

Environmental contamination contributing to the spread of vancomycin-resistant enterococci in nursing homes



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Antibiotic resistance is a growing global concern and a tremendous public health threat.¹ The problem is exacerbated by antibiotic overuse, international travel, and the transfer of resistance determinants from one bacterial species to another.² Infections with multidrug-resistant organisms (MDROs) burden health-care systems, increasing the duration of illnesses, increasing mortality rates, and resulting in enormous costs from diseases formerly treatable by first-line drugs. Antibiotic use also induces changes in the gut microbial composition, reduces microbial diversity, and increases the risk of acquiring MDROs.³ The estimated annual health-care costs in the USA from MDRO-related infections are approximately US\$20 billion, with MDROs causing more than 2.8 million illnesses and 35 000 deaths a year.^{4,5} Most of these infections occur in health-care settings. Although many studies have examined how multicomponent infection-prevention interventions can reduce MDRO prevalence in health-care settings, the gut microbiome's role in the spread of proximate environmental pathogens has yet to be investigated.

Preventing transmission is essential in reducing infections with MDROs in nursing homes. To identify resident characteristics associated with MDRO spread, in *The Lancet Healthy Longevity*, Joyce Wang and colleagues⁶ examined the association between resident characteristics and vancomycin-resistant enterococci (VRE) contamination on proximate room surfaces to identify potential drivers of MDRO transmission in nursing homes. 245 participants were enrolled from six US nursing homes and clinical data and surveillance cultures of participant body sites and room surfaces were collected at intake and during weekly follow-up visits. To investigate the association between the gut microbiota and the culture status of patients and their rooms, the authors did 16S rRNA gene sequencing on perirectal surveillance swabs. The results showed that at baseline 49 (20%) patients were colonised by VRE and, of these, 36 (73%) had VRE-contaminated environmental samples. Further, most of the participants with contaminated environments had their hands also contaminated by VRE. A correlation was found between hand contamination,

colonisation of the participant's groin and perirectal regions, and contamination of various high-touch room surfaces. The microbiota composition of the patients was associated with antibiotic use and VRE colonisation but not environmental contamination among the VRE-colonised participants. Increased physical independence and hand contamination were identified as the major risk factors for VRE environmental contamination, and antibiotic exposure in the past 30 days increased the odds of acquiring VRE. The results suggest a model whereby previous antibiotic treatment leads to gut microbiome disruption, increasing the risk of acquiring MDROs. Acquisition of MDROs leads to pathogen shedding and environmental contamination, increasing the transmission rate. These findings suggest that individuals whose gut microbiomes have been affected by antibiotic use have an increased risk of being infected by an MDRO.

Existing prevention practices for health-care-associated infections include hand-hygiene interventions and environmental cleaning.⁷ Hand-hygiene interventions that include education of patients have been found to reduce the spread of health-care-associated infections and MDROs, showing the important role patients play in transmitting these pathogens.⁸ Interventions emphasising individual characteristics are not current practice for health-care institutions. Wang and colleagues' findings support effective hand-hygiene initiatives in ambulatory residents of nursing homes to reduce the transmission of MDROs in these settings.

Healthcare-associated infections with MDROs are often associated with patients with long-term medical devices, which usually reduces physical independence.⁹ Wang and colleagues' study shows that physical independence plays an important role in environmental contamination, suggesting that an individual's increased susceptibility to acquiring MDROs does not equate to the individual's risk for spreading MDROs. However, the study has some limitations. Since samples were not taken before residents entered the room, the study could not assess with certainty whether the infected residents (ambulatory or otherwise) contaminated their environment or if the contaminated environment led to

disease in the residents. Wang and colleagues consider this in their model as cyclical, with environmental contamination leading to illness and vice versa. Additionally, although Wang and colleagues showed that antibiotic-mediated disruption of the gut microbial community is associated with VRE colonisation in nursing home residents, the authors did not find a significant relationship between the gut microbiome and environmental contamination. Ultimately, the gut microbiome's role in the pathogenicity and transmission of MDROs remains unknown. Further study is needed to understand this relationship better and to help design intervention strategies to reduce the spread of MDROs in health-care settings.

We declare no competing interests.

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