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Background. Colistin is an antibiotic of last resort for treatment of Carbapenem-resistant Enterobacteraceae (CRE) infections. Resistance to colistin is associated with increased mortality and has been observed with increasing frequency in *Klebsiell*a spp. (*K*) Risk factors for colistin-resistant infection have been incompletely studied.

Methods. All patients admitted to academic tertiary medical center and community hospital from 2006-2016, where routine microbiology susceptibility testing includes gold standard broth micro-dilution. From 2006 to 2011, colistin testing was done by request. Starting in 2012, all Gram-negative organisms underwent colistin testing, except urine isolates where only CRE undergo colistin testing. We searched the clinical data warehouse for patients in whom *K* was isolated from any source. Logistic regression models were used to create univariate and multivariable predictive models for colistin resistance. Data were analyzed for complete cases only and were analyzed once per hospital admission.

Results. From 2006-2016, there were 3,837 admissions with *K* isolated and 1360 with complete data. There were 93 admissions with colistin-resistant *K* and 80/93 demonstrated meropenem resistance. Univariate predictors are shown. **Table 1** On unadjusted analysis, days in hospital, male gender, skilled nursing residence, black race, increased age, Elixhauser score, and end-stage renal disease were each significantly associated with increased risk of colistin-resistance. On multivariable analysis, the best model included days hospitalized, gender, skilled nursing residence, and Elixhauser score, with an AUROC of 0.81. **Table 2**

Conclusion. Colistin resistance among patients with *Klebsiella* is significantly associated with skilled nursing facility residence, male gender, prolonged hospitalization, and increased comorbidity. Further studies will look at events within a hospitalization, including patient location, antibiotic exposure to determine modifiable factors associated.

Table 1: Univariate Predictors of Colistin Resistant *Klebsiella* spp. (n=93) among 1,360 admissions where *Klebsiella spp.* were identified.

Predictor	Coefficient	Std Error	p-value
Days since admission	0.013	0.002	0
Male	0.540	0.214	0.012
BMI	-0.012	0.024	0.601
In facility	2.304	0.330	0
Race (ref = White)			
Asian	-0.305	0.438	0.486
Black	0.674	0.268	0.012
Latinx	-0.126	0.300	0.674
Other	0.145	0.477	0.761
Age	0.013	0.006	0.032
Elixhauser Score	0.026	0.007	0.001
Solid Organ Transplant	-0.295	0.293	0.313
Renal Failure	0.796	0.242	0.001
HIV Positive	0.201	1.021	0.844

Table 2: Multivariate Predictors of Colistin Resistant *Klebsiella* spp. (n=93) among 1,360 admissions where *Klebsiella spp.* were identified.

```
Logistic regression                     Number of obs   =      1,360
                                        LR chi2(4)      =      68.40
                                        Prob > chi2     =     0.0000
Log likelihood = -149.7446              Pseudo R2       =     0.1859
```

col_resistant	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
days_to_culture	.014609	.004802	3.04	0.002	.0051973	.0240207
male	.9157987	.3530167	2.59	0.009	.2238986	1.607699
1.in_facility	2.430997	.3459806	7.03	0.000	1.752887	3.109107
elixhauser_score	.0254039	.012699	2.00	0.045	.0005143	.0502934
_cons	-5.464497	.4411761	-12.39	0.000	-6.329186	-4.599807

Disclosures. **L. G. Miller**, Sage Products: Study coordination, Conducting studies in healthcare facilities that are receiving contributed product. Xttrium: Study coordination, Conducting studies in healthcare facilities that are receiving contributed product. Clorox: Study coordination, Conducting studies in healthcare facilities that are receiving contributed product. 3M: Study coordination, Conducting studies in healthcare facilities that are receiving contributed product.

