a 1:4 case–control study. Controls were patients without bloodstream infection (BSI) during the outbreak period.

Results. The cluster included 3 patients. Patient 1 had BSI due to D. acidovorans (2/08), E. absuriae (3/15) and B. cepacia (3/17). Patient 2 had BSI due to D. acidovorans (3/17 and 3/27) and S. maltophilia (4/5). Patient 3 had a urine culture positive for D. acidovorans and S. maltophilia (4/2). The case–control study showed that cases had been dialyzed more often than controls on the third shift ($P < 0.0001$) and at station 2 ($P < 0.0001$), where subsequently a wall box spent dialysate drain connection swab culture yielded D. acidovorans. E. absuriae was recovered from wall boxes and spent dialysate drain connection at two stations and from used prime buckets from two stations; one wall box culture grew S. maltophilia. D. acidovorans and E. absuriae patient isolates were not available for genomic analysis. Observations revealed that waste water was leaking onto the floor from several wall boxes, and that priming buckets were often rinsed with tap water after being disinfected with 1:100 bleach solution and not allowed to dry before reuse. Multiple deficiencies in hand hygiene and station disinfection were observed. No deficiencies in water treatment practices were identified. Multiple water cultures obtained in August were negative for the observed pathogens.

Conclusion. A cluster of unusual Gram-negative infections in outpatient HD patients was most likely due to exposures to contaminated wall boxes or priming buckets; poor hand hygiene and station disinfection can contribute to transmission to patients.

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2455. Outbreak of carbapenemase-producing *Enterobacteriaceae* in cardiology units associated with contaminated water dispenser and sink drain in Korea

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Background. There is a growing concern about the importance of hospital water environment for the transmission of carbapenemase-producing Enterobacteriaceae (CPE). Herein, we report a large outbreak in cardiology units involving intensive care units (ICU) and wards at a tertiary care hospital.

Methods. During a CPE outbreak between July and December 2018, contact tracing and environmental sampling were performed. For outbreak control, we performed education to healthcare workers, hand hygiene enforcement, active surveillance test, preemptive isolation, chlorhexidine bathing for CPE positive patients, and deep terminal cleaning including UV and hydrogen peroxide non-touch disinfection. Patients with CPE were isolated at a single room with dedicated staffs, contact precaution was implemented, and when case patients were located in multi-patient room, we performed surveillance culture for exposed patients in the room.

Results. A total of 87 patients with CPE infection or colonization were identified at two cardiology ICUs and three cardiology wards. CPE from the first two index patients were identified from sputum culture suspecting pneumonia, and the remaining 85 patients were identified to harbor CPE through surveillance culture (exposed patients $n = 22$, active surveillance test $n = 63$). Diverse organisms were identified; organisms with blakpc ($n = 13$), blaNDM-1 ($n = 55$), blaVIM or blaIMP ($n = 12$), blaOXA-48 ($n = 3$), and co-producing organisms ($n = 4$). We performed environmental culture; KPC-producing Escherichia coli was isolated from water dispenser in ICU and NDM-1 producing Citrobacter freundii and Enterobacter cloacae were isolated from sinks in the patient room. Outbreak ended after the removal of water dispenser and the replacement of sink drain with pouring bleach to the sink drain.

Conclusion. Water dispenser and sink drain were suspected for the possible reservoirs of CPE in this outbreak. Replacement of plumbing system and use of bleach for pouring to sink as well as the removal of water dispenser was needed to control outbreak. Investigation of water system is warranted for finding the source of CPE.

