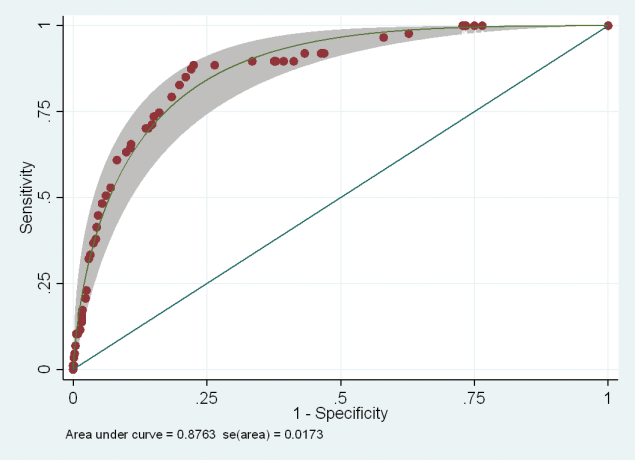
at bedside for patients admitted with sepsis. A future prospective interventional study is needed in order to validate the score, captured at bedside electronically, in terms of improving patients' outcomes.



Disclosures. **All authors:** No reported disclosures.

1205. Emergence of Carbapenemase Producing *Enterobacteriaceae* in South Central Ontario, Canada

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Session: 136. Healthcare Epidemiology: MDR-Gram Negative Infections
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Background. The spread of CPE is an increasing global threat to patient safety. We describe the introduction and evolution of CPE in south-central Ontario, Canada.

Methods. The Toronto Invasive Bacterial Diseases Network has performed population based surveillance for CPE in metropolitan Toronto and Peel region from first identified isolates in 2007. All laboratories test/refer all carbapenem non-susceptible Enterobacterial isolates for PCR testing for carbapenemases. Demographic and medical data and travel history are collected from chart review and patient/physician interview.

Results. Since 2007, 659 patients have been identified as colonized/infected with CPE; 362, 57%) have at least one clinical isolate. Annual incidence has increased from 0 in 2006 to 1.3 per 100,000 in 2016/17 (Figure 1). First bacteremia occurred in 2010, the incidence in 2017 was 0.14 per 100,000 population. 388 (59%) patients were male, median age was 70 years (range 3 months–100 years). Most common genes among first isolates were NDM (306, 46%), OX48 (149, 23%), KPC (122, 19%). Most common species were *K. pneumoniae* (268, 41%) and *E. coli* (259, 39%). Over time, second species/same gene were identified in 113 (16%) patients. In addition, 34/xxx patients with isolates with NDM and/or OXA-48 subsequently had a second isolate with a different gene/gene combination. Of 518 patients whose travel and hospitalization history are available, patients with VIM were less likely than other patients to have a foreign hospitalization or travel history (9/28 vs. 341/490, $P < 0.0001$). Patients with KPC were more likely to have a hospitalization history outside Canada and the Indian subcontinent (25/70, 36%), in Canada (47/164,29%) than to have no hospitalization in the last year (13/93, 14%), or a history of hospitalization in the Indian subcontinent (2/191, 1%) ($P < 0.001$). The number of incident patients with different hospitalization and travel history over time is shown in Figure 2.

Conclusion. CPE is increasingly recognized in southern Ontario, both in patients with a history of exposure in healthcare in other countries, and to healthcare in Canada. Intensification of control programs is urgently needed.

Figure 1. Incidence of clinical isolates of CPE over time.

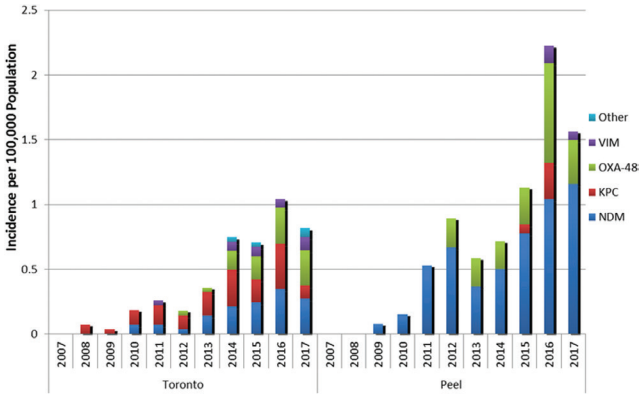
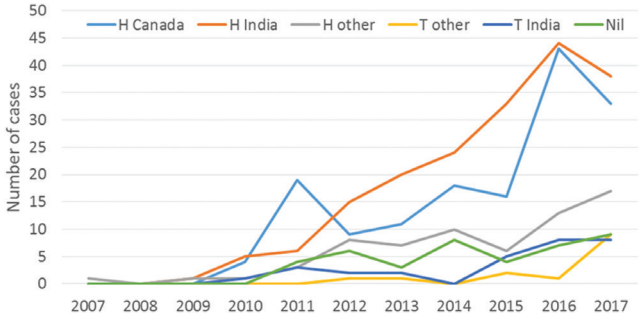


Figure 2. Number of incident CPE cases with different hospitalization (H) and travel (T) history over time.