387. Intestinal Colonization with *Escherichia coli* Sequence Type 131 (ST131) and Other Fluoroquinolone (FQ)-Resistant *E. coli* (FQREC) within Households (HHs) of Veterans

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Background. Among veterans, FQREC infections are caused mainly by *E. coli*ST131, a recently emerged disseminated clonal group that contains multiple virulence genes. Infecting FQREC strains typically arise from the host's gut reservoir. Within-HH transmission therefore may underlie the ST131 pandemic, and may be influenced by host and/or bacterial characteristics.

Methods. We conducted fecal surveillance for 91 veterans and their 157 HH members, including 72 pets. Fecal cultures were processed extensively to resolve unique *E. coli* clones, as defined by random amplified polymorphic DNA (RAPD) analysis and pulsed-field gel electrophoresis (PFGE). Seven *E. coli*phylogenetic groups and 53 extraintestinal virulence genes were detected by multiplex PCR. Patterns of within-HH strain sharing were evaluated statistically in relation to host and bacterial characteristics.

Results. Of the 350 identified fecal *E. coli* clones, 59 (17%) were shared within a HH. Within-HH strain sharing involved 56 (23%) of the 248 subjects and 27 (30%) of the 91 HHs. The prevalence of strain sharing, while not varying significantly by host group, was slightly higher for humans (24%) than pets (19%), and among humans was somewhat higher for children (40%) than adults (18%) and for females (27%) than males (20%). In contrast, strain sharing was significantly more likely for FQREC (32% for ST131, 31% for non-ST131) than for FQ-susceptible strains (10% for ST131, 15% for non-ST131) (P = .007). Likewise, as compared with other strains, the 59 shared strains more frequently contained *gafD, yfcV*, *sat*, *pic*, *fyuA*, *iutA*, *kpsMII*, *usp*, and H7 *fliC* (P < .05 for each), and had significantly higher virulence gene scores (median, 10.0 vs. 7.2: P = .03).

Conclusion. Intestinal *E. coli* strains were shared extensively among veterans and their human and animal HH members. The frequency of strain sharing varied minimally in relation to host characteristics, but was significantly associated with multiple bacterial characteristics, including FQ resistance, specific virulence genes, and virulence gene score. Since such traits may promote intestinal colonization and/or host-to-host transmission, interventions that target them conceivably could reduce colonization and transmission, including for ST131.

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388. Longitudinal Analysis of ICU Surface Multidrug-resistant Organism Contamination in the US and Pakistan

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Background. The objective of the study was to characterize the environmental reservoirs of multidrug-resistant organism (MDROs) in an intensive care unit (ICU) in Pakistan and the US.

Methods. Environmental samples from 4 ICU rooms at Barnes-Jewish Hospital (St. Louis, MO) and Military Hospital (Rawalpindi, Pakistan) were taken every other week for 3 months, for 7 total samplings (Figure 1). Tap water was also cultured at a subsequent time point. MDROs were cultivated using selective agar. DNA extracted from a "sweep" of the growth on blood agar was used as input for metagenomic sequencing. Metaphlan2 was used to identify species in the metagenomic surface samples.

Results. 18 and 928 MDRO isolates were recovered from the US and the Pakistani ICU, respectively. *Acinetobacter baumanii* (*n* = 13) and *Escherichia coli* (*n* = 5) were recovered from the US, from the same room. *A. baumannii* (*n* = 238), *Enterococcus faecium* (*n* = 152), *Klebsiella pneumoniae* (*n* = 136), and *Pseudomonas aeruginosa* (*n* = 108) were the most common isolates obtained from the Pakistan. Carbapenem-resistant strains were recovered at both sites (Table 1). Pakistani tap water culture revealed: *Aeromonas hydrophilia/punctata, Citrobacter freundii, Comomonas aquaticus, A. baumannii, Acinetobacter haemolyticus, Acinetobacter johnsonii*; the first 4 organisms tested positive for a carbapenemase.

Conclusion. The environmental MDRO burden was higher in Pakistan compared with the USA. The MDROs recovered at both sites are nosocomial pathogens. Whole genome sequencing of all recovered isolates and antibiotic susceptibility testing is underway to determine clonality, extent of multidrug resistance, and mechanisms of carbapenem resistance.

