Clinical environments as a potential reservoir for nosocomial infections

ESR11José Laço, Supervisor Margarita Gomila

Microbiologia (Departamento de Biologia) – Universidad de las Islas Baleares

Hospital acquired infections (HAI) or nosocomial infections can be described as the ones that occur within 48 hours of hospital admission, 3 days of discharge or 30 days of an operation. The European Centre for Disease Prevention and Control (ECDC) estimates that there are around 3.1-4.6 million nosocomial infections each year in Europe. HAIs have a direct impact in patient morbidity and mortality in hospitals. As a result, more than 90 000 people die each year in Europe due to the six most common infections in these environments. Furthermore, HAIs also represent an economic burden for hospitals and they represent up to 6% of public hospital budgets.

With HAIs being a serious concern on its own, it gets worse if the infection is caused by antibiotic resistant bacteria (ARB), as they have intrinsic or acquired mechanisms that allow them to defend themselves against the antibiotic. This means that the treatment won't be as effective, extending hospital stays, or may even be impossible, leading to death. Antibiotic resistance is a natural characteristic of bacteria and its increase and spread are inevitable results of antibiotic usage. However, this tendency may rise in time, as a result of abusive use (antibiotic usage to prevent infections may not be needed), insufficient use (when patients don't finish their treatment) or inadequate use (when the chosen antibiotic is incapable of treating the infection due to bad diagnosis).

Bacterial DNA is different from human DNA, as they have a single circular chromosome and also tiny circular parts of DNA called plasmids. They have the ability to share these plasmids between them, even without being from the same species, contributing to the dispersion of all types of genes. In an environment that has strong selective pressure by antibiotic usage (like the hospital), bacteria will share more and more plasmids carrying antibiotic resistance genes (ARG) in order to survive, meaning that the result is a much higher population of resistant bacteria comparatively to non-resistant.

Currently, the emergence of ARB, as well as the spreading of ARG is one of the major health problems around the world, and if no changes are made to the current situation, antimicrobial resistance is set to be the major cause of death by disease by the year 2050, with an estimated 10 million deaths worldwide, far more than the 8.2 million deaths per year attributed to cancer, the current major cause of death worldwide.

Hospital environments can represent a reservoir of microorganism that can develop complex communities, with a relatively high level of microbial diversity. There are several bacterial species associated with nosocomial infections and prone to develop or acquire multi-resistances (resistance to 3 or more antibiotic families), in many cases being environmental bacterial species. As examples, *Staphylococcus aureus*, species of the genus *Enterococcus*, species of the family

Enterobacteriaceae, *Pseudomonas aeruginosa* and species of the genus *Acinetobacter*, especially *Acinetobacter baumanii*, are the most relevant ones. As mentioned before, the antibiotic selection pressure in hospital environments is especially important if the resistance genes are associated with mobile genetic elements, such as plasmids, since they facilitate their dissemination among microorganisms. Keeping this in mind, hospital environments would not only act as a reservoir of bacteria capable of triggering an infection, but also as the perfect environment for the dissemination or emergence of new resistances to antibiotics or mechanisms of virulence. Potentially infectious agents present in the environment can enter the hospital in a handful of ways, such as the water supplies and the distribution systems. Bacteria have the ability to form biofilms, an arrangement of bacteria cells attached to a surface through secretions which protect the cells within it, and these structures serve as a great reservoir to all kinds of bacteria, including potential pathogens or ARG carriers. Additionally, they represent a source of microorganisms that can contaminate all types of hospital material and come into direct contact with patients and staff, as well as being very difficult to eliminate once they have established themselves in the hospital environment.

Previous studies performed in our laboratory have shown that even in strictly controlled hospital waters, such as haemodialysis waters, complex microbial communities can be present, with a relatively high microbial, which will make direct contact with patients with renal failure during treatment. Evidently, disinfection and control of these systems is done regularly in order to control the access and proliferation of microorganisms. However, these results provide evidence that environmental bacteria have mechanisms that allow them to surpass the applied safety measures to prevent or reduce, as much as possible, the entry of microorganisms that may pose a danger for patients and, once inside, proliferate.

The study and characterization of the microorganisms present in the different hospital environments is therefore crucial since few studies have been performed to determine their role as a reservoir of microorganisms or clinically relevant genes. Hopefully, by identifying the microbial composition of these environments over time, as well as to study their mobile genetic elements associated to virulence and antibiotic resistance, we can have a better understanding of the problem we are facing, and of ways to protect ourselves against it.

As of now, 40 different species of bacteria have been identified through samplings, amongst them being species well known to cause nosocomial infections, such as *Pseudomonas aeruginosa, Klebsiella pneumoniae* and several *Staphylococcus* species, but also emerging pathogens such as *Stenotrophomonas maltophila*, *Brucella anthropi* and *Achromobacter* species, which are already confirmed to have mechanisms of antibiotic resistance.