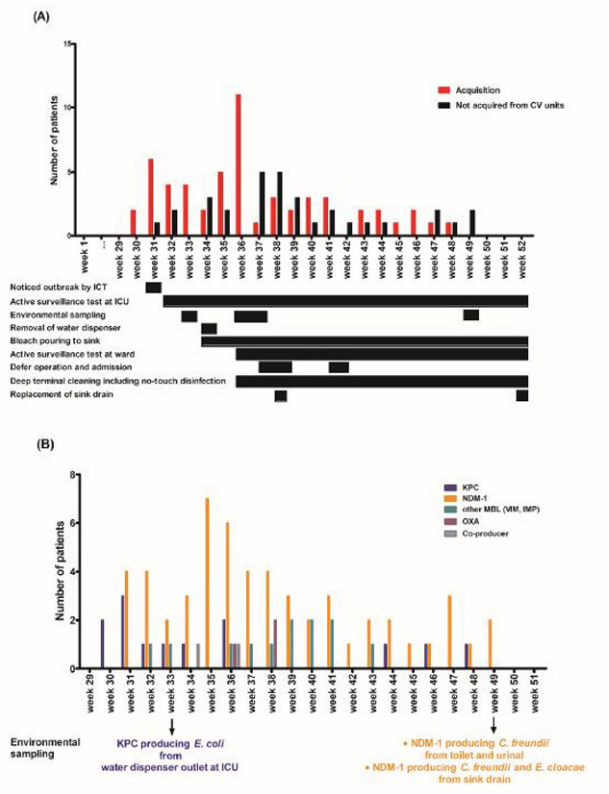
Figure 1. Epicurve and interventions to control outbreak. (A) Epicurve stratified by acquisition sites (cardiology units or other units) and intervention. (B) Epicurve stratified by genotype of carbapenemase and results from environmental sampling.



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

2456. *Stenotrophomonas maltophilia* (SM) Pseudo-outbreak Associated with Bronchoscope

Siobhan Eichenblat, CCRN[1]; Eileen Campbell, CIC[1]; Shelley Kester, CIC, MHA[1]; Jessica Layell, CIC[1]; Catherine Passaretti, MD[2]; [1]Atrium Health, Charlotte, North Carolina; [2]Carolinas HealthCare Systems, Charlotte, North Carolina

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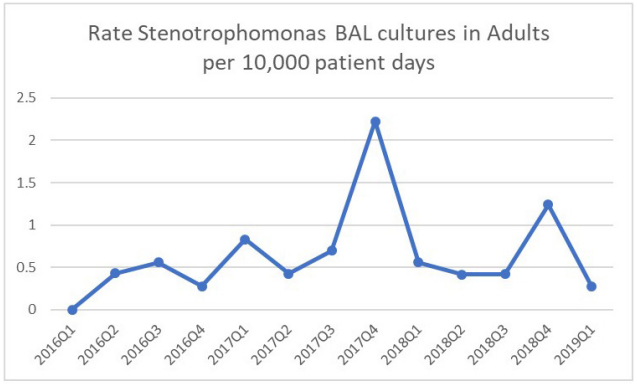
Background. Stenotrophomonas maltophilia (SM) is a multi-drug-resistant Gram-negative organism that typically impacts patients with long hospital stays or severe immunocompromise. In Q4 2017, an increase in rates of SM from adult bronchoscopic alveolar lavage (BAL) specimens was detected.

Methods. The charts of all patients with SM from BAL specimens during the time frame in question were reviewed for commonalities, clinical symptoms and antibiotic treatment for Stenotrophomonas. Incidence rate ratios for the 21 months prior to, 3 months during and 15 months after the increase were compared using Fisher exact test.

