Table 1 – Incidence Rate Ratios (95% CI) from stratified regression model associated with the amount of time other family members spent hospitalized in prior 90-days

Total time other family members spent in hospital (prior 90 days)	All CDI Cases (N CDI = 224,818)	No prior CDI in family (N CDI – 223,744)	No prior CDI in family and no prior hospitalization (N CDI = 164,650)
≤5 days	(reference)	(reference)	(reference)
5-10 days	1.28 (1.12-1.46)	1.32 (1.12-1.55)	1.58 (1.28-1.96)
11-20 days	1.49 (1.22-1.82)	1.60 (1.25-2.04)	1.99 (1.44-2.76)
21-30 days	1.68 (1.19-2.37)	1.91 (1.25-2.92)	2.45 (1.38-4.36)
31-40 days	1.92 (1.19-3.11)	2.19 (1.20-3.99)	3.22 (1.45-7.14)
41-50 days	2.00 (1.03-3.87)	2.27 (1.00-5.19)	3.79 (1.32-10.89)
>50 days	4.05 (2.65-6.19)	4.30 (2.51-7.38)	6.14 (2.98-12.64)

conducted a retrospective cohort study using the Truven Marketscan database from 2001 through 2017; both commercial claims and Medicare supplemental data were included. We categorized enrollees by age, sex, month, year, exposure to a family member with CDI, hospitalization, or high- or low-risk antibiotic use in the prior 90 days. We then subdivided these groups based on the total amount of time that other family members spent hospitalized in the prior 90 days: ≤4 days, 5–10, 11–20, 21–30, 41–50 or >50 days. Within each subgroup, we computed the incidence of CDI. We then used a stratified regression model (log-linear quasi-Poisson) to estimate the incidence of CDI in each enrollment bin. Finally, we repeated our analysis using all CDI cases, CDI cases with no prior CDI in the family, and cases without prior hospitalization. **Results:** Over the 17-year study period, >5.1 billion enrollment months were represented in our dataset. We identified 224,818 cases of CDI, 223,744 cases without prior CDI in a family member and 164,650 CDI cases where the case patient had no prior hospitalization. Table 1 depicts the estimated risk (incident rate ratios) associated with the amount of time that other family members spent hospitalized in the prior 90 days. There is a very clear dose–response curve, and the relative risk for CDI increase as the amount of time other family members spent hospitalized increased. Other risk factors included prior hospitalization, low- and high-risk antibiotics, age, female sex and exposure to a family member with CDI. **Conclusions:** Having a family member who has been hospitalized in the prior 90 days significantly increases the risk for CDI, even if the family member did not have CDI. The total amount of time other family members spent in the hospital is positively associated with the level of risk.

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Presentation Type:
Distinguished Oral

Repeated Prevalence Surveys and Admission Screening for *Candida auris* at One Long-Term Acute-Care Hospital, Chicago, 2016–2019

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Background: Since the initial identification of *Candida auris* in 2016 in Chicago, ongoing spread has been documented in the Chicago area, primarily among older adults with complex medical issues admitted to high-acuity long-term care facilities, including long-term acute-care hospitals (LTACHs). As of October 2019, 790 cases have been reported in Illinois. Knowing *C. auris* colonization status on admission is important for prompt implementation of infection control precautions. We describe periodic facility point-prevalence surveys (PPSs) and admission screening at LTACH A. Methods: Beginning September 2016, we conducted repeated PPSs for *C. auris* colonization at LTACH A. After a baseline PPS, we initiated admission screening in May 2019 for patients without prior evidence of *C. auris* colonization or infection. *C. auris* screening specimens consisted of composite bilateral axillary/inguinal swabs tested at public health laboratories. We compared a limited set of patient characteristics based on admission screening results. Results: From September 2016 through October 2019, 277 unique patients were screened at LTACH A during 10 PPSs. Overall, 36 patients (13%) were identified to be colonized. The median facility *C. auris* prevalence increased from 2.8% in 2016 to 37% in 2019 (Fig. 1). During May–September 2019, among 174 unique patients admitted, 151 (87%) were screened for *C. auris* colonization on admission, of whom 18 (12%) were found to be colonized. Overall, 14 patients were known to have *C. auris* colonization on admission and were not rescreened, and 9 patients were discharged before screening specimens could be collected. A significantly higher proportion of patients testing positive for *C. auris* on admission had a central venous catheter or a peripherally inserted central catheter or were already on contact precautions (Table 1). The PPS conducted on October 1, 2019, revealed 5 new *C. auris* colonized patients who had screened negative on admission. **Conclusions:** Repeated PPSs at LTACH A indicated control of *C. auris* transmission in 2016–2017, followed by increasing prevalence beginning in May 2018, likely from patients admitted with unrecognized *C. auris* colonization and subsequent facility spread. Admission screening allowed for early detection of *C. auris* colonization. However, identification during subsequent PPS of additional colonized patients indicates that facility transmission is ongoing. Both admission screening and periodic PPSs are needed for timely detection of colonized patients. Given the high *C. auris* prevalence in LTACHs and challenges in identifying readily apparent differences between *C. auris* positive and negative patients on admission, we recommend that all patients being admitted to an LTACH in endemic areas should be screened for *C. auris*.

