

Figure. Relatedness of seven NDM-producing *Klebsiella pneumoniae* carrying hypervirulence markers, and associated epidemiology and molecular features.

Fig. 1.

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Background: In April 2019, the Georgia Department of Public Health (DPH) initiated whole-genome sequencing (WGS) on NDM-producing Enterobacteriaceae identified since January 2018. The WGS data analyzed at CDC identified related *Klebsiella pneumoniae* isolates with hypervirulence markers from 2 patients. Carbapenemase-producing hypervirulent *K. pneumoniae* (CP-hvKP) are rarely reported in the United States, but they can cause serious, highly resistant, invasive infections. We conducted an investigation to identify cases and prevent spread. **Methods:** We defined a case as NDM-producing *K. pneumoniae* with ≥ 4 hypervirulence markers identified by WGS, isolated from any specimen source from a Georgia patient. We reviewed the case patient's medical history to identify potentially affected facilities. We also performed PCR-based colonization screening and retrospective and prospective laboratory-based surveillance. Finally, we assessed facility infection control practices. **Results:** Overall, 7 cases from 3 case patients (A, B, and C) were identified (Fig. 1). The index case specimen was collected from case-patient A at ventilator-capable skilled nursing facility 1 (vSNF1) in May 2018. Case-patient A had been hospitalized for 1 month in India before transfer to the United States. Case-patient B's initial isolate was collected in January 2019 on admission to vSNF2 from a critical access hospital (CAH). The CAH laboratory retrospectively identified case-patient C, who overlapped with case-patient B at the CAH in October 2018. The CAH and the vSNF2 are geographically distant from vSNF1. Case-patients B and C had no known epidemiologic links to case-patient A. Colonization screening occurred at vSNF1 in May 2018, following detection of NDM-producing *K. pneumoniae* from case-patient A ~1 year before determining that the isolate carried hypervirulence markers. Among 30 residents screened, 1 had NDM and several had other carbapenemases. Subsequent screening did not identify additional NDM. Colonization screening of 112 vSNF2 residents and 13 CAH patients in 2019 did not reveal additional case patients; case-patient B resided at vSNF2 at the time of screening and remained colonized. At all 3 facilities, the DPH assessed infection control practices, issued recommendations to resolve lapses, and monitored implementation. The DPH sequenced all 27 Georgia NDM-*K. pneumoniae* isolates identified since January 2018; all were different multilocus sequence types from the CP-hvKP

isolates, and none possessed hypervirulence markers. **Conclusions:** We hypothesize that CP-hvKP was imported by a patient hospitalized in India and spread to 3 Georgia facilities in 2 distinct geographic regions through indirect patient transfers. Although a response to contain NDM at vSNF1 in 2018 likely limited CP-hvKP transmission, WGS identified hvKP and established the relatedness of isolates from distinct regions, thereby directing the DPH's additional containment activities to halt transmission.

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Treatment Outcomes and Subsequent Healthcare Utilization Among Patients With Injection Drug Use–Associated Endocarditis

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Background: Addiction medicine consultation and medication-assisted treatment (MAT) have been promoted as a way to improve outcomes for patients hospitalized with injection drug use–associated endocarditis (IDU-IE). However, IDU-IE outcomes have not been evaluated in settings where these services are commonplace. **Objective:** In this study, we evaluated IDU-IE outcomes in a setting where involvement of addiction medicine consultants and use of MAT is well integrated into patient care. **Methods:** Medical records of patients hospitalized with a diagnosis of bacteremia or infective endocarditis (IE) between October 1, 2015, and December 31, 2017, at a safety-net hospital in Boston were screened for evidence of active injection drug use (IDU) within 6 months of hospitalization (as documented by providers or as supported by urine toxicology assays) for suspected or definite IE using modified Duke criteria. Patients without active IDU or IE were excluded, as were those with a diagnosis of IDU-IE over the 6 months prior to the index hospitalization. Demographic parameters, receipt of antibiotics and MAT, other clinical information, and details of rehospitalizations were recorded. Analyses of descriptive statistics were performed. **Results:** Of 567 subjects screened for inclusion, 47 patients met inclusion criteria. All had opiate use disorder (OUD); 41 patients (87.2%) had polysubstance abuse. Addiction medicine consultation was completed for 41 patients (87.2%). Of the 47 subjects, 23 patients (54.8%) received MAT (methadone or buprenorphine/naloxone) over their entire hospitalization, and 31 patients (73.8%) received MAT for