Results. Quarter 4 2017 rates of SM isolated from BALs performed in patients >/ = 18 years of age increased significantly from baseline of 0.46 to 2.22 per 10,000 patient-days. Upon chart review 75% (12/16) of patients with SM during the increase had BALs performed with a specific bronchoscope. Q4 2017, 22 patients had a BAL performed with the scope in question with 16 sent for culture. 75% (12/16) of the BALs done with this scope during Q4 2017 grew SM. The scope was pulled from use once the association was identified. ATP and high-level disinfection records were reviewed with no failures noted. The scope was sent to an independent lab where boroscope evaluation showed epoxy lifting. Cultures from the scope were unrevealing. After the scope was removed from service, rates of SM from adult BALs dropped significantly back to 0.58 per 10,000 patient-days (Figure 1). Upon clinical review, SM was deemed clinically insignificant in all but 1 case, however, 8 of the 12 patients received antibiotic treatment for this pathogen. To date, none of the patients in question had subsequent cultures with SM. No adverse events due to antibiotic therapy have been noted 10 of the patient isolates were retrieved and sent for pulsed-field gel electrophoresis testing. All came back with identical PFGE patterns strongly suggesting a point source.

Conclusion. While the bronchoscope culture did not grow SM, the identical PFGE patterns in patients without evidence of active infection suggested a point source. Return of SM rates to baseline following removal of the scope from service strongly suggest a pseudo-outbreak resulting from a reusable bronchoscope.



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

2457. Data Science for Outbreak Investigation: Identifying Risk Factors, Tracing Contacts, and Eliciting Transmission Pathways in a Vancomycin-Resistant Enterococci (VRE) Outbreak

Stefan Zahnd, PhD[1]; Theus Hossmann, PhD[1]; Andrew Atkinson, PhD[2]; Sabine Herbel[2]; Luisa Salazar-Vizcaya, PhD[3]; Michael Dahlweid, MD[1]; Jonas Marschall, MD[3]; [1]University Hospital Bern, Bern, Bern, Switzerland; [2]Bern University Hospital, Bern, Bern, Switzerland; [3]University of Bern, Bern, Bern, Switzerland

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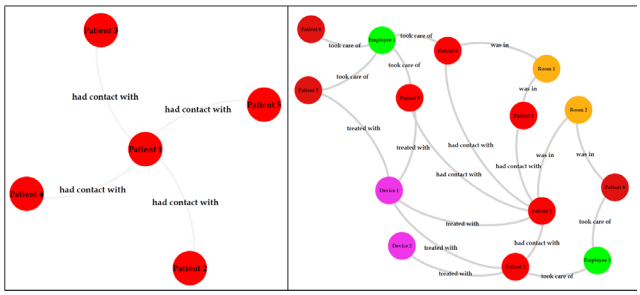
Background. In 2018 we experienced a nosocomial outbreak due to vancomycin-resistant enterococci (VRE) in our hospital network. Our goals were to characterize risk factors for VRE acquisition, elicit potential hot spots of transmission, and delineate an optimized approach to tracing contacts.

Methods. We assembled diverse datasets of variable quality and covering different aspects of care from electronic medical records generated during the outbreak period (1/2018–9/2018). Patients who tested VRE-positive during this period were compared with controls with up to 3 negative screenings. First, we identified risk factors for VRE colonization by means of uni- and multivariate analyses. Next, we elicited transmission pathways by detecting commonalities between VRE cases, and determined whether patients with characteristics and connections similar to VRE cases were missed by our current contact tracing strategy.

Results. We compared 221 VRE patients to 33,624 controls. Independent predictors of VRE colonization were ICU admission (OR 4.9, with 95% confidence interval [3.7–6.5], $P < 0.001$)], number of records in the database (a proxy for severity-of-illness, OR 1.1 [1.1–1.1], $P < 0.001$), length of hospital stay (OR 2.7 [2.0–3.5], $P < 0.001$), age (OR 1.3 [1.2–1.4], $P < 0.001$), and weeks of antibiotics (OR 1.2 [1.1–1.3], $P < 0.001$). By using complex network analysis, we were able to establish three main pathways by which the 221 VRE cases are connected: healthcare personnel, medical devices, and patient rooms. This multi-dimensional network extends beyond our current contact tracing strategy, which captures inpatients based on geographical proximity (cf. figure).

