains from patients in Germany: common features and differences to other regions of the world. Eur J Clin Microbiol Infect Dis 2008:27:29–36.
- Fry NK, Alexiou-Daniel S, Bangsborg JM, et al. A multicenter evaluation of genotypic methods for the epidemiologic typing of *Legionella pneumophila* serogroup 1: results of a pan-European study. Clin Microbiol Infect 1999;5:462–477.
- Amemura-Maekawa J, Kura F, Chang B, Watanabe H. Legionella pneumophila Serogroup 1 isolates from cooling towers in Japan form a distinct genetic cluster. Microbiol Immunol 2005;49:1027–1033.
- Sabria M, Yu VL. Hospital-acquired legionellosis: solutions for a preventable infection. *Lancet Infect Dis* 2002:2:368–373.

A. Bianchi* F. Pregliasco M. Consonni M. Tesauro M.G. Galli

Dipartimento di Sanità Pubblica, Microbiologia e Virologia, Università degli Studi di Milano, Milano, Italy

* Corresponding author. Address: Dipartimento di Sanità Pubblica, Microbiologia e Virologia, Università degli Studi di Milano, Via Pascal 36, 20133 Milano, Italy.

Tel.: +39 02 50315109; fax: +39 02 50315100. E-mail address: annalisa.bianchi@unimi.it (A. Bianchi)

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Prevalence of nosocomial infections in a tertiary heart centre in Iran, 2006 and 2007

Madam,

Hospital-acquired infection (HAI) surveillance is an important component of an infection control programme. Iran HAI has not been quantified by a nationwide surveillance study to date, and only some localised surveillance data from individual hospitals have been reported. The lack of valid nationwide surveillance study data in Iran influenced our hospital infection control committee to conduct a prospective, on-site continuous, hospital-wide surveillance study at

Tehran Heart Centre, a major referral and educational cardiac hospital affiliated to Tehran University of Medical Sciences, from 2006 to 2007.

Approximately 19 256 coronary angiography and 7221 cardiac surgeries were performed in this hospital in the two-year period. Using the Centers for Disease Control and Prevention (Atlanta, GA, USA) definitions, all patients hospitalised for >48 h with clinically and paraclinically documented infections were included. All patients who had an operative procedure were followed up for one month if no implant was left in place and for one year if an implant (e.g. prosthetic valves, non-human vascular grafts, mechanical heart, implantable cardioverter defibrillator) was in place. The required data were collected from HAI cases diagnosed by on-site observation of the infection control team and also from hospital information system and laboratory information system reports as well as cases of potential infection notified by nursing staff.

All culture samples referred to the laboratory were cultured and samples with colonisation or contamination were excluded.

In the year 2006, 215 (29.25%) of detected infections fulfilled the criteria for HAI whereas 520 (70.75%) did not. The equivalent numbers for 2007 were 266 (37.78%) and 438 (62.22%) respectively. A total of 140 infected patients from 3451 surgical procedures in the year 2006 and 169 infected from 3770 procedures in the year 2007 were included in this study. According to our findings the total nosocomial infection rate after surgery was 4.06% in 2006 and 4.48% in 2007. The distribution stratified by infection site was, for 2006: bloodstream infection (BSI) 1.01%, respiratory tract infection (RTI) 0.70%, urinary tract infection (UTI) 0.58%, surgical site infection (SSI) 1.71%; and for 2007: BSI 0.82%, RTI 0.53%, UTI 0.61%, SSI 2.41%. The prevalence varied between sites. In the year 2006 the most frequent site of HAI was SSI (30.2%), followed by RTI (23.3%), UTI (20.9%) and BSI (16.3%); the top five sites of non-HAI in descending order were UTI (78.1%), RTI (10.8%), BSI (6.9%) and SSI (0.8%). The pattern in 2007 was very similar.

The overall two-year nosocomial infection rate among our post-operative cardiac patients was 4.27% which was within the HAI rate of between 3.5% and 11.6% in large multicentre studies conducted in European countries.^{2,3} This rate was higher than that found in a Turkish study, and lower than that in a Canadian study.^{4,5}

The relatively low HAI rate in our hospital may be due to an active infection control committee and a well-established administrative support system by the hospital's executive director. Furthermore, the infection control aims and strategies are planned prospectively annually and all staff are trained accordingly. Moreover, a separate routine infection feedback report is provided for all surgeons every six months which informs them about the rate of surgical infections and relevant prevention strategies.

Staphylococcus aureus (20.0%) and *Enterobacter* spp. (27.0%) were the two most frequently recorded pathogens for BSI in both 2006 and 2007, in line with two previous studies. In the current study, *Escherichia coli* accounted for approximately half (51.75%) of the UTIs, similar to the findings of other studies. $^{2-4,6-8}$

The pathogens most frequently responsible for RTIs were *S. aureus* (16.3%) and *Pseudomonas aeruginosa* (16.3%) in 2006, and *Enterobacter* spp. (16.4%) and *Klebsiella* spp. (14.8%) in 2007, in keeping with the results of a national surveillance programme in the USA. *P. aeruginosa* has been the most frequent isolate from nosocomial RTIs recorded in the literature. *2.4,6–8* According to our study, *S. aureus* (36.95%) was the most frequent isolate from SSIs, again similar to other studies. *2–4*

In conclusion, in our single-centre study from a tertiary referral cardiac hospital in Iran, we surveyed the prevalence and distribution of HAIs and the most frequently isolated pathogens in each site in a high risk subset of patients who should benefit from targeted HAI programmes. This may help to enhance the current infection prevention interventions. Further nationwide studies are required to identify risk factors and preventive measures for monitoring HAI in Iran.