wards. Nonestablished practices (staff resistance) were related to the time taken to don full PPE and reluctance to arrange for an isolation bed due to increased workload and unavailability of isolation beds. A shift was noted in the control chart for HO-*Clostridium difficile* after the implementation of the CDI bundle in May 2019. **Conclusions:** The categorization of practices into established and nonestablished practices can help to identify barriers that may interfere with successful implementation of an infection prevention bundle.

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Presentation Type:
Poster Presentation

Cluster of Infections Associated With Contaminated Stem-Cell Products

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Background: The unapproved and unregulated use of umbilical stem-cell products has been identified as a possible source of adverse events and infection. In 2018, a national outbreak of multiple bacterial infections was associated with use of umbilical stem cells products. From December 2018 through March 2019, the Los Angeles County Department of Public Health (LACDPH) identified 4 cases of bacterial infection in patients that had received therapies using umbilical stem-cell products. Although 2 cases were associated with the national outbreak of a single company's product, 2 additional cases of *Enterobacter cloacae* were instead associated with a second stem-cell distributer. **Methods:** In December 2018, LACDPH staff received notification from a hospital infectious disease physician of 2 cases of *E. cloacae* infection in patients of a freestanding ambulatory surgery center following allogenic umbilical cord stem-cell injections on the same day in August 2018. LACDPH reviewed the medical records of these patients and conducted an on-site visit to the ambulatory surgery center, which included observation of infection prevention practices, interview of staff, and review of logs. The 2 isolates from each patient were sent to the CDC laboratory for relatedness testing. **Results:** The 2 case patients received products via intra-articular injection from different lot and donor numbers for lumbar spine pain. In addition to the stem-cell product, both patients also received antibiotics and pain medications during their procedures, though from different vials. Both patients were seen by the same surgeon, anesthesiologist, and nurse during their procedures. No additional cases occurred. The case patients were hospitalized for 12 and 27 days, respectively. Whole-genome sequencing indicated that the isolates from the 2 patients were related. No major gaps in infection prevention practices were identified at the surgery center. **Conclusion:** This report describes a cluster of 2 *E. cloacae* infections in patients who had received unapproved-use stem-cell products via spinal injection. Given molecular laboratory results and infection prevention observations, we hypothesize that the stem-cell products used on these 2 cases were likely contaminated before distribution. This cluster demonstrates that contamination of stem-cell products extends beyond the single outbreak previously described and points to the systematic inability to ensure the safety of unapproved use of umbilical stem- cell products.

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Cobweb Chart for Infection Rates, Infectometer, and Outbreak Alert System: Real-Time Systems for Summarizing Nosocomial Data

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Background: Reporting nosocomial surveillance data can be difficult because the quantity of statistics, graphics, tables, and numeric data may confuse people. Another issue related to feedback regarding healthcare infections rate is that gaps exist between collecting data, the analysis, and implementation of actions based on the information produced. Even when a statistical process control chart (SPC) is used, it is interpreted retrospectively. Here, we present 3 epidemiological tools: (1) a cobweb chart for infection rates, (2) the infectometer, and (3) an outbreak alert system. **Methods:** For the cobweb chart, the first step is to choose how many and which infection rates will be summarized. Thereafter, all infection rates, respective benchmarks, endemic level, and actual values are placed in a spreadsheet. Although each infection rate has different units (eg, %, rates per 100 discharges, and/or rates per 1,000 denominator days), when we compare the respective endemic level and actual rate with the benchmark, dimensionless quantities are generated for each indicator, making it possible to build the cobweb graph. Using the infectometer for calculations, we (1) built an SPC chart for each infection or microorganism; (2) estimated the average month and standard deviation of the infection cases, excluding outlier data, and (3) calculated the monthly expected incidence, assuming that nosocomial infection occurrence follows a normal distribution. If the supposition of normal distribution fails, a percentile method is used. The outbreak alert system predicts outbreaks using the infectometer parameters, the last month's observed infection cases, and a Poisson model for predicting the chance of new cases of each infection above monthly expected incidence. **Results:** With the adapted radar chart, we can report many infection rates in only 1 chart (Fig. 1). The SPC charts for infection rates, stratified by all the types of healthcare infections or by microorganism, can be built, and the infectometer can then be produced, showing weekly and monthly expected cases of an endemic condition. The outbreak alert system is presented as a speedometer that is analyzed at the beginning of each month (Fig. 2). **Conclusions:** The idea behind the cobweb chart for infection rate method is to report all infection rates in only 1 graph. With the infectometer, it is not necessary to wait until the end