Figure 1: Sampling and Specimen Analysis

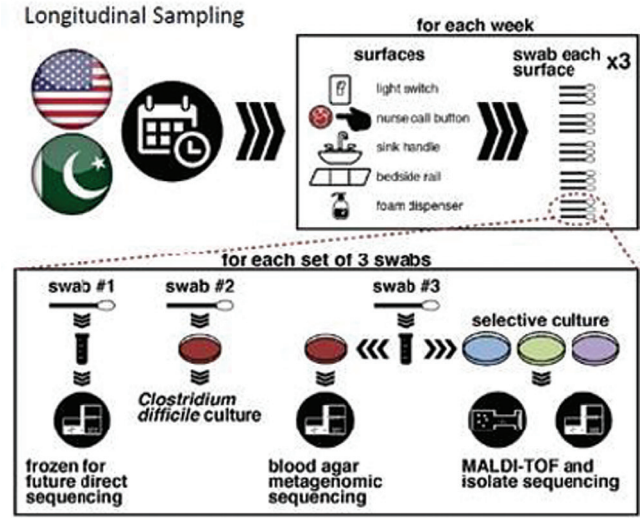

Table 1: Carbapenem-resistant Strains

	Meropenem-Resistant Isolates		Isolates Positive for Carbapenemase	
	US	Pak	US	Pak
Enterobacteriaceae	0	57 (R) 11 (I)	0	60
Acinetobacter spp.	10	83	0	73
Pseudomonas aeruginosa	0	16	0	1
Others	0	19	0	13

Disclosures. **C. A. D. Burnham**, bioMerieux: Grant Investigator, Research grant ThermoFisher: Consultant, Salary. Cepheid: Grant Investigator, Research grant

389. Evaluation of the Management of ESBL Producing Enterobacteriaceae Infections: CHI health Omaha

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Background. Extended spectrum β-lactamase producing Enterobacteriaceae are concerning for appropriate anti-infective treatment. The CDC estimates 1,700 deaths per year and $40,000 in excess hospital costs/ESBL bacteremia. This study evaluated appropriateness of treatment regimens used for ESBL-producing bacteria within the CHI Omaha health system.

Methods. Hospitalized patients were identified by the Microbiology Department within CHI Health System for 2015. Patients > 18 years of age were included in the study if culture results determined an ESBL-producing organism. Treatment appropriateness (TA) was defined as using a carbapenem, (or fosfomycin for UTI only) as definitive therapy. ESBL-production was determined using Clinical Laboratory Standards Institute (CLSI) approved microbiological methods. SPSS (ver 24) was used to analyze the data. A p-value of ≤ 0.05 was considered significant.

Results. A total of 172 patients (107 (62%) female) had positive ESBL-producing organisms and 30% of patients were admitted from nursing homes. *E. coli* was predominant organism cultured (78%). No differences in sex, age, incidence of diabetes, or chronic kidney disease between TA (n = 114) and treatment inappropriate (TI) (n = 58) patients. Forty-six (27%) patients had bacteremia on presentation. Duration of intravenous (IV) antimicrobial therapy was significantly shorter in TI bacteremia patients (TA 13.4 ± 4.3; TI 6.6 ± 5.1, $P < 0.001$). A total of 10% of ESBL patients expired. Significantly more TI patients were diagnosed with urinary tract infections (UTI) compared with TA patients [88% vs. 75%, $P < 0.05$]. Infectious Diseases (ID) was consulted for 65% of ESBL infections. More than two-thirds (40/58) of TI patients did not consult ID ($P < 0.001$). ID consultation resulted in significantly more appropriate duration of IV therapy (ID consult 12.3 ± 7.7, no ID consult 2.2 ± 2.4 days, $P < 0.001$). Majority (53%) of hospitalized TI patients were administered oral antimicrobials for definitive UTI therapy.

Conclusion. In patients with ESBL-producing organisms, TA antimicrobial use with ID consultation leads to more appropriate outcomes.