Table 1. Characteristics of 87 patients with carbapenemase-producing *Enterobacteriaceae* (CPE) during outbreak

Patient characteristics	
Age, years, median (IQR)	64 (56-73)
Male gender	55 (63)
Underlying disease or condition	
Valvular heart disease	24 (28)
Myocardial infarction or angina	16 (18)
Heart failure	15 (17)
Infective endocarditis	8 (9)
Arrythmia	3 (3)
Acute aortic syndrome	3 (3)
Other underlying disease	18 (21)
End stage renal disease on hemodialysis	11 (14)
ICU stay (>2 days) before CPE isolation	25 (29)
Underwent cardiac surgery before CPE isolation	20 (23)
Days from admission to first positive CPE isolation, median (IQR)	8 (3-19)
Location of acquisition	
Acquisition from CV/CS units	55 (63)
CCU	6/55 (11)
CSICU	4/55 (7)
133 ward	20/55 (36)
143 ward	18/55 (33)
144 ward	7/55 (13)
Acquisition from other units	14 (16)
CPE isolation within 2 days after admission	18 (21)
Location of first positive CPE isolation	
CCU	15 (17)
CSICU	18 (21)
133 ward	19 (22)
143 ward	16 (18)
144 ward	9 (10)
Other ward	10 (11)
First positive specimen	
Clinical specimen (sputum)	2 (2)
Surveillance culture specimen (stool or rectal swab)	85 (98)
Exposed patients	22 (25)
Active surveillance test on admission	38 (44)
Active surveillance test on discharge from ICU	5 (6)
Weekly active surveillance test	20 (23)
Infection	2 (2)
Colonization	87 (98)
Use of antibiotics before isolation of CPE within 1 month	49 (56)
Carbapenem	6 (7)
Piperacillin/tazobactam	10 (11)
Cephalosporin	30 (34)
Quinolone	10 (11)

Data are number (%) of patients, unless otherwise indicated.

Abbreviation. IQR, interquartile range; ICU, intensive care units; CCU, cardiac intensive care unit; CSICU, cardiac surgery intensive care unit; CV, cardiovascular; CS, cardiac surgery

Table 2. Microbiologic results of 85 patients with carbapenemase-producing *Enterobacteriaceae*

Genotype and organism	Number (%)
KPC producing organism	**13 (15)**
Escherichia coli	9 (10)
Klebsiella pneumoniae	2 (2)
E. coli and *K. pneumoniae*	1 (1)
Xpert positive but not isolated on culture	1 (1)
NDM-1 producing organism	**55 (63)**
Citrobacter freundii	17 (20)
Enterobacter cloacae	5 (6)
K. pneumoniae	5 (6)
E. coli	5 (6)
Other[a]	10 (11)
Xpert positive but not isolated on culture	13 (15)
Other MBL (VIM, IMP-1) producing organism	**12 (14)**
K. pneumoniae	7 (8)
Other[b]	3 (3)
Xpert positive but not isolated on culture	2 (2)
OXA-48 producing organism	**3 (3)**
E. coli and *K. pneumoniae*	1 (1)
Xpert positive but not isolated on culture	2 (2)
Co-producing (NDM-1 plus IMP, and NDM-1 plus VIM)	**4 (5)**

Abbreviation. KPC, *Klebsiella pneumoniae* carbapenemase; NDM-1, New Delhi metallo-beta-lactamase 1; MBL, metallo-beta-lactamase; VIM, Verona integron-encoded metallo-beta-lactamase; IMP-1, imipenemase-1.

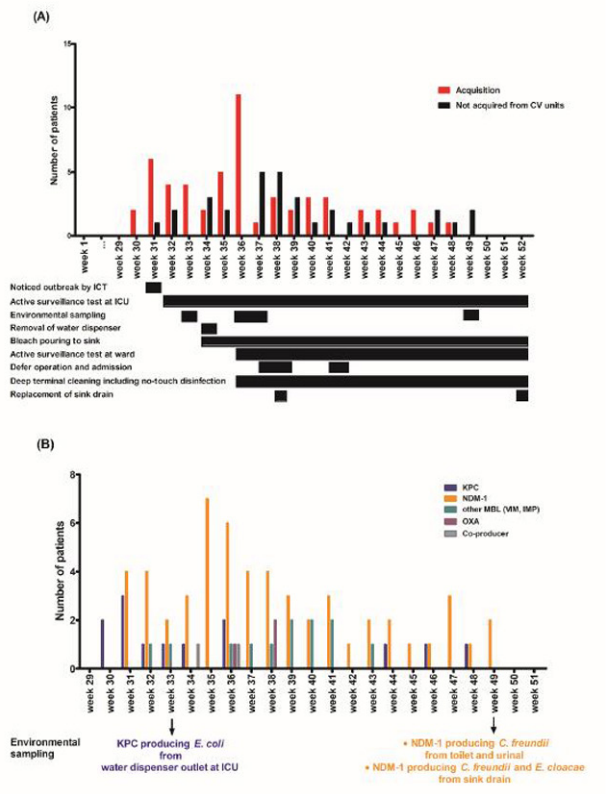
[a]*Klebsiella oxytoca* (n=1), *Klesiella variicola* (n=1), *Citrobacter braakii* (n=1), *Enterobacter asburiae* (n=1), *E. kobei* (n=1), *E. cloacae* and *C. freundii* (n=1), *K. pneumoniae* and *E. coli* (n=3), *Raoultella ornithinolytica* and *C. freundii* (n=1)

