Fig. 1.

Main graph: Legionella positivity is significantly different between eras except between 1800s and 1980-2019 (p<0.05, Chi square)
Inset graph: Legionella positivity is significantly different between decades except between 1980 and 2010 (p<0.05, Chi square)

environmental *Legionella* data set in the Veterans Health Administration (VHA) healthcare system to examine infrastructure characteristics and *Legionella* positivity. Methods: VHA medical facilities across the country perform quarterly potable water sampling of healthcare buildings for *Legionella* detection as part of a comprehensive water safety program. Results are reported to a standardized national database. We did an exploratory univariate analysis of facility-reported *Legionella* data from routine potable water samples taken in 2015 to 2018, in conjunction with infrastructure characteristics available in a separate national data set. This review examined the following characteristics: building height (number of floors), building age (reported construction year), and campus acreage. Results: The final data set included 201,936 water samples from 819 buildings. Buildings with 1–5 floors (n = 634) had a *Legionella* positivity rate of 5.3%, 6–10 floors (n = 104) had a rate of 6.4%, 11–15 floors (n = 36) had a rate of 8.1%, and 16–22 floors (n = 9) had a rate of 8.8%. All rates were significantly different from each other except 11–15 floors and 16–22 floors ($P < .05, \chi^2$). The oldest buildings (1800s) had significantly less ($P < .05, \chi^2$) *Legionella* positivity than those built between 1900 and 1939 and between 1940 and 1979, but they were no different than the newest buildings (Fig. 1). In newer buildings (1980–2019), all decades had buildings with *Legionella* positivity (Fig. 1 inset). Campus acreage varied from ~3 acres to almost 500 acres. Although significant differences were found in *Legionella* positivity for different campus sizes, there was no clear trend and campus acreage may not be a suitable proxy for the extent or complexity of water systems feeding buildings. **Conclusions:** The analysis of this large, real-world data set supports an assumption that taller buildings are more likely to be associated with *Legionella* detection, perhaps a result of more extensive piping. In contrast, the assumption that newer buildings are less associated with *Legionella* was not fully supported. These results demonstrate the variability in *Legionella* positivity in buildings, and they also provide evidence that can inform implementation of water safety programs.

Presentation Type:
Oral Presentation
Burden of *Clostridium difficile* Infection (CDI) Across Whole Healthcare Economies and European Borders; COMBACTE-CDI Results

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Background: The burden of *C. difficile* infection (CDI) on healthcare facilities is well recognized. However, studies focusing on inpatient settings, in addition to ascertainment bias in general, have led to a paucity of data on the true burden of CDI across whole healthcare economies. **Methods:** Sites testing both inpatient and community samples were recruited from 12 European countries (1 site per 3 million population). On 2 selected days, all diarrheal fecal samples (regardless of tests requested) were sent to the European Coordinating Laboratory (ECL) for *C. difficile* toxin testing and culture. The CDI results and tests not requested at each submitting site were compared with the ECL results to determine the number of missed CDIs. Contemporaneous *C. difficile* isolates from food and animal sources were collected. All isolates underwent PCR ribotyping and toxinotyping; prevalences of ribotypes among regions of Europe and reservoir settings were compared. **Results:** Overall, 3,163 diarrheal fecal samples were received from 119 sites. The burden of CDI varied by country (positivity rates, 0–15.8%) and by European region; the highest positivity rate in Eastern Europe was 13.1%. The testing and positivity rates in community samples were 29.6% and 1.4% vs 74.9% and 5.0% in hospital samples; 16% and 55% of samples positive for CDI at ECL were not diagnosed in hospitals and the community. The most common *C. difficile* ribotypes from hospital samples were 027 (11%), 181 (12%), and 014 (8%), although prevalence varied by country. The highest prevalence of toxinotype IIIb (ribotypes 027, 181, and 176) was seen in Eastern Europe (55% of all isolates), which also had the lowest testing rate. For hospital samples, the proportion of toxinotype IIIb was inversely related to the testing rate (r = −0.79) (Fig. 1). The most common ribotypes from food sources were 078 (23%) and 126 (13%) (toxinotype V), and most common ribotypes from community samples were 078 (9%) and 039 (9%). Overall, 106 different ribotypes were identified: 25 in both the hospital and community and 16 in the hospital, community, and food chain. **Conclusions:** The diagnosed burden of CDI varies markedly among countries in both hospital and community settings. Reduced sampling/testing in Eastern Europe is inversely related to the proportion of toxinotype IIIb strains identified, suggesting that lack of suspicion leads to underdiagnosis and
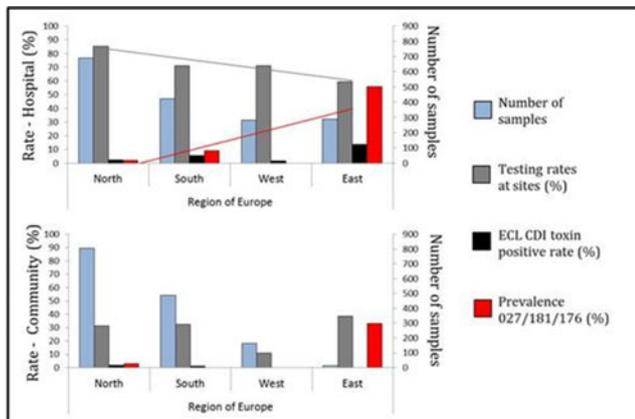
Figure 1. Testing rate, prevalence of toxinotype IIIb (RBT 027, 181 and 176) and CDI positivity rate in Hospital and Community locations. In Hospital setting, we observed an inverse correlation between testing rate at sites (grey trendline) and prevalence of toxinotype IIb (red trendline) (r=-0.79), and between testing rate and CDI toxin positivity rate identified at the European coordinating laboratory (ECL) (r=-0.81).