Conclusion. In this outbreak investigation based on a large electronic healthcare data collection, we found three main risk factors for being a VRE carrier (ICU admission, length of hospital stay, antibiotic exposure), along with three important links between VRE cases (healthcare personnel, medical devices, patient rooms). Data science is likely to provide a better understanding of outbreaks, but interpretations should take data maturity, the scope of included sources, and potential confounding factors into account.



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

2458. A comprehensive approach to ending an outbreak of rare OXA-72 producing carbapenem-resistant *Acinetobacter baumannii* at a Community Hospital, Kansas City, MO, 2018

David S. McKinsey, MD[1]; Carolyn Gasser, RN, MSN, CIC[1];

Joel P. McKinsey, MD[2]; Geri Ditto, RN[1]; Alyssa Agard, RN[1];
Brianna Zellmer, RN[1]; Carrie Poteete, MPH[1];
Paula Snippes Vagnone, MT(ASCP)[3]; Jennifer Dale, PhD[3]; John Bos, BS[4];
Rachael Hahn, BS[4]; George Turabelidze, MD, PhD[4]; Madison Poiry, BS[4];
Patrick Franklin, BS[4]; Nick Vlachos, MS[5]; Gillian A. McAllister, BS[5];
Alison L. Halpin, PhD[5]; Janet Glowicz, PhD, RN[5]; David Ham, MD, MPH[5];
Lauren Epstein, MD MSc[5]; [1]Research Medical Center, Kansas City, Missouri; [2]David S McKinsey M D, Kansas City, Missouri; [3]Minnesota Department of Health Laboratory, St. Paul, Minnesota; [4]Missouri Department of Health and Senior Services, Jefferson City, Missouri; [5]Centers for Disease Control and Prevention, Atlanta, Georgia

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Background. In 2018, an outbreak of carbapenem-resistant *Acinetobacter baumannii* (CRAB) containing a rare β-lactamase (OXA-72) was detected at Research Medical Center, a 511 bed community hospital in Kansas City, MO. We describe a coordinated effort among hospital infection control personnel and public health to control the outbreak.

Methods. We defined a case as isolation of OXA-72-producing CRAB from any clinical culture collected from a hospitalized patient during 2018. We assessed infection control practices, including adherence to transmission-based precautions and hand hygiene, environmental cleaning and patient transfers. After patients with CRAB were discharged, terminal cleaning was performed using bleach and environmental cultures were collected; rooms were closed to new patients until CRAB was not isolated. Whole-genome sequencing and bioinformatics analyses were performed.

Results. From January through October, CRAB was isolated from clinical cultures among 20 patients; 6 OXA-72-positive cases were identified during June and July. We found practices for cleaning and disinfection of shared medical equipment were not clearly delineated among nursing and environmental services staff and we ensured responsibilities were well defined. W restricted all patients with CRAB to certain medical units in order to limit the spread. In total, 248 environmental cultures were collected; 151 (61%) from inside patient rooms and 97 (39%) from shared medical equipment or surfaces outside patient rooms. Overall, *Acintobacter baumannii* was isolated from 39 (16%) environmental cultures (21 from inside rooms and 18 from outside rooms); 5 isolates were confirmed to contain OXA-72. Using WGS, we compared 6 clinical and 5 environmental OXA-72 CRAB isolates; all were determined to be genetically related (0–6 single nucleotide polymorphisms, 88.4% core genome) (figure). No additional cases were identified after these interventions.

Conclusion. We identified widespread CRAB environmental contamination, illustrating the challenges of eradicating CRAB from the hospital environment. We developed a comprehensive approach focusing on infection control, environmental cleaning and culturing, and patient movement to stop the outbreak.

