

blood culture attributable to a contaminant; and O-CLABSI-4 is a patient injecting line, though not officially documented. Descriptive analyses were performed using the  $\chi^2$  and the Fisher exact tests. **Results:** We found a large number of O-CLABSIs on chart review (79 of 192, 41%). Overall, 56 of 192 (29%) LCBSIs were attributable to a primary infectious source not meeting NHSN definition. O-CLABSI proportions between the 2 hospitals were statistically different; hospital A identified 34 of 59 (58%) of their NHSN-identified CLABSIs as O-CLABSIs, and hospital B identified 45 of 133 (34%) as O-CLABSIs ( $P = .0020$ ) (Table 1). When comparing O-CLABSI types, hospital B had a higher percentage of O-CLABSI-1 compared to hospital B: 76% versus 64%. Hospital A had a higher proportion of O-CLABSI-2: 21 versus 7%. Hospitals A and B had similar proportion of O-CLABSI-3: 15% versus 18%. These values were all statistically significant ( $P < .0001$ ). **Discussions:** The results of these 2 geographically proximate systems indicate that O-CLABSIs are common. Attribution can vary significantly between institutions, likely depending on differences in incidence of true CLABSI, patient populations, protocols, and protocol compliance. These findings have implications for interfacility comparisons of publicly reported data. Most importantly, erroneous attribution can result in missed opportunity to direct patient safety efforts to the root cause of the bacteremia and could lead to inappropriate treatment.

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### Presentation Type:

Poster Presentation

### Aggressive Colonization Screening and Infection Control Measures in Containment of NDM-5 Carbapenemase-Producing CRE

Ishrat Kamal-Ahmed, University of Nebraska Medical Center; Margaret Drake, Kate Tyner, Nebraska ICAP, Nebraska Medicine; Teresa Fitzgerald, Nebraska Medicine; Erisa Sula; Heather Adele Moulton-Meissner, Centers for Disease Control; Gillian McAllister, Centers for Disease Control and Prevention; Alison Halpin, US Centers for Disease Control and Prevention; Muhammad Salman Ashraf, University of Nebraska Medical Center; Tom Safranek, Epidemiology DHHS Nebraska; Maroya Walters, Centers for Disease Control and Prevention; Maureen Tierney, Nebraska DHHS

**Background:** In April 2019, Nebraska Public Health Laboratory identified an NDM-producing *Enterobacter cloacae* from a urine sample from a rehabilitation inpatient who had recently received care in a specialized unit (unit A) of an acute-care hospital (ACH-A). After additional infections occurred at ACH-A, we conducted a public health investigation to contain spread. **Methods:** A case was defined as isolation of NDM-producing carbapenem-resistant Enterobacteriaceae (CRE) from a patient with history of admission to ACH-A in 2019. We conducted clinical culture surveillance, and we offered colonization screening for carbapenemase-producing organisms to all patients admitted to unit A since February 2019. We assessed healthcare facility infection control practices in ACH-A and epidemiologically linked facilities by visits from the ICAP (Infection Control Assessment and Promotion) Program. The recent medical histories of case patients were reviewed. Isolates were evaluated by whole-genome sequencing (WGS). **Results:** Through June 2019, 7 cases were identified from 6 case patients: 4 from clinical cultures and 3 from 258 colonization screens including 1 prior unit A patient detected as an outpatient (Fig. 1). Organisms isolated were *Klebsiella pneumoniae* ( $n = 5$ ), *E. cloacae* ( $n = 1$ ), and *Citrobacter freundii* ( $n = 1$ ); 1 patient had both NDM-producing *K. pneumoniae* and *C. freundii*. Also, 5 case patients had overlapping stays in unit A during February–May 2019 (Fig. 2); common exposures in unit A included rooms in close proximity, inhabiting the same room at different times and shared caregivers. One case-patient was not admitted to unit A but shared caregivers, equipment, and devices (including a colonoscope) with other case patients while admitted to other ACH-A units. No case patients reported travel outside the United States. Screening at epidemiologically linked facilities and clinical culture surveillance showed no evidence of transmission beyond ACH-A. Infection control assessments at ACH-A revealed deficiencies in hand hygiene, contact precautions adherence, and incomplete cleaning of shared equipment within and used to transport to/from a treatment room in unit A. Following implementation of recommended infection control interventions, no further cases were identified. Finally, 5 *K. pneumoniae* of ST-273 were related by WGS including carriage of NDM-5 and IncX3 plasmid supporting transmission of this strain. Further analysis is required to relate IncX3 plasmid carriage and potential transmission to other organisms and sequence types identified in this study. **Conclusions:** We identified a multi-organism outbreak of NDM-5–producing CRE in an ACH specialty care unit. Transmission was controlled through improved

