perform antimicrobial susceptibility testing, and whole-genome sequencing to identify resistance mechanisms.

Results. Among the 24 patients with culture-confirmed *Shigella* infection, 4 were hospitalized and 2 died. All isolates were multidrug-resistant (Table 1) and harbored mechanisms for resistance to ampicillin, ceftriaxone, trimethoprim-sulfamethoxazole, azithromycin, and ciprofloxacin. Fifteen patients received one course of ciprofloxacin, 5 received multiple courses of antibiotics, and 4 received no antibiotics. Overall, 6 patients had treatment failure (Table 2); all 4 patients who received azithromycin had subsequent clinical failure and 2 also had microbiologic failure. Two patients had failure after ciprofloxacin (1 clinical, 1 microbiologic).

Conclusion. This outbreak of highly resistant shigellosis highlights the importance of comprehensive susceptibility testing and systematic outcome studies. Evidence of treatment failure after azithromycin suggests that an appropriate clinical breakpoint is needed to inform clinical decision-making. Ciprofloxacin treatment failures were observed in patients with a susceptible strain harboring a resistance mechanism, warranting further investigation.

Table 1. Antibiotic susceptibility of *Shigella sonnei* outbreak isolates (n=24).

Antibiotic	Minimum inhibitory concentration (MIC)	Interpretation[1]
Amoxicillin-clavulanic acid	4–8 µg/ml	S
Ampicillin	> 32 µg/ml	R
Azithromycin	> 32 µg/ml	NS
Cefoxitin	2–4 µg/ml	S
Ceftriaxone	32–64 µg/ml	R
Ciprofloxacin	0.12 µg/ml	S
Meropenem	≤0.06 µg/ml	S
Nalidixic acid	≥32 µg/ml	R
Streptomycin[2]	32–>64 µg/ml	R
Tetracycline	≥32 µg/ml	R
Trimethoprim-sulfamethoxazole	> 4 µg/ml	R

[1] Interpretation of MIC is characterized according to Clinical and Laboratory Standards Institute (CLSI) breakpoints (S = susceptible; R = resistant; NS = non-susceptible) when available. Non-susceptibility is defined based on the epidemiological cutoff value (ECV) for *Shigella sonnei* of ≥32 µg/ml established by CLSI in 2015. The ECV should not be used as a clinical breakpoint to predict clinical effectiveness.
[2] CLSI breakpoints are not established for streptomycin; interpretive standards used are NARMS-established breakpoints for resistance monitoring and should not be used to predict clinical efficacy.

Table 2. Patients with treatment failures during an outbreak of multidrug-resistant shigellosis (n=6).

Age (years)	Sex	Antibiotic course (listed in sequence given)[1]	Clinical failure following completion of antibiotics?	Days to diarrhea resolution[2]	Microbiologic failure following completion of antibiotics?	Days to negative culture or PCR[3]
90	F	Azithromycin 250–500mg PO QD x4d[4]	Yes	6	Unknown[5]	-
		Ceftriaxone 1000mg IV QD x5d[4]	Yes	5	Unknown[5]	-
		Ampicillin 500mg IV QD x5d[4]	Yes	3	No	8
88	M	Ceftriaxone 1000–2000mg IV QD x3d	Yes	1	Unknown[5]	-
		Ciprofloxacin 250mg PO BID x3d	No	-1	No	12
88	F	Ciprofloxacin 500mg PO BID x3d	Yes	4	No	7
82	F	Azithromycin 500mg PO TID x3d	Yes	2	No	11
79	F	Azithromycin 500mg IV QD x2d[4]	Yes	12	Yes	-
		Ceftriaxone 1000–2000mg IV QD x4d[4]	Yes	9	Yes	43
42	M	Azithromycin 500mg PO QD x3d	Yes	3	Yes	-
		Ciprofloxacin 500mg PO BID x3d	No	-14	Yes	-
		Ciprofloxacin 500mg PO BID x3d	No	-25	No	1

[1] Median days between courses was 1 day (range 0–15).
[2] Days from end of antibiotic course to end of diarrhea (defined as ≥3 loose stools per day).
[3] Days from end of antibiotic course to first negative culture obtained. Daily cultures following antibiotic completion were not obtained for any patients; therefore these values should not be interpreted as days to microbiologic cure.
[4] Administered concurrently.
[5] Patients who did not have cultures between antibiotic courses are listed as having unknown microbiologic outcomes for these courses.