Figure: Single Nucleotide Polymorphism Analysis Matrix of OXA-72 CRAB Isolates obtained from Clinical and Environmental cultures*

		Environmental Isolates					Clinical Isolates					
		ICU medicine cabinet	Patient chart	Computer (patient room)	Nursing station	Cabinet (patient room)	Case 1: Blood	Case 2: Foot wound	Case 3: Sputum	Case 4: Hip wound	Case 5: Abdominal wall abscess	Case 6: Bronchial lavage
Environmental Isolates	ICU medicine cabinet	-	1	0	1	0	2	0	0	0	0	4
	Patient chart	1	-	1	0	1	1	1	1	1	1	5
	Computer (patient room)	0	1	-	1	0	2	0	0	0	0	4
	Nursing station	1	0	1	-	1	1	1	1	1	1	5
	Cabinet (patient room)	0	1	0	1	-	2	0	0	0	0	4
Clinical Isolates	Case 1: Blood	2	1	2	1	2	-	2	2	2	2	6
	Case 2: Foot wound	0	1	0	1	0	2	-	0	0	0	4
	Case 3: Sputum	0	1	0	1	0	2	0	-	0	0	4
	Case 4: Hip Wound	0	1	0	1	0	2	0	0	-	0	4
	Case 5: Abdominal wall abscess	0	1	0	1	0	2	0	0	0	-	4
	Case 6: Bronchial lavage	4	5	4	5	4	6	4	4	4	4	-

*All isolates are multilocus sequence type 2 and 208/1806 (Pasteur and Oxford schemes, respectively)

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

2459. Control of a Healthcare–associated Infection Outbreak with Carbapenem-resistant *Klebsiella pneumonia* at a Respiratory Intensive Care Unit (RICU) in an Acute Care Hospital

Liping Guo, Medical Doctor & Helthcare Administration Master[1];
Duochun Wang, Doctor Degree[2]; Binghuai Lu, Doctor Degree[1]; [1]China Japan Friendship Hospital, Beijing, China (People's Republic); [2]Chinese Center For Disease Control And Prevention, Beijing, China (People's Republic)

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Background. Carbapenem-resistant *Klebsiella pneumonia* (CRKP) is among the most serious pathogens of healthcare–associated infections and accounts for significant morbidity and mortality. The study was conducted in a tertiary 1,600-bed hospital where we once reported a suspicious outbreak of ventilator-associated pneumonia caused by *Burkholderia cepacia* at a surgical intensive care unit (SICU) in 2015. From April 2017, the infection control team (ICT) reported that more cases with positive CRKP cultures from endotracheal aspirate and bronchoalveolar lavage fluid (BALF) were detected than previously in a respiratory intensive care unit (RICU).

Methods. ICT embarked on a field epidemiology investigation immediately to confirm the possibility of a healthcare-associated infection outbreak. The quick reaction to probable outbreak consisted of a serial protocols including contact precaution and antibiotic prescribing to support urgent contain of potential risks. Microbiological investigation was done for patients with epidemiologic traces of any with CRKP infection and colonization in RICU. VITEK 2 compact was used for initial antimicrobial susceptibilities. For those suspected CRE isolates, E-tests were performed as a confirmation for the resistance. The Carbapenem Inactivation Method (CIM) was utilized for detecting the production of carbapenemase. The homology was analyzed by pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST) .

Results. Between April and October in 2017, 13 cases with CRKP infection were identified (Figure 1 and Table 1). Multiple environmental samples of 668 were collected during 7 months. Nearly 75 percent of the involved patients received the first anus swab screening within 48 hours upon RICU admission. The number of the resistance positivity was 26 clinical specimens, 39 anal swabs, and 6 environmental samples. Most of the isolated strain ID and genetic characterization was illustrated as the Figure 2 and 3.

Conclusion. The origin of the CRKP isolates in RICU probably due to the dissemination of diverse groups. The standardization of the novel and more innovative interventions in tackling such the epidemicity should be implemented further.