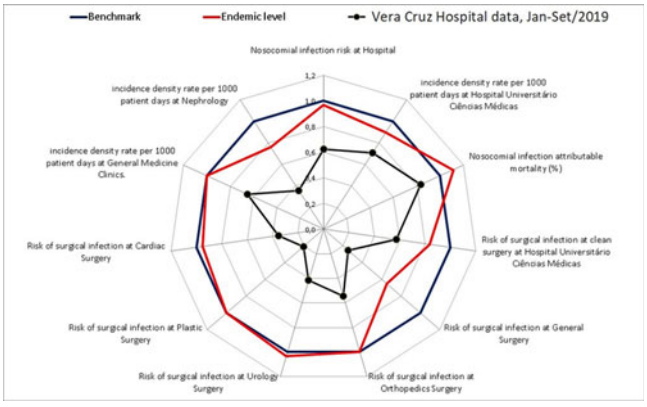

Fig. 1.

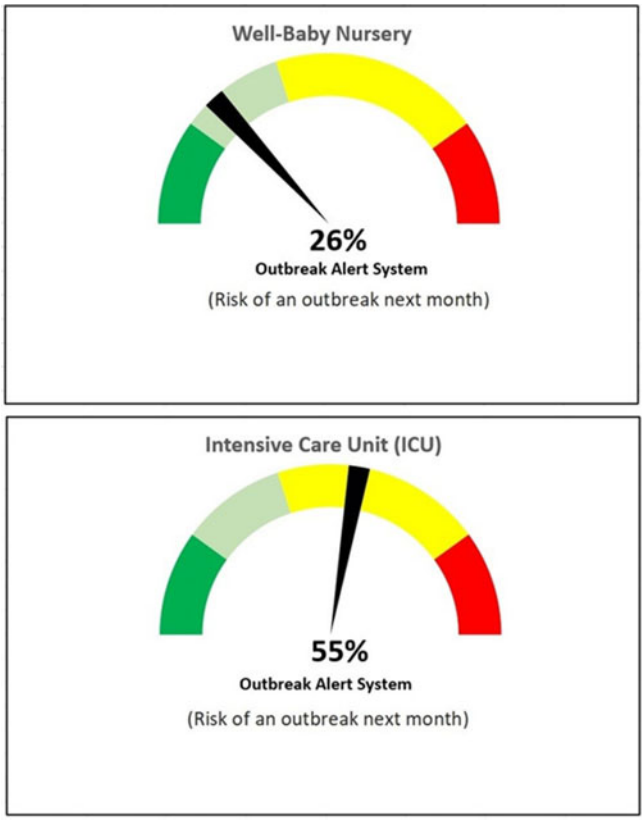

Fig. 2.

of the month to analyze the surveillance data; the analysis becomes prospective and timely. The outbreak alert system brings the future to the present, showing the risk of an outbreak.

