



Fig. 1.

Pseudomonas spp, and *P. aeruginosa*) increased on the second floor after the clinic opened (eg, from 23% to 42% for *C. difficile* and from 7% to 46% for MRSA; $P < .05$). The play devices showed small increases in bacterial load after clinic opening, most notably *Pseudomonas* spp. **Conclusions:** This study provides evidence that a shift from bacterial species associated with soil (eg, *Bacillus* spp) toward species commonly associated with humans occurred in waiting rooms after construction in this children's outpatient clinic. Increases for MRSA, *Pseudomonas* spp, and *P. aeruginosa* were linked to patient presence. These data suggest that patients, their families, and clinic staff transport bacteria into clinic waiting

rooms. This outpatient clinic environmental contamination may increase potential for HAIs and may represent a target for intervention.

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Bad Bugs Move Alike: Regional Transmission of Antibiotic-Resistant Organisms

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Background: Upon admission, 56.8% of patients entering 6 Michigan nursing facilities from regional acute-care hospitals (ACHs) were colonized with 1 or more antibiotic-resistant organisms (AROs) (Mody 2018, CID). This observation raises 2 questions critical to regional infection control strategies: (1) Is the high ARO burden entering nursing facilities driven by dominant epidemic lineages or diverse circulating strains? and (2) What are the relative roles of patient characteristics (eg, high-risk patients) and exposure to specific ACHs (eg, high-risk facilities) in determining whether patients are colonized with AROs upon nursing facility admission? Here, we integrated whole-genome sequencing, patient transfer, and clinical data to answer these questions for the 4 most prevalent ARO species in the region: methicillin-resistant *Staphylococcus aureus*

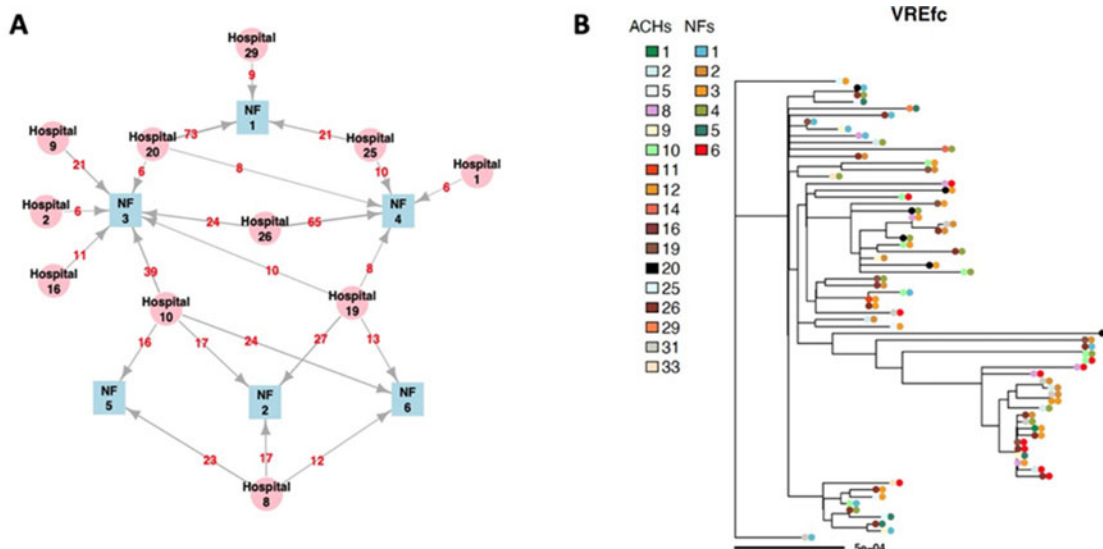


Figure 1. A) Visualization of patient sharing network involving six nursing facilities (NFs; blue nodes) and 11 acute-care hospitals (pink nodes) in southeast Michigan, 2013–2016. Directed arrows represent patient flow from an ACH to a NF, with the number of patients transferred shown in red. **B)** A representative phylogenetic tree (vancomycin-resistant *Enterococcus faecalis*; VREfc) labeled with nursing facilities (NFs) and acute-care hospitals (ACHs) to demonstrate the intermixing of strains across facilities. The trees were inferred from maximum likelihood (RAxML) analysis. Tip colours indicate different NFs and ACHs, and scale bar represents substitutions per nucleotide site.

Fig. 1.