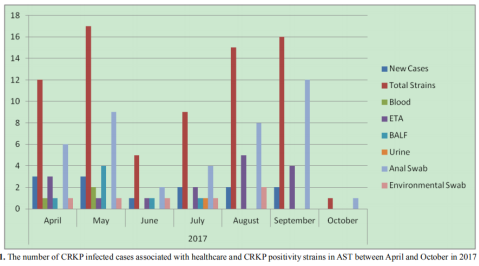

Fig. 1. The number of CRKP infected cases associated with healthcare and CRKP positivity strains in AST between April and October in 2017

Note. CRKP, carbapenem-resistant *Klebsiella pneumonia*; AST, antimicrobial susceptibility test; EAT, endotracheal aspirate; BALF, bronchoalveolar lavage fluid

Table 1. Clinical characteristics of patients with CRKP positivity in AST

Age (years)	Gender	Date from Admission to Discharge of RICU (day/month, year); (Total staying RICU days)	Major Diagnosis (On Admission)	Underlying Disease	Duration of Ventilator Care (Date Range; Total Utilization Hours)	Clinical Specimen	Date of Isolation (day/month/year)	Susceptibility Pattern	Treatment before Isolation	Treatment after Isolation	Outcome
34	Male	28/3-14/4, 2017; (22 Days)	IIP	No other illness	6/4-18/4, 2017; 477	ETA	11/4/2017	CRE	IPM+TLC	TLC+CEF+MIN	Deceased
70	Male	13/4-25/4, 2017; (13 Days	IIP	Metabolism syndrome	13/4-25/4,2017; 295	BALF	17/4/2017	PDR	CEF+TLC	IPM	Deceased
63	Male	8/4-15/5, 2017; (38 Days)	Severe pneumonia	Liver cancer	12/4-15/5, 2017; 784	Blood	29/4/2017	PDR	ETP/IPM+LVX	IPM+ETM	Survived
79	Male	1/5-17/5, 2017; (17 Days)	Severe pneumonia	Lung cancer	1/5-17/5, 2017; 373	BALF	3/5/2017	CRE	AZM+NOR+SPI	IPM+CEF+TLC	Deceased
49	Male	9/5-21/5, 2017; (13 Days)	Peritonitis	Severe pancreatitis	9/5-15/5, 2017; 299	BALF	19/5/2017	PDR	MOX+IPM+LE	IPM+CTZ	Survived
71	Male	26/5-8/6, 2017; (14 Days)	Severe pneumonia	PTB	Non-invasive ventilator	BALF	27/5/2017	CRE	IPM+LVX	MOX+TLC+CEF	Survived
78	Male	4/6-12/6, 2017; (9 Days)	Severe pneumonia	COPD, Silicosis	4/6-12/6, 2017; 202	BALF	9/6/2017	PDR	IPM+MOX+MZ	CEF+AMK+LVX	Deceased
58	Male	21/6-13/7, 2017; (23 Days)	Severe pneumonia	Lung cancer	21/6-28/6 & 8/7-13/7, 2017; 501	ETA & Urine	5/7 & 11/7, 2017	CRE/PDR	CEF+VAN+VOI	No treatment received	Deceased
80	Male	5/7-22/7, 2017; (18 Days)	IIP	Metabolism syndrome	8/7-13/7, 2017; 133	BALF	18/7/2017	PDR	PIP+LVX+CTZ	CIZ+TLC	Deceased
73	Male	18/7-7/8, 2017; (21Days)	Severe pneumonia	Metabolism syndrome	26/7-3/8, 2017; 433	BALF	2/8/2017	PDR	IPM+MIN+TEI	TLC+LVX+AMK	Deceased
73	Male	2/8-5/9, 2017; (35 Days)	Severe pneumonia	Metabolism syndrome	18/8-29/8, 2017; 777	ETA	10/8/2017	PDR	IPM+VOR	CEF+TLC+AMK	Deceased
82	Male	2/9-10/10, 2017; (39 Days)	Severe pneumonia	Metabolism syndrome	12/9-10/10, 2017; 688	ETA	20/9/2017	PDR	LVX+CTZ+MEI	MEM+AMK+CTZ	Deceased
31	Male	1/9-8/10, 2017; (48 Days)	IIP	No other illness	1/9-11/12	ETA	26/9/2017	PDR	CTZ+MIN+MEI	MIN+CEF+VAN	Survived