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1206. Risk Factors of Antibiotic Resistance in *E. coli* Isolated from the MAL-ED Birth Cohort Study in Rural Tanzania

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Background. The emergence and spread of antimicrobial resistance is a serious global public health crisis. Drug-resistant Gram-negative bacteria, like *Escherichia coli*, are particularly concerning given their significant morbidity and mortality. Despite the increasing prevalence of drug-resistant Gram-negative bacteria worldwide, there are significant knowledge gaps in low resource countries. We aimed to characterize the prevalence, phenotypes, and risk factors of drug-resistant *E. coli* carriage in children up to age 5 from stool collected in the Etiology, Risk Factors, and Interactions of Enteric Infections and Malnutrition and the Consequences for Child Health and Development (MAL-ED) birth cohort study in rural Tanzania.

Methods. Two hundred sixty-two children were enrolled in the MAL-ED Tanzania site. We randomly selected 100 children who had *E. coli* specimens archived every 6 months through 60 months. Up to five lactose-fermenting colonies were selected from growth on MacConkey agar. Drug susceptibility testing of 18 antibiotics was performed by disk diffusion. CLSI interpretive criteria were used for determination of resistance. Generalized estimating equations were used to create a multivariate Poisson regression model for drug resistance risk factors.

Results. Eight hundred twenty-three *E. coli* specimens were available for testing. The highest rates of resistance were to ampicillin, cefazolin, and cotrimoxazole, respectively. No carbapenem resistance was found. 1.8% met criteria for extended-spectrum β-lactamase production based on combination disk testing. 696 (84.6%) specimens met criteria for multi-drug resistance (nonsusceptible to at least 1 drug in at least three drug categories). In terms of dynamic risk factors, there was no association between antibiotic use or episodes of diarrhea and antibiotic resistance. For static risk factors, there was an association between higher income and increased antibiotic resistance.

Conclusion. Antibiotic resistance carriage is an under recognized problem in this setting. Resistance rates at 6 months of age are higher than expected, with surprisingly little variance explained by individual-level risk factors for resistance in this community.

Disclosures. **All authors:** No reported disclosures.

1207. Acquisition and Quantification of Antimicrobial Resistance Genes in the Gut Microbiome of Ugandan Women Exposed to Small-Scale Chicken Farming

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Session: 136. Healthcare Epidemiology: MDR-Gram Negative Infections

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Background. Antibiotic use in livestock farming is thought to be a major contributor to the spread of antimicrobial resistance (AMR) genes in humans. However, quantitative data in this in this field are rare. To address this gap in the literature, we examined the prevalence of clinically important AMR genes before and after the introduction of chicken farming among women in rural Uganda.

Methods. We recruited a subset of women participating in a waitlist-randomized controlled trial of small-scale hybrid chicken farming in rural Uganda. Tetracycline is routinely administered to chicks during brooding. Stool samples before and one year after chicken introduction were obtained from six women randomized to the control arm, from five women randomized to the intervention arm, and from chickens. Microbial DNA was extracted from chicken and human stool and screened for 87 AMR genes using validated qPCR arrays (Qiagen).

Results. The median age was 35 years. At baseline, 10 of the women reported animal contact, most commonly goats (n = 8), free ranging village chickens (n = 7), cats (n = 4), and dogs (n = 4). During baseline testing of the women's stool, we detected 18 genes conferring AMR to aminoglycosides, fluoroquinolones, macrolides, lincosamides, streptogramin B, Class A-C β-lactamases and tetracycline efflux pumps. Chickens harbored 23 AMR genes from the same classes as found in humans, and were also found to have vancomycin resistance genes (Van B and C) and Group D β-lactamases (OXA-58 and OXA-10). At one year, six new AMR genes emerged in controls, including one present in chickens; CTX-M-1, a Class A β-lactamase. In contrast, seven new AMR genes emerged in the intervention group, including four present in chickens: SHV, SHV(238G240E), (Class A β lactamases) and QnrS, QnrB-5 (fluoroquinolone resistance genes). Two AMR genes gained by both control and intervention groups were not present in chickens.

Conclusion. Women exposed to small-scale chicken farming acquired more AMR genes compared with unexposed participants. Chickens harbored many of the genes that emerged in humans. Introduction of antibiotic-treated animals may result in the transfer of AMR genes from animals to humans, even among humans exposed to a wide range of animals at baseline.

Disclosures. **All authors:** No reported disclosures.