Fig. 1.

outbreaks of infection. The proportion of missed CDIs in the community was ~3.5× higher than in hospitals, indicating major underrecognition in the former setting. There were marked differences in ribotypes in different reservoir settings, emphasizing the complex epidemiology of *C. difficile.*
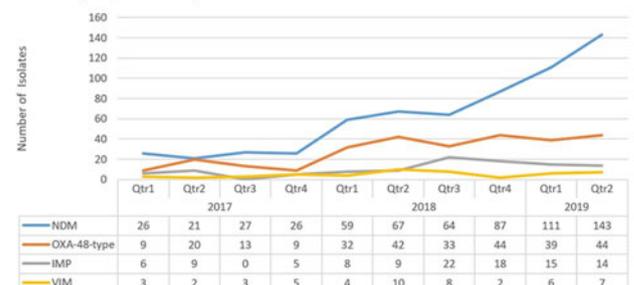
Presentation Type:
Oral Presentation

Changing US Epidemiology of NDM-Producing Carbapenem-Resistant Enterobacteriaceae, 2017–2019

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Background: Due to limited therapeutic options and potential for spread, carbapenem-resistant Enterobacteriaceae (CRE)-producing New Delhi metallo-β-lactamases (NDMs) are a public health priority. We investigated the epidemiology of NDM-producing CRE reported to the CDC to clarify its distribution and relative prevalence. **Methods:** The CDC's Antibiotic Resistance Laboratory Network supports molecular testing of CRE for 5 carbapenemases nationally. Although KPC is the most common carbapenemase in the United States, non-KPC carbapenemases are a growing concern. We analyzed CRE with any of 4 non-KPC plasmid-mediated carbapenemases (NDM, VIM, IMP, or OXA-48 type) isolated from specimens collected from January 1, 2017, through June 30, 2019; only a patient's first isolate per organism–carbapenemase combination was included. We excluded isolates from specimen sources associated with colonization screening (eg, perirectal). We compared the proportion of NDM-producing CRE to all non-KPC–producing CP-CRE between period A (January to June 2018) and period B (January to June 2019). Health departments and the CDC collected additional exposure and molecular information in selected states to better describe current NDM-producing CRE epidemiology. **Results:** Overall, 47 states reported 1,013 non–KPC-producing CP-CRE (range/state, 1–109 isolates; median, 11 isolates); 46 states reported 631 NDM-producing CRE (range/state, 1–84; median, 6). NDM-producing CRE increased quarterly from the third quarter of 2018 through the second quarter of 2019; CP-CRE isolates with other non-KPC carbapenemases remained stable (Fig. 1). In period A, 124 of 216 emerging CP-CRE had NDM (57.1%), compared with 255 of 359 emerging CP-CRE (71.0%) during period B ($P = .1179$). Among NDM-producing CRE, the proportion of *Enterobacter* spp increased from 10.5% in 2018 to 18.4% in 2019 ($P = .0467$) (Fig. 2). In total, 18 states reported more NDM-producing CRE in the first 6 months of 2019 than in all of 2018. Connecticut, Ohio, and Oregon were among states that conducted detailed investigations; these 3 states identified 24 NDM-producing CRE isolates from 23 patients in period B. Overall, 5 (21.7%) of 22 patients with history available traveled internationally ≤12 months prior to culture; 17 (73.9%) acquired NDM-producing CRE domestically. Among 15 isolates sequenced, 8 (53.3%) carried NDM-5 (6 *E. coli*, 1 *Enterobacter* spp and 1 *Klebsiella* spp) and 7 (46.7%) carried NDM-1 (6 *Enterobacter* spp and 1 *Klebsiella* spp). Species were diverse; no single strain type was shared by >2 isolates. **Conclusions:** Detection of NDM-producing CRE has increased across the AR Lab Network. Among states with detailed information available, domestic acquisition was common, and no single variant or strain

Figure 1. Number of isolates with NDM, OXA-48-type, IMP, and VIM carbapenemase genes reported, among emerging CP-CRE isolates from specimens collected January 1, 2017 through June 30, 2019, United States (N=1,013 isolates*)

	Qtr1	Qtr2	Qtr3	Qtr4	Qtr1	Qtr2	Qtr3	Qtr4	Qtr1	Qtr2
			2017				2018			2019
NDM	26	21	27	26	59	67	64	87	111	143
OXA-48-type	9	20	13	9	32	42	33	44	39	44
IMP	6	9	0	5	8	9	22	18	15	14
VIM	3	2	3	5	4	10	8	2	6	7

*Among the 75 isolates with more than one of these carbapenemase genes detected, each emerging carbapenemase was counted separately.

Fig. 1.