Note. IIP, idiopathic interstitial pneumonia; COPD, chronic obstructive pulmonary disease; PTB, pulmonary tuberculosis; EI/ ET: endotracheal intubation/ tracheotomy; ventilator care , invasive ventilator care ; ETA, endotracheal aspirate; BALF, bronchoalveolar lavage fluid; CRE, carbapenem-resistant Enterobacteriaceae; PDR, pandrug-resistant; IPM, imipenem and cilastatin; TLC, tigecycline; CEF, cefoperazone sulbactam; MIN, minocycline; ETP, ertapenem; LVX, levofloxacin; AZM, azithromycin; NOR, norfloxacin; MOX, moxifloxacin; LE, linezolid; CTZ, ceftazidime; MZL, mezlocillin sulbactam sodium; AMK, amikacin; VAN, vancomycin; VOR, voriconazole; PIP, piperacillin and sulbatam sodium; TEI, teicoplanin; MEM, meropenem.

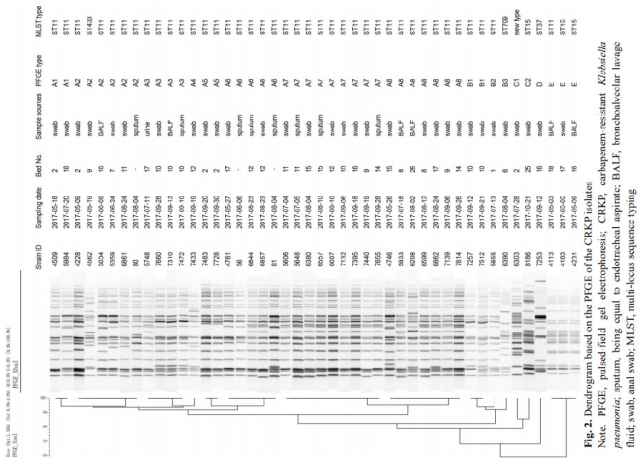

Fig. 2. Dendrogram based on the PFGE of the CRKP isolates
Note. PFGE, pulsed field gel electrophoresis; CRKP, carbapenem-resistant *Klebsiella pneumonia*; sputum, being equal to endotracheal aspirate; BALF, bronchoalveolar lavage fluid; swab, anal swab; MLST, multi-locus sequence typing

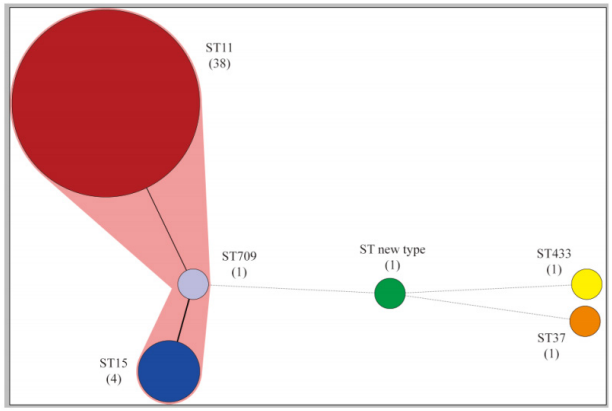

Fig. 3. Dendrogram based on the MLST tree of the CRKP isolates
Note. MLST, multi-locus sequence typing; CRKP, carbapenem-resistant *Klebsiella pneumonia*;

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