>75% of the index admission. Moreover, 43 patients (91.5%) survived to discharge, of whom 28 (59.6%) completed antibiotic therapy. Relapsed IDU was observed in 33 patients (76.7%). Relapsed IDU trended toward significance among undomiciled patients (OR, 4.07; 95% CI, 0.93–17.85; $P = .06$). Also, 24 patients (55.8%) were rehospitalized within 1 year due to infectious complications of IDU; undomiciled patients were readmitted more frequently (OR, 20.45; 95% CI, 1.09–383.99; $P = .04$). Completion of IDU-IE antibiotic therapy, relapse of IDU, and rehospitalization were not associated with prior AMA discharges, duration or variety of IDU, receipt of MAT during the index admission, or addiction medicine consultation. The rate of readmission due to an infectious complication of IDU within 1 year was unrelated to the proportion of hospital days where MAT was prescribed. **Conclusions:** In settings with high rates of addiction medicine consultation and in-hospital MAT administration, inpatient interventions targeting OUD may not necessarily be protective against morbidity and rehospitalization. Focusing on housing instability and outpatient continuation of MAT may be beneficial.

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Trends and Clinico-Epidemiological Features of Human Rabies Cases in Bangladesh, 2006–2018

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Background: Vaccinating dogs against rabies is an effective means of reducing human rabies. **Methods:** We analyzed 1,327 clinically diagnosed human rabies deaths and mass dog vaccination (MDV) data during 2006–2018 to quantify the impacts of MDV on human rabies incidence in Bangladesh and a subset of rabies death data ($n = 422$) for clinico-epidemiological analysis. **Results:** We found a positive and increasing trend of dog population vaccination ($P = .01$ and $\tau = 0.71$) and a negative and declining trend ($P < .001$ and $\tau = -0.88$) of human rabies cases (correlation coefficient, -0.82). Among 422 human rabies death cases, most victims (78%) sought treatment from traditional healers, and 12% received postexposure prophylaxis (PEP). The mean incubation period of rabies cases with exposure sites on the head and neck (35 days) was shorter than the upper limb (mean, 64 days; $P = .02$) and lower limb (mean, 89 days; $P < .01$). MDV is effective for reducing human rabies cases in Bangladesh. **Conclusions:** Creating awareness among the animal bite victims to stop relying on traditional healers rather seeking PEP, addressing the role of traditional healers through an awareness education program in respect to the treatment of dog bites, ensuring availability of PEP, and continuing to scale up MDV can help prevent human rabies deaths.

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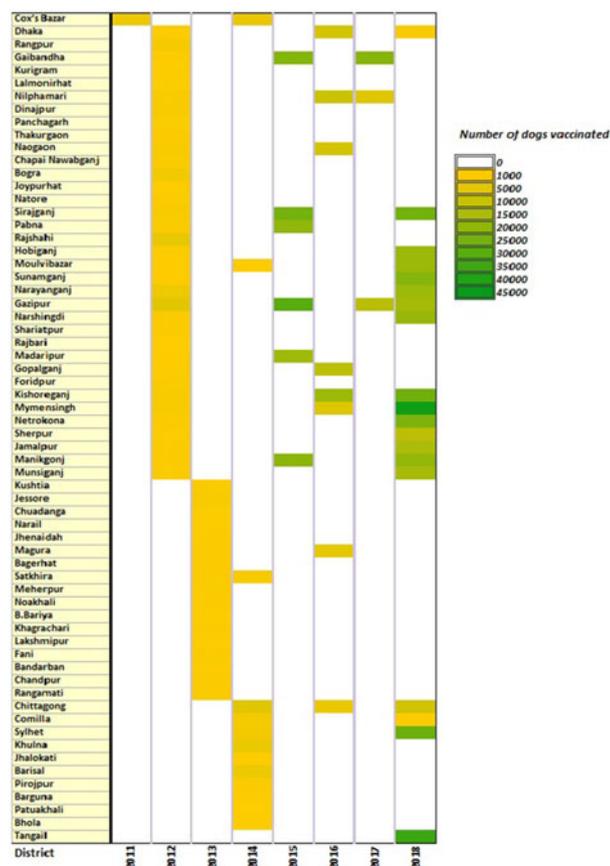


Fig. 1.