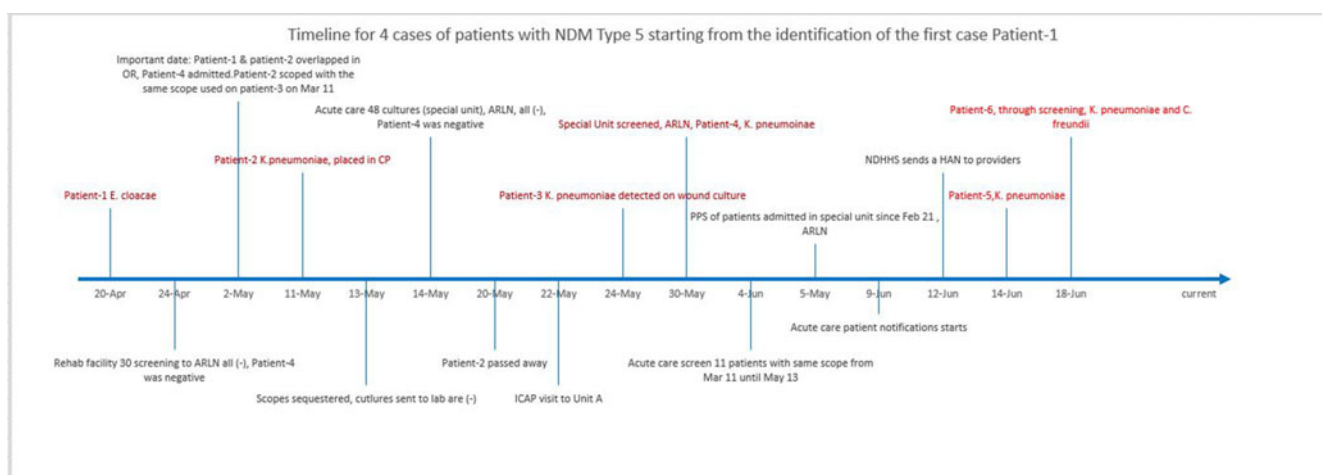


Fig. 1

Figure 2. Patient movement between facilities

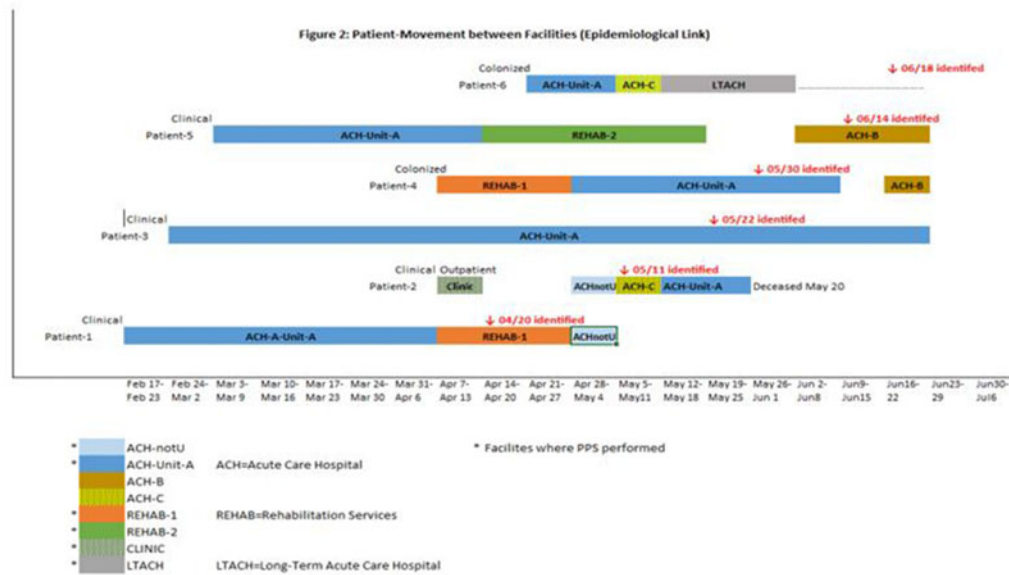


Fig. 2.

Table: Whole Genome Sequencing Results

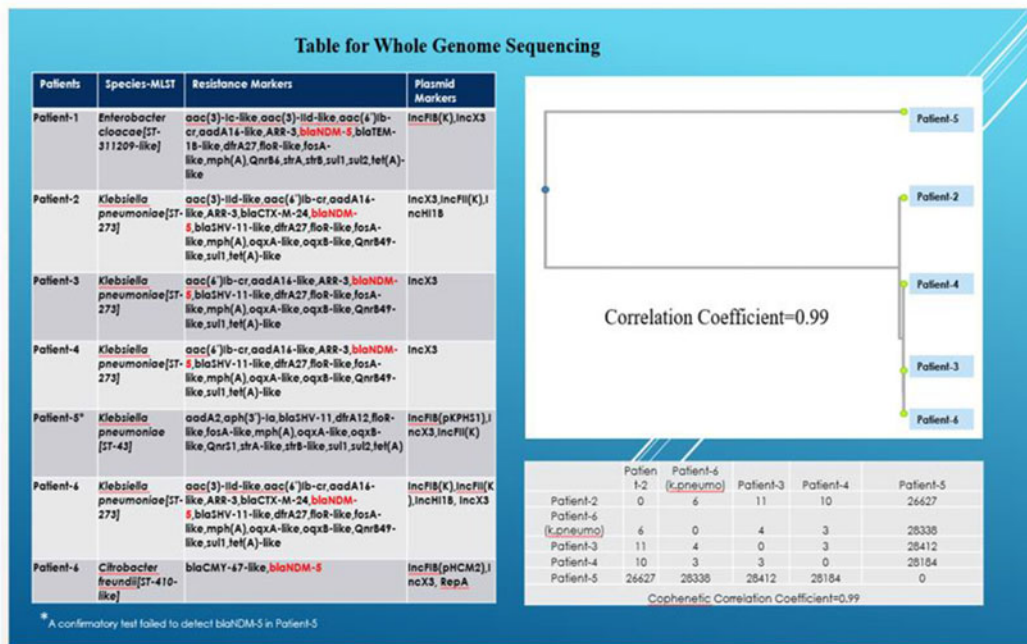


Fig. 3.

infection control practices and extensive colonization screening to identify asymptomatic case-patients. Multiple species with NDM-5 were identified, highlighting the potential role of genotype-based surveillance.

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Poster Presentation

**Antibiotic Overuse at Discharge in Hospitalized Patients with Bacteriuria or Treated for Pneumonia: A Multihospital Study**

Valerie M Vaughn, University of Michigan Medical School; Lindsay A. Petty, University of Michigan Medical School; Tejal N. Gandhi, University of Michigan Medical School; Keith S. Kaye, University of Michigan Medical School; Anurag Malani, St. Joseph Mercy Health System; Steven J. Bernstein, University