1604. Response to a Cluster of *Haemophilus influenzae* Serotype A Cases in a Small Alaska Community, 2018

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Background. Between May and July 2018, four invasive cases of *Haemophilus influenzae* type a (Hia) occurred in a remote Alaska community. A public health response was performed to prevent further illness and to understand local Hia transmission.

Methods. The team identified close contacts of the Hia patients, collected oropharyngeal (OP) swabs and provided prophylactic rifampin. Close contacts were persons who spent ≥4 hours with a Hia patient for ≥ 5 of the 7 days preceding hospitalization. Five days later, OP swabs were collected community-wide and prophylactic rifampin was offered to community members aged <10 years. Eight weeks later, OP swabs were collected from all willing community members. Samples were tested using PCR and culture to identify Hi carriage.

Results. No Hia cases occurred in this community after the response. The pre-treatment carriage prevalence is shown in Figure 1. There was a significant difference in prevalence of Hia carriage between contacts (4/27, 14.8%) and non-contacts (7/364, 1.9%) ($P = 0.0043$). Contacts aged <10 years were significantly more likely to carry Hia compared with contacts aged ≥10 years (11/18 [61.1%] vs. 3/34 [8.8%], $P = 0.0001$). The case households had the highest proportion of individuals who carried Hia at any time, with 54%–60% of individuals in three case households carrying Hia at least once. Hia carriage was eliminated in two carriers who completed treatment and were tested immediately after rifampin prophylaxis. Testing 8 weeks later found that the prevalence of carriage did not significantly change in the contacts (5/42 [11.9%] to 6/25 [24%], $P = 0.18$) or the non-contacts (7/368 [1.9%] to 2/114 [1.8%], $P = 0.47$).

Conclusion. Children aged <10 years who had close contact with the Hia patients were the most likely to carry Hia. These findings suggest that people who do not have close contact do not benefit from prophylaxis as they have very low Hia carriage. While rifampin prophylaxis eliminated carriage of Hia in the short term, carriage prevalence did not change in the long term. Further research is needed to understand why contacts have such a high prevalence of carriage even after receiving appropriate prophylactic medication.

Figure 1: *Haemophilus influenzae* carriage prior to antimicrobial treatment, Alaska 2018.
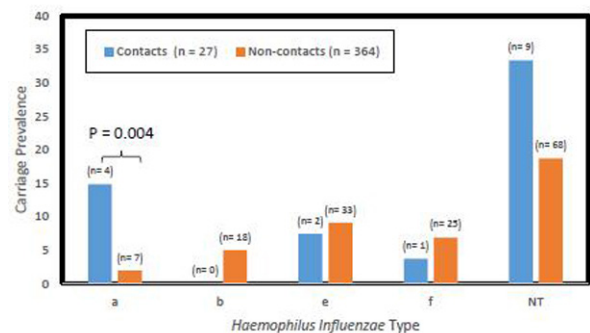
1605. Temperature Modulates the Rate of Increase of Antibiotic Resistance Across Europe

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Background. Widely recognized as a major public health threat globally, the rapid increase of antibiotic resistance in bacteria could soon render our most effective method to combat infections obsolete. Factors influencing the burden of resistance in human populations remain poorly described, though temperature is known to play an important role in mechanisms of bacterial growth and transmission.

Methods. Here, we present the first evidence that ambient temperatures may modulate the rate of increase of antibiotic resistance across Europe. Using a comprehensive dataset containing information across 28 countries, for 17 years (2000–2016), 3 common bacterial pathogens, and 4 antibiotic classes collectively representing over 4 million tested isolates, we show that antibiotic resistance has increased more rapidly in warmer regions over a period of nearly 2 decades.

Results. Specifically, we show that European countries with 10°C warmer ambient temperatures have experienced more rapid increases in antibiotic resistance to *E. coli* and *K. pneumoniae* over the 17-year period, ranging between 0.33%/year (95% CI 0.2, 0.5) and 1.2%/year (0.4, 1.9), even after accounting for recognized drivers of resistance including antibiotic consumption and population density. We found a decreasing relationship for *S. aureus* and methicillin of -0.4%/year (95% CI −0.7, 0.0), reflecting widespread declines in MRSA across Europe over the study period.