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

390. Enhanced Gram-Negative Resistance Gene Surveillance in Clinical Samples using a Rapid Microarray System

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Background. Extended-spectrum β lactamases (ESBLs) are clinically significant due to the limited treatment availability and associated increased healthcare costs. They are caused by point mutations arising on chromosomal genes or are encoded from plasmid genes, such as bla_{CTX-M} class genes. These mobile genetic elements can spread to create extensive environment reservoirs, which can, in turn, result in the carriage of resistant bacteria by humans in clinical and non-clinical settings.

Methods. All patients admitted to a large London teaching hospital between January and May 2015 were screened. ESBL-carrying organisms were isolated on chromogenic media for ESBL and DNA was extracted. Enterobacteriaceae were analysed for resistance genes using the microarray system Check-MDR CT103XL® (Check-Points), which detects most carbapenemase and ESBL genes, including plasmid-mediated AmpC genes.

Results. A total of 4,567 patients were approached and 4,006 screened; prevalence of ESBLs-carrying organisms was 8.2%. Most patients carried only one organism, of which *E. coli* was the most common (77.8%), followed by *K. pneumoniae* (8.4%), *C. freundii* (3.6%) and *E. cloacae* (2.8%). 20.7% of patients carried more than one ESBL-resistant organism, 3.3% of which belonging to a different species; when of the same species, organisms were considered different based on their resistance genes. The most prevalent ESBL genes identified were the plasmid-mediated $bla_{CTX-M-15}$ (57.4%) and $bla_{CTX-M-9}$ (20.7%), and AmpC CMY-2 (6.4%). Notably, 8.6% of isolates carried more than one gene, and 1.4% more than 2 genes, with AmpC genes (CMY-2 and DHA) and ESBL genes (bla_{CTX-M}) being the most common co-carried genes.

Conclusion. The use of the Microarray system Check-MDR CT103XL® (Check-Point) allows for a rapid and comprehensive identification of resistance genes in clinical samplse. In this study, this system revealed a much more diverse resistance genetic composition of the *Enterobacteriaceae* population circulating in South London than previously estimated, perhaps due to the unselected patient group screened. It also reveals the co-existence of more than one resistance gene in a proportion of organisms. Moreover, composite genetic profiles could be useful to identify hotspots for transmission or novel risk factors.

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

391. Discordant Ertapenem/Imipenem Susceptibilities in *Enterobacter* Bacteremia: Frequency and Outcomes

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Background. *Enterobacter* spp. are an important cause of infections and antibiotic resistance, including carbapenem resistance. Recent studies suggest that infections due to carbapenem-resistant Enterobacteriaceae (CRE) carrying carbapenemase-encoding genes carry a worse prognosis than CRE that do not carry a carbapenemase-encoding gene, but it is unknown whether there are differences by different bacterial genera/species. CRE that are resistant only to one carbapenem –almost always ertapenem –have been reported, but the frequency of discordance between ertapenem and imipenem/meropenem is not known for *Enterobacter* spp.

Methods. We examined all cases of *Enterobacter* bacteremia from January 2012 to December 2016 at the Michael E. DeBakey VA Medical Center in Houston, Texas, USA. Clinical and microbiological data were independently extracted by two investigators. Antibiotic suscepitibilty testing results were interpreted according to current CLSI breakpoints.

Results. Discordance between ertapenem and imipenem susceptibilities was found in 14/67 (20.9%) isolates; eight isolates were ertapenem susceptible/imipenem non-susceptible, and six isolates were ertapenem non-susceptible/imipenem susceptible. Bacteremia cleared in 94.5% (3/55) of all patients who had follow-up cultures, including infection by all (13/13) isolates with discordant carbapenem susceptibilities. Fourteen-day mortality was not different between the patients with concordant and discordant carbapenem susceptibilities (7.5% vs. 21.4%; $P = 0.3408$, Fisher's exact test); four patients died within 48 hours of bacteremia and the remaining three deaths had documented clearance of bacteremia.