HealthManagement
Promoting Management and Leadership

Volume 12, Issue 2 / 2010 - Matrix

The Geographical Dimension of Hospital-Acquired Infections

Hospital-acquired infections (HAIs) are a constant battle for hospitals, often making the headlines. But how do these infections spread and what can be done to stop them? This article investigates the use of mapping tools for epidemiological investigation, which could allow for early warning and response for hospital infections.

The Epidemiology of Hospital- Acquired Infections

Hospital-acquired infections resemble each other. They are likely to be caused by opportunistic pathogens carried by patients as part of their 'normal' flora and are usually associated – in some way or the other – with antibiotic consumption, either of the patient himself or among the fellow patients in the rest of the ward or hospital. It therefore comes as no surprise that in hospitals, where on average about one of third patients are receiving systemic antibiotic chemotherapy, most bacteria that cause nosocomial infections express some type of resistance to first or second line antibiotics or occasionally even compounds of "last resort". This provides them with the edge over their susceptible competitors.

Moreover, de novo emergence of antibiotic resistance in hospitals is a relatively rare event and mainly restricted to some special bacteria or resistance mechanisms. Most antibiotic resistance is encoded by genes and more often assemblages of genes so called genetic elements which are frequently mobile and can spread between different bacteria. Antibiotic resistance of this type is mainly disseminated by bacterial strains which have acquired these elements and are carried by patients. Naturally, these antibiotic resistant strains are also more frequently transmitted between patients who share the same facilities and some have evolved into notorious hospital clones (groups of bacteria that are all genetically related and descended from a single, common ancestor) with the potential to cause outbreaks if given the chance. In absence of the high antibiotic selection pressure and the multiple opportunities for transmission that exist in hospitals, these strains are constrained in their ability to spread far and wide in the community and if this paradigm holds one should be able to observe a geographical concentration of typically hospital- acquired clones.

The European Network Approach of the Staphylococcal Reference Laboratories

We have tested this hypothesis by utilising one of the most successful networks for the surveillance of antimicrobial resistance, the European Antimicrobial Resistance Surveillance System (EARSS). With this approach we intended to identify the geographic distribution of Staphylococcus aureus clones that cause invasive infections in patients treated in European hospitals.

S. aureus lives on the skin and in the nose of about a third of healthy people. These bacteria usually coexist peacefully with their human hosts but occasionally can cause trivial infections such as spots or boils, or even less frequent, serious, life-threatening conditions such as blood poisoning and pneumonia. These latter infections require professional management in hospitals and treatment with antibiotics. Unfortunately, in some parts of Europe many of the S. aureus clones that are typically encountered in hospitals are resistant to most frequently prescribed group of antibiotics the betalactams and are then referred to as methicillin-resistant.

Epidemic clones of methicillin-resistant S. aureus (MRSA) infections can be a particular problem in hospitals and other healthcare facilities (so-called hospital-acquired MRSA), but a few clones can also occur in otherwise healthy people who have not been admitted to a hospital and are then called community- acquired MRSA. With the help of the EARSS network, we were able to garner the support of Staphylococcal Reference Laboratories (SRLs) from 26 European countries.

Together with the experts from these laboratories, we agreed on a standardised approach to identify different clones of S. aureus using the most advanced genetic characterisation consisting of sequencing the DNA of a particularly variable gene the so called spa gene. The SRLs also secured the participation of up to 25 hospitals per country. These hospitals were chosen to provide a representative geographic as well as demographic coverage at the national level. Using a common sampling frame, participating hospitals collected successive methicillin-susceptible (MSSA) and MRSA isolates from patients with invasive S. aureus infection. All isolates were then sequenced at the spa locus at the respective national SRL and all data were aggregated into a single database.

The Geographical Distribution of S. Aureus

In the course of the study, we were able to collect data on approximately 3,000 isolates from 450 hospitals of which one third consisted of MRSA the others were MSSA. The non antibiotic resistant isolates, the MSSA showed a very large diversity with individual clones distributed all across Europe. However, the genetic diversity of MRSA differed considerably between countries. Especially for the most dominant MRSA clones, we could identify distinctive geographical clusters. Some of these clones were clearly confined to national boundaries. Others had spread regionally and had become mainly prevalent in neighbouring countries. Others still were found in single hospitals which most likely resulted form local outbreaks.

For visualisation and interrogation we built an interactive web-based mapping tool that provides detailed information for clinicians, diagnostic microbiologists, infection control teams and hospital management on the dynamics of the S. aureus and especially the MRSA population. We also made this tool freely available at www.spatialepidemiology.net/srl-maps/.

The Role of Hospital Networks in the Dissemination of Nosocomial Pathogens

Obviously, the difference in geographic concentration between resistant and susceptible isolates was intriguing. The most plausible explanation lay in the fact that acquisition of resistance by MSSA to become MRSA is a relatively rare event. Therefore, there are far fewer MRSA clones compared to MSSA clones and they are very young in evolutionary history since they mainly emerged since the availability of antibiotic chemotherapy during the last 40-60 years. MSSA on the contrary is much older and therefore had time to diversify.

Since hospital-acquired MRSA clones have their special selective advantages over MSSA when antibiotic use is high, they expand in hospitals and attain geographic spread by repeated admissions and referrals between hospitals by patients that carry them. These patients typically belong to a frailer or more ill segment of the population, which normally don't travel large distances. We therefore have reasons to believe that the geographic concentration of MRSA clones is a reflection of patient movement between hospitals that are part of a collaborative referral structure.

By analysing the admission pattern of patients in the Netherlands and England we could show that indeed, all hospitals in each country are interconnected by means of patients that they share over a single year. This patient traffic mainly happens at national level since hospital referral structures only occasionally reach out over national borders, and we believe that it is this national healthcare utilisation pattern that determines the spread of nosocomial pathogens in modern healthcare systems.

Improving the Understanding by Collaborative Mapping Exercises

By establishing a large collaborative network and then combining molecular and spatial analytic techniques, we were able to map specific strains across large geographic regions. At its most basic, we could show that MRSA clones were not randomly distributed but clustered. But the study also illustrated other potential applications of this approach. Combining demographic with clinical outcome data and more detailed genetic characteristics such as toxin genes or virulence properties, these mapping-tools may become extremely versatile for epidemiological investigation.

They will allow for early warning and response to emerging hospital as well as community pathogens. This information may provide a better understanding of transmission, also across the interface between distinct ecological habitats such as farm animals, environmental reservoirs and humans, risk factors such as occupation or exposures to healthcare, nursing homes, etc and may therefore be able to help protect vulnerable populations.

Author:

Prof. Hajo Grundmann

National Institute for Public Health and the

Environment (RIVM)

The Netherlands

Hajo.Grundmann@RIVM.nl

Published on : Sun, 1 Aug 2010