

insurance type, presence of coexisting conditions or medical devices at enrollment, hospitalization or residence in a nursing home in the year before enrollment, receipt of anti-MRSA antibiotics, protocol adherence, and randomization strata. **Results:** USA300 was identified in 420 of the 783 participants who attended all visits and had strains genetically tested. MRSA infections occurred in 27 of 207 education group participants (0.149 per person year) and in 19 of 213 decolonization group participants (0.099 per-person year). Point estimates from the unadjusted hazard ratios of infection reduction were similar (0.59; 95% CI, 0.32–1.09) to the full trial population (0.61; 95% CI, 0.44–0.85), suggesting nondifferential benefit for the USA300 strain type. Adjusted models were highly similar. **Conclusions:** The reduction in MRSA infection associated with postdischarge decolonization in the subgroup of participants who harbored the USA300 strain-type was consistent with overall trial findings. Although the original trial was not powered for the evaluation of a USA300 subset, this RCT provides a valuable design for assessing the magnitude of strain-specific responsiveness to decolonization during a time when national rates of MRSA invasive disease have plateaued and USA300 is responsible for an increasing proportion of infections. These data suggest that postdischarge decolonization should be similarly effective in carriers of either USA300 or healthcare-associated MRSA strains.

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Presentation Type:

Top Rated Posters

Prevalence of Healthcare-Associated Infections and Antimicrobial Resistance in Rural Alberta Acute-Care Facilities
Jennifer Ellison, Infection Prevention & Control, Alberta Health Services; Uma Chandran, Royal Alexandra Hospital & Glenrose Rehabilitation Hospital; Jennifer Happe, Alberta Health Services; Ye Shen, Infection Prevention & Control, Alberta Health Services; Jayson Shurgold, Public Health Agency of Canada; Geoffrey Taylor, University of Alberta; Kathryn Bush, Alberta Health Services

Background: Antibiotic-resistant organisms (AROs) are associated with greater disease severity and poor outcomes. Previous studies have investigated AROs and healthcare-associated infections (HAIs) within larger urban acute-care settings, but similar data for rural settings are scarce. In this study, we aimed to fill this gap. **Methods:** Data on antimicrobial resistance (AMR), additional precautions and HAI were collected from 8 rural Alberta acute-care facilities over a 24-hour period from February 4–28, 2019. Data were gathered as part of the national Canadian, Rural, and Northern Acute Care Point Prevalence (CNAPP) survey. All inpatients on included units were reviewed. CNAPP protocol surveillance definitions were used. **Results:** In total, 961 patients were surveyed, of whom 94 of 961 (9.8%) were on additional precautions. Contact precautions only were most common (54 of 94, 57.4%) and were

predominantly in place for MRSA (30 of 94, 31.9%). Of 961 patients, 100 (~10%) met the surveillance definitions for any infection. The most common infections were skin and soft-tissue infections (29 of 100, 29.0%) and bloodstream infections (28 of 100, 28.0%). An HAI occurred in 30 of 961 patients (3.1%); the most common HAIs were surgical site infections (8 of 30, 26.7%) and urinary tract infections (8 of 30, 26.7%). An antimicrobial was prescribed to 333 of 961 patients (34.6%) at the time of the survey, with ceftriaxone the most commonly prescribed (68 of 333, 20.4%). Most patients receiving an antimicrobial (237 of 333, 71.2%) did not meet the surveillance definition for any infection. The most common reason for any antimicrobial administration was empiric therapy (167 of 333, 50.1%). **Conclusions:** Investigations into antimicrobial use and the burden of HAIs in rural acute-care settings have been limited. In this study, we (1) established provincial baseline data for burden of disease in these facilities due to HAIs and (2) demonstrated that antimicrobial use is common, though most patients who were prescribed an antimicrobial did not meet study definitions for infection. It will be important to continue this type of surveillance in this understudied population to monitor the burden of HAIs over time, to establish antimicrobial utilization trends, and to continue to identify potential antimicrobial stewardship initiatives.

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Top Rated Posters

Public Health Oversight of Interfacility Transfers During a *Candida auris* Outbreak—Orange County, California, 2019

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Background: In February 2019, the Orange County Health Care Agency (OCHCA) identified an outbreak of *Candida auris*, an emerging fungus that spreads rapidly in healthcare facilities. Patients in long-term acute-care hospitals (LTACHs) and skilled nursing facilities that provide ventilator care (vSNFs) are at highest risk for *C. auris* colonization. With assistance from the California Department of Public Health and the Centers for Disease Control and Prevention, OCHCA instituted enhanced surveillance, communication, and screening processes for patients colonized with or exposed to *C. auris*. **Method:** OCHCA implemented enhanced surveillance by conducting point-prevalence surveys (PPSs) at all 3 LTACHs and all 14 vSNFs in the county. Colonized patients were identified through axilla/groin skin swabbing with *C. auris* detected by PCR and/or culture. In facilities where >1 *C. auris* colonized patient was found, PPSs were repeated every 2 weeks to identify ongoing transmission. Retrospective case finding was instituted at 2 LTACHs with a high burden of colonized patients; OCHCA contacted patients discharged after January 1, 2019, and offered *C. auris* screening. OCHCA tracked the admission or discharge of all colonized patients, and facilities with ongoing transmission were required to report transfers of any patient, regardless of colonization status. OCHCA tracked all patients discharged from facilities with ongoing transmission to ensure that accepting facilities conducted admission

Figure 1. *Candida auris* colonized patient transfer network- Orange County, CA healthcare facilities

Orange County *C. auris* colonized patient transfer network
February 1- October 31, 2019
(N=96)

