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Association between *Pseudomonas aeruginosa* positive water samples and healthcare-associated cases: nine-year study at one university hospital

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SUMMARY

Objective: To study the association between the results of water samples and *Pseudomonas aeruginosa* healthcare-associated cases in a French university hospital.
Methods: Generalized Estimating Equations were used on complete case and imputed datasets. The spatial unit was the building and the time unit was the quarter.
Results: For the period 2004–2013, 2932 water samples were studied; 17% were positive for *P. aeruginosa*. A higher incidence of *P. aeruginosa* cases was associated with a higher proportion of positive water samples ($P=0.056$ in complete case analysis and $P=0.031$ with the imputed dataset). The association was no longer observed when haematology and intensive care units were excluded, but was significant in analyses of data concerning intensive care units alone ($P<0.001$).
Conclusion: This study suggests that water outlet contamination in hospitals can lead to an increase in healthcare-associated *P. aeruginosa* cases in wards dealing with susceptible patients, but does not play a significant role in other wards.

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Introduction

Pseudomonas aeruginosa infections may cause severe morbidity and mortality.[1] The possible presence of *P. aeruginosa* in water systems is well established.[2] Some mechanisms of exposure are common and can occur even when guidelines for the control of *P. aeruginosa* are adhered to, such as when showering or bathing, via drinking water or through contact with contaminated surfaces. Outbreaks of infection with *P. aeruginosa* have also been reported in relation to failure to comply with guidance, such as use of contaminated water to rinse endoscopes or surgical equipment, or use of non-sterile water for antiseptic dilution.[3]

The literature review of Anaissie *et al*. provided a summary of water-borne healthcare-associated infections other than *Legionella* spp.[3] Most of the reports related to *P. aeruginosa*, and all were concerned with outbreaks of infection; no large-scale long-term studies were found. Many of the studies went no further than to report on the relationship between micro-organisms found in water systems and those identified in patients using genotyping methods.

Two recent literature reviews reported a link between water system contamination and *P. aeruginosa* infections.[4,5] However, although a link between water network contamination and healthcare-associated infection is suspected, the strength of the association is still not clear. As a result, water sampling remains controversial and guidelines differ between countries.

This study aimed to examine the association between the results of water samples and cases of healthcare-associated infection with *P. aeruginosa*.

Methods

Study setting and population

The University Hospital of Dijon is located in France and has 1800 beds, with medical and surgical wards and intensive care units (ICUs). There are 10 buildings across five sites, one of which was constructed recently (wards occupied since 2010).

All *P. aeruginosa* positive samples from 1st January 2005 to 31st March 2013 were extracted from the bacteriology laboratory database. Duplicates (isolates with the same antibiogram according to the Antimicrobial Committee of the French Society for Microbiology,[6] and identified within six months of an earlier isolate from the same patient) were excluded. Patients were also excluded if they had been hospitalized for less than 48 h when their samples were collected.

Water samples

In the study facility, water samples had to be taken from taps, showers and drinking fountains in each ward for testing once every quarter. Water points that were sampled on each occasion were selected at random; however, rooms that housed patients and those 'disfavoured' outlets furthest away from the water supply entry point into the hospital had to be tested at least annually. Samples from water outlets on the ICUs with filters fitted were taken after removing the filter. Filters in the study hospital are ready to use and are changed every 31 days. Samples were taken according to French standards: after disinfection of the water point and a short flush (1 or 2 min), 100 mL of water was sampled in sterile bottles containing 20 mg/L of sodium thiosulphate and filtered through a sterile membrane (pore size 0.45 μm).[7] The membranes were placed face upwards on a selective agar medium with cetrimide, and were incubated for 44±4h at 36°C. The culture results for the water samples were obtained from the bacteriology laboratory database and were available from 1st July 2004 to 15th February 2013. A water outlet was considered positive if either the cold or hot water contained *P. aeruginosa*.

Temperature and relative humidity

Data on mean outdoor temperatures and relative humidity by month were obtained from the French meteorological database (Météo France).

Building

Several wards moved during the study period, either within the same building or to a new building. This led to potential changes in the risk profiles of patients for acquiring *P. aeruginosa* in any building over time. To overcome this, data for the quarter that patients moved between buildings were erased from the database for the affected buildings, and for analysis purposes, the building was regarded as two different buildings, pre- and post-ward movement. This led to 12 buildings being considered in the analysis, instead of 10 actual buildings within the hospital complex.

Population at risk

The number of person-days (population at risk) was obtained from administrative databases, which record all hospitalizations for each ward.

Analyses

Data about water sample results were aggregated by building and by quarter in order to study the association between water results and cases. Generalized Estimating Equations (GEE) were used in order to take autocorrelation in time within each building into account, with binomial negative regression of the number of *P. aeruginosa* cases, with patient-days as the exposure variable. Exchangeable, first-order autoregressive and independent autocorrelation structures were tested. The autocorrelation structure was chosen with regard to the Quasi-likelihood Information Criterion (QIC),[8] the correlation coefficient between the different periods for the same building, and the graphical evolution of the incidence of *P. aeruginosa* cases in the different buildings. Robust variance estimators were used and allowed standard errors to overcome poor specification of the correlation structure.[9] The proportions of positive water samples among the number of samples in the building during the current, previous and next quarters were tested. A time trend was examined. The effect of quarter and mean outdoor temperature during the quarter and the previous quarter were tested in separate models to avoid collinearity. The QIC was used to choose the model among the models with the same correlation structure. Analyses were repeated without ICUs and haematology units, in which patients are more susceptible to *P. aeruginosa* infections. Finally, due to the small number of