1208. Impact of Admission to an Inpatient Infectious Disease Unit on Methicillin-Resistant *Staphylococcus aureus* Bloodstream Infections

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Session: 137. Healthcare Epidemiology: MSSA, MRSA and Other Gram Positive Infections

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Background. Methicillin-resistant *Staphylococcus aureus* (MRSA) blood stream infection (BSI) remains a condition with high mortality. Despite the introduction of new antibiotics, the mortality in the past 10 years at our institution remains unchanged. To evaluate measures that improve outcomes in these patients (patients), we studied the impact of admission to an inpatient infectious disease (ID) unit.

Methods. We identified a retrospective cohort of patients with MRSA BSI at an 800-bed hospital in urban Detroit from January 2013 to February 2017. Patients were assigned to one of the three groups: group 1 was admission to inpatient ID unit where the ID doctors were the attending physicians, group 2 was ID consultation (without admission to ID unit), and group 3 was no ID consultation. Demographics, clinical information, and 30 day mortality from index blood culture were collected. Source of BSI was classified into four categories: primary (endovascular infection); secondary (respiratory, skin, osteomyelitis, abdominal and genitourinary infections); central line associated; unknown. Unpaired t-test and Fisher's exact test were used to compare groups.

Results. A total of 477 patients were identified with MRSA BSI during the study period. 89 (18.7%) were in group 1, 299 (62%) in group 2 and 89 (18.7%) in group 3. Pt clinical characteristics and outcomes are shown in Table 1. Overall 30-day mortality was 21.4%. Comparison of mortality between groups are shown in Table 2.

Conclusion. While it is well established that ID consultation has improved outcomes in MRSA BSI, this is the first study that shows that admission to an inpatient ID unit decreases mortality even further.

Table 1: Patient Clinical Characteristics and Outcomes

	Group 1	Group 2	Group 3
	N = 89 (%)	*N* = 299 (%)	*N* = 89 (%)
Age mean (±SD)	51.53 (17.58)	62.86 (17.47)	64.6 (17.60)
Male	48 (53.9)	186 (62.2)	61 (68.5)
Mean duration of BSI (±SD)	3.19 (2.502)	3.09 (2.525)	2.94 (2.503)
Source			
Primary	17 (19.5)	26 (8.9)	7 (7.9)
Secondary	48 (55.2)	138 (47.1)	41 (46.1)
Central line associated	10 (11.5)	60 (20.5)	14 (15.7)
Unknown	12 (13.8)	69 (23.5)	27 (30.3)
30-day mortality	8 (9.0)	54 (18.2)	40 (44.9)
Readmission	14 (16.7)	42 (15.4)	16 (18.0)
Recurrence	10 (11.2)	13 (4.8)	5 (5.6)

Table 2. Comparison of 30-Day Mortality Between Groups

	P value
Group 1 vs. group 2	0.0383
Group 2 vs. group 3	P <0.0001
Group 1 vs. group 3	P <0.0001

Disclosures. **All authors:** No reported disclosures.

1209. Expanding an Economic Evaluation of the Veterans Affairs Initiative to Prevent Methicillin-Resistant *Staphylococcus aureus* Infections to Include Prevention of Gram-Negative Bacteria

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Session: 137. Healthcare Epidemiology: MSSA, MRSA and Other Gram Positive Infections

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Background. In October 2007, the Department of Veterans Affairs (VA) launched the National MRSA Prevention Initiative, a nationwide effort to reduce MRSA transmission through (1) universal screening, (2) contact isolation for MRSA+ patients, (3) institutional culture change that "infection prevention is everyone's business," (4) emphasis on hand hygiene, and (5) increased infection control resources. While the initiative focused on MRSA, recent evidence suggests that it also led to a significant decrease in hospital-onset (HO) Gram-negative rod (GNR) bacteremia. The objective of this analysis was to evaluate the cost-effectiveness and the budget impact of the initiative taking into account both MRSA and GNR infections.

Methods. We developed an economic model using published data on the rate of MRSA HAIs and HO-GNR bacteremia in the VA from October 2007 to September 2015, estimates of the attributable cost and mortality of these infections, and the costs associated with the intervention obtained through a microcosting approach. We explored several different assumptions for the rate of infections that would have occurred if the initiative had not been implemented. Effectiveness was measured in life-years (LYs) gained.

Results. We found that during fiscal years 2008–2015, the initiative resulted in an estimated 4,761–9,236 fewer MRSA HAIs and 1,447–2,159 fewer HO-GNR bacteremia. The initiative itself was estimated to cost $206 million over this 8-year period while the cost savings from prevented MRSA HAIs ranged from $75–165 million and from prevented HO-GNR bacteremia ranged from $42–62 million. The incremental cost-effectiveness of the initiative ranged from $12,146–$46,500/LY when just including MRSA HAIs and from $7,945–$24,387/LY when including HO-GNR bacteremia. The overall impact on the VA's budget ranged from $200–$334 million.