[b]*R. ornithinolytica* (n=1), *K. oxytoca* (n=1), *C. freundii* (n=1)

Table 3. Results of environmental culture

	Location of environmental sampling	Number (%) of sampling of positive CPE results	Description of positive CPE results	
			Location	Organisms
Week 33	ICU (Portable EKG machine, ultrasonography machine, computer keyboard and mouse of healthcare worker, sink U-trap and bowl, patient area, and water dispenser)	1/136 (0.7)	Water dispenser	KPC producing *Escherichia coli*
Week 36	Water dispenser and sink around water dispenser at ward	0/19 (0)	-	-
Week 37	Eight hand hygiene sinks (faucet, bowl, and U-trap) and toilet at ward	0/40 (0)	-	-
Week 49	Ward (Computer keyboard, mouse, telephone, EKG machine, nursing cart, wheelchair, toilet, urinal, sink U-trap ,bowl, and faucet, water dispenser, and patient area)	6/402 (1.5)	Toilet and urinal in the shared bathroom (n=3)	NDM-1 producing *Citrobacter freundii*
			Sink U-traps in the bathroom in patient room (n=3)	NDM-1 producing *Enterobacter cloacae* and *C. freundii*

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.



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

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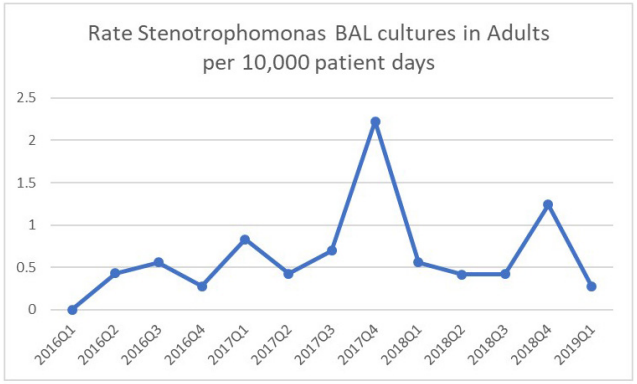
Background. Stenotrophomonas maltophilia (SM) is a multi-drug-resistant Gram-negative organism that typically impacts patients with long hospital stays or severe immunocompromise. In Q4 2017, an increase in rates of SM from adult bronchoscopic alveolar lavage (BAL) specimens was detected.

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

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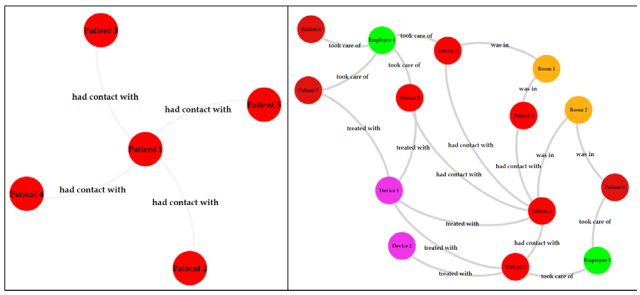
Background. In 2018 we experienced a nosocomial outbreak due to vancomycin-resistant enterococci (VRE) in our hospital network. Our goals were to characterize risk factors for VRE acquisition, elicit potential hot spots of transmission, and delineate an optimized approach to tracing contacts.

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

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