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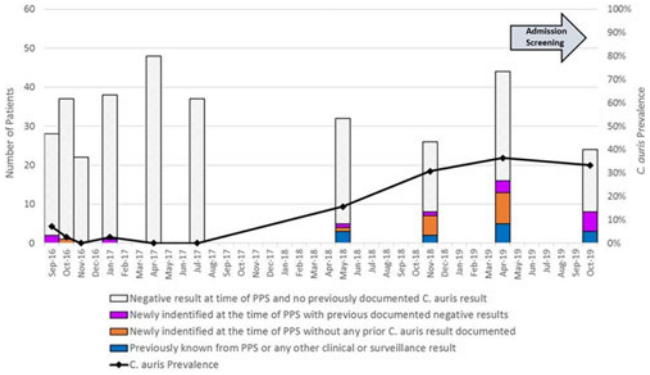

Figure. Patient *C. auris* colonization status identified during point prevalence surveys, LTACH A, September 2016-October 2019.

Fig. 1.

Table. Characteristics of patients screened for *C. auris* on admission to LTACH A, May 2019-September 2019.

Covariate	*C. auris* colonized patients on admission (N=18)	Patients testing negative for *C. auris* colonization on admission (N=133)	P value
	Demographics		
Male, n (%)	10 (56)	88 (66)	>0.05
Age, mean y	64.6	59.2	>0.05
	Clinical Risk Factors		
Gastrostomy tube, n (%)	12 (67)	59 (44)	>0.05
Hemodialysis, n (%)	4 (22)	28 (21)	>0.05
Intravenous devices‡, n (%)	**10 (56)**	**40 (30)**	**0.03**
Mechanical ventilation, n (%)	6 (33)	41 (31)	>0.05
Tracheostomy, n (%)	8 (44)	49 (37)	>0.05
	Prior MDRO† history		
Contact Precautions*, n (%)	**12 (67)**	**40 (30)**	**0.01**
XDRO record**, n (%)	2 (11)	5 (4)	>0.05

† Multi-Drug Resistance Organism (MDRO)

‡ Intravenous devices represent central venous catheter or peripherally inserted central catheter.

* Documented indications for Contact Precautions include: *Clostridioides difficile*, carbapenem-resistance *Enterobacteriaceae* (CRE), carbapenemase-producing organisms (CPO), Extended spectrum beta-lactamase organism, Lice, Methicillin-resistant *Staphylococcus aureus*, and Vancomycin-resistant *Enterococcus*, Shingles, and other MDRO (e.g., *Serratia* sp.).

** Extensively Drug Resistant Organism (XDRO) record indicates documented CRE or CPO history in the Illinois web-based registry.

Presentation Type:
Distinguished Oral

Simplifying Surveillance Sampling: Can Environmental Surveillance Replace Perianal Screening?

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Background: Although active surveillance for multidrug-resistant organism (MDRO) colonization permits timely intervention, obtaining cultures can be time-consuming, costly, and uncomfortable for patients. We evaluated clinical differences between patients with and without attainable perianal cultures, and we sought to determine whether environmental surveillance could replace perianal screening. **Methods:** We collected active surveillance cultures from patient hands, nares, groin, and perianal area upon enrollment, at day 14, and monthly thereafter in 6 Michigan nursing homes. Methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE), and resistant gram-negative bacilli (RGNB) were identified using standard methods. Patient characteristics were collected by trained research professionals. This substudy focused on visits during which all body sites were sampled. To determine the contribution of perianal screening to MDRO detection, site of colonization was categorized into 2 groups: perianal and non-perianal. We evaluated the utility of multisite surveillance (eg, type 1 and type 2 error) using nonperianal sites and environment surveillance. To evaluate

Table 1. Active Surveillance of Multidrug-Resistant Organisms in Six Nursing Homes.

Characteristic[a]	Any MDRO+ No. (%)	MRSA+ No. (%)	VRE+ No. (%)	RGNB+ No. (%)
MDRO Burden (N=1026 Visits)[b]				
All Body Sites	620 (60.4)	155 (15.1)	363 (35.4)	386 (37.6)
Hands	248 (24.2)	100 (9.8)	135 (13.2)	57 (5.6)
Nares	134 (13.1)	98 (9.6)	4 (0.4)	33 (3.2)
Groin	261 (25.4)	17 (1.7)	147 (14.3)	161 (15.7)
Perianal Area	465 (45.3)	31 (3.0)	304 (29.6)	284 (27.7)
Environmental Surveillance	672 (65.5)	250 (24.4)	442 (43.1)	302 (29.4)
Return on MDRO Detection Using Multiple Non-Perianal Sites and Environmental Surveillance[c]				
Hands	248 (40.0)	100 (64.5)	135 (37.2)	57 (14.8)
Hands + Nares	302 (48.7)	140 (90.3)	135 (37.2)	80 (20.7)
Hands + Nares + Groin	437 (70.5)	143 (92.3)	213 (58.7)	212 (54.9)
Environmental Surveillance Only[d]	471 (76.0)	122 (78.7)	261 (71.9)	132 (34.2)
Hands + Nares + Groin + Environment[d]	549 (88.6)	148 (95.5)	301 (82.9)	262 (67.9)
Total Body Site Colonization	**620 (100)**	**155 (100)**	**363 (100)**	**386 (100)**

[a] Study visits were eligible for analysis if all body sites (hands, nares, groin, and perianal area) were collected.

[b] MDRO burden was calculated as the percent of colonized visits divided by the total number of sampling visits.

[c] MDRO detection was defined as the number of colonized visits detected by the screening panel divided by the total number of colonized visits.

[d] Specificity of room environment surveillance was 50.5%, 85.3%, 72.7%, and 73.4% for Any MDRO, MRSA, VRE, and RGNB, respectively.

Abbreviations: MDRO, multidrug-resistant organism; MRSA, methicillin-resistant *Staphylococcus aureus*; VRE, vancomycin-resistant enterococci; RGNB, resistant gram-negative bacteria.

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