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Cohorting KPC+ *Klebsiella pneumoniae* (KPC-Kp)–Positive Patients—A Genomic Exposé of Cross-Colonization Hazards

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Background: Long-term acute-care hospitals (LTACHs) are disproportionately burdened by multidrug-resistant organisms (MDROs) like KPC-Kp. Although cohorting KPC-Kp+ patients into rooms with other carriers can be an outbreak-control strategy and may protect negative patients from colonization, it is unclear whether cohorted patients are at unintended increased risk of cross colonization with additional KPC-Kp strains. **Methods:** Cohorting KPC-Kp+ patients at admission into rooms with other positive patients was part of a bundled intervention that reduced transmission in a high-prevalence LTACH. Rectal surveillance culturing for KPC-Kp was performed at the start of the study, upon admission, and biweekly thereafter, capturing 94% of patients. We evaluated whole-genome sequencing (WGS) evidence of acquisition of distinct KPC-Kp strains in a convenience sample of patients positive for KPC-Kp at study start or admission to identify plausible secondary KPC-Kp acquisitions. **Results:** WGS multilocus sequence type (MLST) strain variability was observed among the 452 isolates from the 254 patients colonized by KPC-Kp (Fig. 1). Among the 32 patients who were positive at the beginning of the study or admission and had a secondary isolate collected at a later date (median, 89 days apart, range, 2–310 days), 17 (53%) had secondary isolates differing by MLST from their admission isolate. Although 60% of the KPC-Kp in the study was ST258, there was substantial genomic variation within ST258 isolates from the same patient (range, 0–102 genetic variants), suggesting multiple acquisitions of distinct ST258 isolates. Among the 17 patients who imported ST258 and had ST258 isolated again later, 11 (65%) carried secondary isolates genetically closer to isolates from other importing patients than to their own ST258 (Fig. 2). Examination of spatiotemporal exposures among patients with evidence of multiple acquisitions revealed that 11 (65%) patients with multiple MLSTs shared a room with a patient who was colonized with an isolate matching the secondary MLST, and 6 (35%) patients who carried multiple distinct ST258 isolates shared a room with a patient who imported these closely related isolates prior to secondary acquisition. **Conclusions:** Half of patients who imported KPC-Kp and had multiple isolates available had genomically supported secondary acquisitions linked to roommates who carried the acquired strains. Although cohorting is intended to protect negative patients from acquiring MDROs, this practice may promote multiple strain acquisitions by colonized patients in the cohort, potentially prolonging the period of MDRO carriage and increasing time at risk of infection. Our findings add to the debate about single-patient

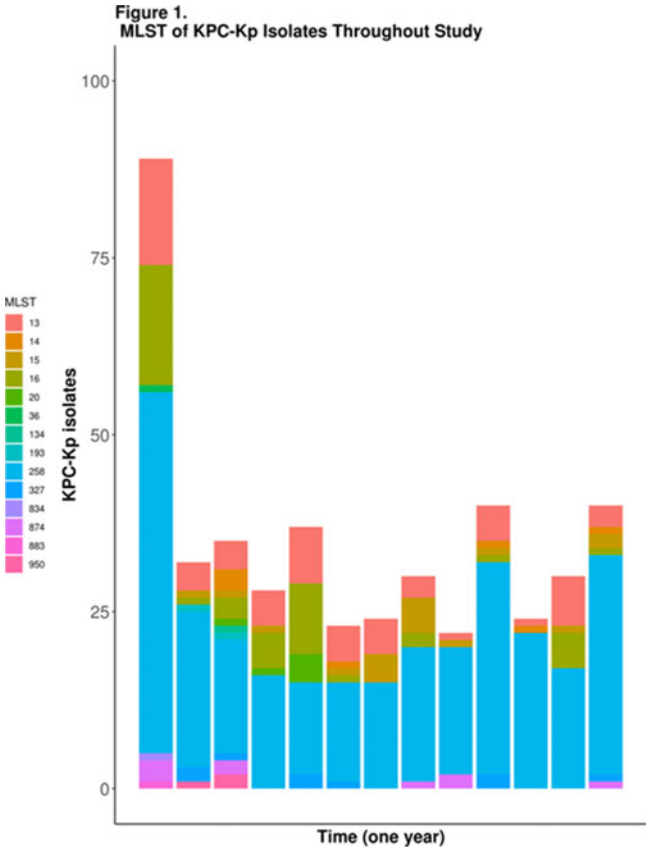

Fig. 1.