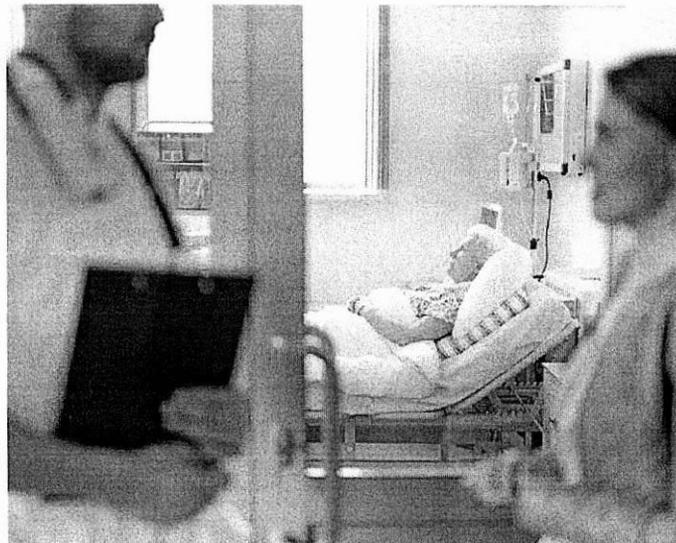


What's to Blame?

Looking at the Sources of Healthcare-Associated Infections

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It shouldn't come as a surprise to us that the most likely cause of a patient's Escherichia coli (E. coli) urinary tract infection (UTI) is probably the patient's own E. coli.

“Wash your hands!” and “The hand-washing police are here!” are not uncommon phrases for infection preventionists to hear. And many of us have been taught that “Handwashing is the single most effective way to prevent the spread of infections.” A few years ago, a famous infection preventionist, Marguerite Jackson, researched that quote and found it most likely first came from a lesson on food safety, not healthcare-associated infections (HAIs). However, Ignaz Semmelweis clearly demonstrated hand hygiene was important in saving patient lives in his hospital.

In the intervening years since Semmelweis, the role of the environment has also been recognized as a driver of infections. For some infections like Legionella, the environment is the sole source of the infection, but for organisms including methicillin-resistant Staphylococcus aureus (MRSA) the environment has also been implicated in transmission to patients. As a response to some studies, many products aimed at reducing bacteria in the healthcare environment have been developed.

Lastly, the patient's own biome has been recognized as the source of infections to the patient. It shouldn't come as a surprise to us that the most likely cause of a patient's Escherichia coli (E. coli) urinary tract infection (UTI) is probably the patient's own E. coli.

While other sources of infections, such as zoonosis, has been recognized as causing some HAIs, there is no significant body that suggests these other causes are a major driver of HAIs. Lastly, no one studying the field of clinical epidemiology and infection prevention believes any one of the above sources causes all the HAIs, we know each makes up a fraction of the HAI sources.

So, the question logically must be asked, what is source of the majority or plurality of HAIs in the developed world? The implications are enormous. If the largest number of HAIs are associated with the environment, then spending resources, —

human, supply and technological — to increase the cleanliness of the room is imperative if we want to improve our patients' outcomes. Researchers should invest aggressively in new technologies to make that happen. If, alternatively, the greatest source is the patient's own biome, antimicrobial stewardship, daily patient chlorhexidine gluconate (CHG) bathing begin to be much more important and resources dedicated to the environment have a lower return on investment. Respectively, if it is healthcare workers carrying the bacteria from patient to patient, then hand hygiene technology is imperative in lowering HAI numbers.

There has been no lack of articles implicating the environment as a source of HAIs. A recent analysis of 18 studies, though, found a mixed bag of when the environment was likely the source. To quote the authors, “Multiple studies reported positive associations between infection and exposure to roommates with influenza and group A streptococcus, but no associations were found for Clostridium difficile, methicillin-resistant Staphylococcus aureus, Cryptosporidium parvum, or Pseudomonas cepacia; findings were mixed for vancomycin-resistant enterococci (VRE). Positive associations were found between infection/colonization and exposure to rooms previously occupied by patients with Pseudomonas aeruginosa and Acinetobacter baumannii, but no associations were found for resistant Gram-negative organisms; findings were mixed for C. difficile, methicillin-resistant S. aureus, and VRE.”

Some studies have found very strong associations and are frequently cited by those wishing greater expenditure of resources on environmental cleaning. However, while the findings using traditional epidemiological techniques showed significant associations between the environment and acquisition of pathogens, what was important was what percent of total cases could be attributed to the environment compared to other sources. Susan Huang, MD, the author of one of the papers, even noted that although the adjusted odds ratio

was 1.4 for the acquisition of either VRE or MRSA ($p < 0.05$) if the prior room occupant had these pathogens, "These excess risks accounted for 5.1 percent of all incident MRSA cases and 6.8 percent of all incident VRE cases, with a population attributable risk among exposed patients of less than 2 percent for either organism."

So, the environment, even though a significant risk factor for acquiring MRSA or VRE, made up less than 2 percent of the total cases, suggesting that focusing on the environment to squeeze out these infections may not yield a lot of juice.

Whole genome sequencing, which gained prominence years after the Huang article, have borne out her conclusion. Studies from the UK showed 45 percent of the strains were not closely related to any other strains in the multi-hospital, multi-year study. When the data set the parameters even more narrowly, suggesting a need for both a visit to the same hospital and a close genetic link, the percent of cases that fell into that category was 10.3 percent — meaning about 90 percent of the cases had the environment in the hospital eliminated as the source of transmission. In fact, a recent review noted many sources in the community were linked to later healthcare cases.

Other studies around MRSA found even less transmission occurring in the hospital. Two studies, one involving 1,854 patients with or without MRSA and another involving 398 patients with MRSA bacteremia found rates of MRSA acquisition linked to the environment in the first study of 8 percent and in the later study of transmission of 0 percent, clearly suggesting in the western hospital environment that the focus of the environment to reduce HAI infections would gain little in the way of reduction.

If these findings were limited to MRSA and *C. difficile*, then the environment could play a role in other infections, but one study looking at ICU clinical cultures revealed that only 8.7 percent belonged to a genomically related clonal lineage. While clearly other bacteria, specifically *Pseudomonas*, has showed strong links to the environment, these studies identified sources such as sink drains and potable water that cannot be eliminated by increased cleaning.

One study did a deep dive to prove that the patient's own flora were responsible for their infections. This study showed that among patients with central line-associated bloodstream infections (CLABSI) with mucosal barrier injuries (MBI) the patients did have genetically identical bacteria identified in their stool before developing the infection. Interestingly, the data showed

that organisms like *Staphylococcus epidermidis*, normally thought of as skin flora, could be found in the gut and subsequently cause infections presumably from the GI system. However, it was already well established that the patient's own biome was most likely to cause the infections, with the exception of organisms not found on the CDC's MBI organism list. Given the genetic diversity seen in whole genome sequencing (WGS) studies, we can conclude that the environment is not the source of the majority of infections occurring in western healthcare today. So, maybe in the future, infection preventionists won't be known as the "handwashing police" but as the "bathe your patients" police. 

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Given the genetic diversity seen in Whole Genome Sequencing (WGS) studies we can conclude that the environment is not the source of the majority of infections occurring in western healthcare today.