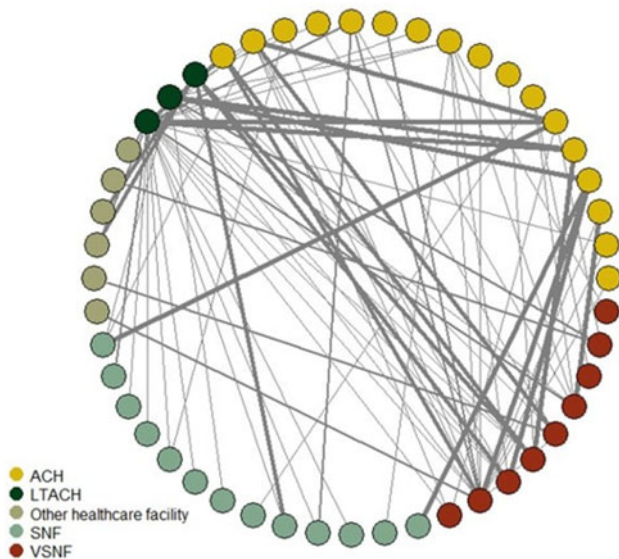


Fig. 1.

surveillance testing of exposed patients and implemented appropriate environmental and contact precautions. **Result:** From February–October 2019, 192 colonized patients were identified. All 3 LTACHs and 6 of 14 VSNFs had at least 1 *C. auris*–colonized patient identified on initial PPS, and 2 facilities had ongoing transmission identified on serial PPS. OCHCA followed 96 colonized patients transferred a total of 230 times (an average of 2.4 transfers per patient) (Fig. 1) and 677 exposed patients discharged from facilities with ongoing transmission (Fig. 2). Admission screening of 252 exposed patients on transfer identified 13 (5.2%) *C. auris*–colonized patients. As of November 1, 2019, these 13 patients were admitted 21 times to a total of 6 acute-care hospitals, 2 LTACHs, and 3 vSNFs. Transferring facilities did not consistently communicate the colonized patient’s status and the requirements for isolation and testing of exposed patients. **Conclusion:** OCHCA oversight of interfacility transfer, though labor-intensive, improved identification of patients colonized with *C. auris* and implementation of appropriate environmental and contact precautions, reducing the risk of transmission in receiving healthcare facilities.

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Top Rated Posters

Recurrent *Clostridioides difficile* infection can be predicted using inflammatory mediator and toxin activity levels Jonathan Motyka, University of Michigan Medical School; Aline Penkevich, University of Michigan Medical School; Vincent Young, University of Michigan Medical School; Krishna Rao, University of Michigan

Figure 2. Flow chart of exposed patient tracking for patients discharged from facilities with ongoing transmission

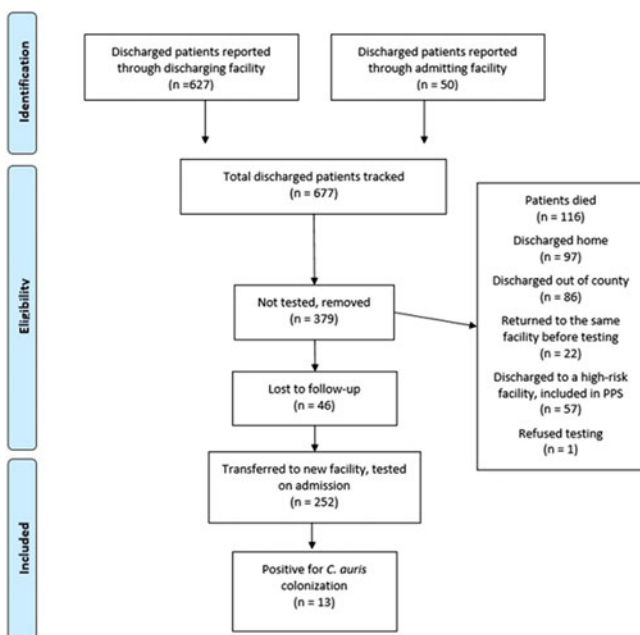


Fig. 2.

Background: *Clostridioides difficile* infection (CDI) frequently recurs after initial treatment. Predicting recurrent CDI (rCDI) early in the disease course can assist clinicians in their decision making and improve outcomes. However, predictions based on clinical criteria alone are not accurate and/or do not validate other results. Here, we tested the hypothesis that circulating and stool-derived inflammatory mediators predict rCDI. **Methods:** Consecutive subjects with available specimens at diagnosis were included if they tested positive for toxigenic *C. difficile* (+enzyme immunoassay [EIA] for glutamate dehydrogenase and toxins A/B, with reflex to PCR for the *tcdB* gene for discordants). Stool was thawed on ice, diluted 1:1 in PBS with protease inhibitor, centrifuged, and used immediately. A 17-plex panel of inflammatory mediators was run on a Luminex 200 machine using a custom antibody-linked bead array. Prior to analysis, all measurements were normalized and log-transformed. Stool toxin activity levels were quantified using a custom cell-culture assay. Recurrence was defined as a second episode of CDI within 100 days. Ordination characterized variation in the panel between outcomes, tested with a permutational, multivariate ANOVA. Machine learning via elastic net regression with 100 iterations of 5-fold cross validation selected the optimal model and the area under the receiver operator characteristic curve (AuROC) was computed. Sensitivity analyses excluding those that died and/or lived >100 km away were performed. **Results:** We included 186 subjects, with 95 women (51.1%) and average age of 55.9 years (± 20). More patients were diagnosed by PCR than toxin EIA (170 vs 55, respectively). Death, rCDI, and no rCDI occurred in 32 (17.2%), 36 (19.4%), and 118 (63.4%) subjects, respectively. Ordination revealed that