	MRSA (n = 67) OR (95% CI)	VREfm (n = 101) OR (95% CI)	VREfc (n = 49) OR (95% CI)	CipREc (n = 34) OR (95% CI)
Urinary catheter use in past 30 days	1.37 (0.7 - 2.6)	1.69 (0.94 - 3)	-	-
Physical self-maintenance score	1.15 (1.08 - 1.23)	1.08 (1.02 - 1.15)	1.07 (1 - 1.14)	1.11 (1.02 - 1.2)
Length of hospital stay	-	1.06 (1.02 - 1.11)	-	-
Charlson comorbidity score	-	1.05 (0.91 - 1.19)	1.17 (1.01 - 1.35)	-
Exposure to third/fourth-generation Cephalosporins in ACH	2.48 (1.03 - 5.81)	3.96 (1.97 - 8.09)	-	-
Exposure to Glycopeptides in ACH	2.95 (1.23 - 6.93)	2.77 (1.29 - 5.94)	2.62 (1.02 - 6.41)	-
ACH 8	0.63 (0.19 - 1.8)	1.18 (0.45 - 2.94)	0.43 (0.09 - 1.43)	0.7 (0.1 - 3.03)
ACH 10	0.77 (0.32 - 1.8)	0.83 (0.35 - 1.9)	0.59 (0.22 - 1.47)	2.27 (0.82 - 6.46)
ACH 19	1.3 (0.44 - 3.54)	2.48 (1.06 - 5.83)	0.7 (0.18 - 2.18)	1.64 (0.33 - 6.42)
ACH 20	0.51 (0.17 - 1.35)	0.63 (0.22 - 1.61)	0.51 (0.16 - 1.42)	1.53 (0.47 - 4.76)
ACH 26	0.93 (0.37 - 2.25)	1.6 (0.7 - 3.61)	1.2 (0.47 - 2.92)	1.53 (0.42 - 5.06)

Table 1. Associations between patient characteristics, facility exposure and colonization with an antibiotic-resistant organism (ARO) upon admission to a nursing facility by ARO. Results of multivariate analysis adjusting for patient factors and recent hospital exposure are presented. "-" indicates that the covariate was not included in the final model because the p value was ≥ 0.1 in the univariate analysis. Risk factors significantly associated with ARO colonization at admission are bolded. Functional status was measured by physical self-maintenance score. Hospitals with fewer than 50 discharges were collapsed and used as the referent group. Abbreviations: ACH, acute-care hospital; MRSA, methicillin-resistant *Staphylococcus aureus*; VREfm, vancomycin-resistant *Enterococcus faecium*; VREfc, vancomycin-resistant *Enterococcus faecalis*; CipREc, ciprofloxacin-resistant *Escherichia coli*, OR (95% CI) = odds ratio and 95% confidence interval.

Table 1.

(MRSA), vancomycin-resistant *Enterococcus faecalis* (VREfc), *Enterococcus faecium* (VREfm), and ciprofloxacin-resistant *Escherichia coli* (CipREc). **Methods:** We studied colonizing isolates collected via active surveillance of 584 patients in 6 Michigan nursing facilities between 2013 and 2016. The whole genome of the first isolate of each ARO species collected from each patient was sequenced and analyzed to identify sequence types (STs) and to infer the transmission network by species. We determined the connectedness between nursing facilities based on the number of patients received from the same ACHs and assigned each ARO to the most recent ACH using curated transfer information. The associations between patient characteristics and recent ACH exposures with colonization by ARO were examined using multivariable models. **Results:** Most of the sequenced ARO isolates belonged to major healthcare-associated lineages: MRSA (ST5, N = 78 of 117); VREfc (ST6, N = 68 of 75); CipREc (ST131, N = 50 of 64); and closely related VREfm isolates (N = 129). Phylogenetically closely related isolates were found across study facilities, indicating that endemic ARO lineages have permeated local healthcare networks (Fig. 1). Patient characteristics played a dominant role in determining patient risk of ARO colonization on admission to a nursing facility. Only in the case of VREfm was a hospital significantly associated with colonization after adjustment for covariates (Table 1). **Conclusions:** ARO lineages were widely disseminated and colonization of specific ARO lineages at nursing facility entry could not be attributed to recent exposure to a specific ACH. Thus, for the ARO lineages studied here, a broader transmission system crosses ACHs, nursing facilities and probably the community. Therefore, the best indicators of ARO colonization were patient clinical characteristics, particularly poor functional status and antibiotic exposure. These findings suggest that intervention efforts targeting patients with characteristics associated with ARO colonization may help limit further spread among regional facilities.

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Barriers and Facilitators to Improving Hospital Cleanliness in a Brazilian Hospital

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Background: Antimicrobial resistance is a global public health threat. Integrated actions are necessary to reduce multidrug-resistant organisms (MDROs) in healthcare settings, including antimicrobial stewardship, infection prevention measures, and optimal environmental hygiene. We developed a project to improve hospital hygiene that involves 3 phases: (1) diagnostic, compounded by assessment of cleanliness and identification of barriers and facilitators for environment cleanliness improvement; (2) intervention, based on review of structure and processes followed by a training program focused on major weaknesses identified; and (3) evaluation, impact of the intervention assessment. **Objectives:** We performed group interviews to identify barriers and facilitators for improving environment cleanliness. **Methods:** The project was performed by the infection control team and the housekeeping manager in a 350-bed, private hospital located in the city of São Paulo (Brazil). Two group interviews were conducted, one involving supervisors and the other involving housekeeping cleaners. All professionals were invited to participate. A semistructured questionnaire was used to guide the discussion, which was compounded by the following topics: working process, availability of human and material resources, training on institutional norms and routines, perception regarding work conditions, and quality of cleanliness. **Results:** In total, 33 professionals attended the interviews: 12 were supervisors and 21 were housekeeping cleaners. The