Conclusion. Our findings suggest that rising temperatures globally may hasten the spread of resistance and complicate efforts to mitigate it.

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1606. Legionellosis Cluster Associated with Direct and Indirect Hot Tub Exposure—West Virginia, 2018

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Background. In October 2018, the West Virginia Bureau for Public Health (BPH) notified CDC of one *Legionella* urinary antigen test (UAT)-positive case of Legionnaires' disease (LD) in a worker at a racetrack facility. Following investigation by BPH and the county health department, five additional LD cases were identified among facility workers within a one-month period. Our objective was to determine the extent of the outbreak and identify potential sources of exposure.

Methods. We interviewed the previously identified patients and conducted case-finding among racetrack workers. Our case definitions included confirmed LD (pneumonia with a positive UAT), suspected LD (pneumonia without a UAT completed), and Pontiac fever (PF) (self-limited, nonspecific flu-like symptoms) among employees with exposure to the facility within 14 days prior to symptom onset. We conducted an environmental assessment of the facility and the surrounding area for sources of potential *Legionella* exposure.

Results. We identified 17 cases (71% in men, 35% in current smokers, median age 55 years): six confirmed LD, four suspected LD, and seven suspected PF cases. Our environmental assessment revealed a poorly maintained hot tub in the first floor jockey area. All samples collected from the hot tub (which was chlorinated before our arrival) tested negative for *Legionella*. Two employees with confirmed LD (33%), three with suspected LD (75%), and six with suspected PF (86%) had direct exposure to the hot tub or adjacent hallway; the remaining six were exposed only to a second floor office suite. Further investigation identified deficiencies in the facility's ventilation systems and a crack in the floor between the hot tub and office areas. These factors created a pathway for *Legionella*-containing aerosols from the hot tub to pass into the second floor office space and air-handling unit for recirculation to occupied areas.

Conclusion. Our investigation suggests that both direct and indirect exposure to a *Legionella* reservoir can cause illness. This finding supports analysis of ventilation systems and airflow dynamics in future LD outbreak investigations. Clinicians should consider LD in pneumonia patients with direct or indirect exposure to suspected *Legionella* sources to ensure appropriate testing and treatment.

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1607. Temporal Patterns and Spatial Synchrony in Pertussis Incidence—the United States, 2000–2017

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Background. Pertussis is a highly contagious, vaccine-preventable respiratory disease. Historically, pertussis incidence was cyclic with peaks in disease every 3–5 years. In the United States, reported pertussis has increased over the past few decades despite high vaccination coverage; however, there is currently no clear national spatiotemporal pattern. We aimed to assess whether geographically distinct areas in the United States: (1) share similar temporal patterns (trend and periodicity), and (2) were synchronous in peaks in pertussis incidence.

Methods. We used pertussis cases reported through the National Notifiable Diseases Surveillance System, and CDC Wonder bridged-race county population estimates, for 2000–2017. County-level pertussis case counts were aggregated by month, and counties were aggregated into population areas of ≥300,000 persons. For each

population area, trend and dominant periods across the study period were extracted using wavelet analysis. Common temporal patterns were identified using hierarchical cluster analysis of trend and periodicity. Synchrony between population area pairs, and between each area and the country as a whole, were assessed using wavelet coherence and phase difference.

Results. There was substantial variability in temporal patterns, though geographically distinct population areas clustered by trend and similar dominant periods of 8 to <19 months, 19 to <38 months, and 38 to 71 months, with three main patterns accounting for 79% (400/506) of all population areas (Figures 1 and 2). The majority of areas had a background period of at least 38 months, and 87% (439/506) of population areas experienced a positive trend. However, only 37% (185/506) of areas were synchronous with the national time series at any time during 2000–2017.

Conclusion. Spatiotemporal patterns in pertussis incidence are complex, and are heterogeneous across the United States. Although a background period of at least 38 months was identified in the majority of areas, similar to the historic perception of a 3–5-year cycle, higher frequency components were also identified. A better understanding of the current spatiotemporal patterns of pertussis will allow us to better characterize current epidemiology and improve prediction of future outbreaks.

Figure 1. Temporal patterns in pertussis incidence in the United States, from 2000 to 2017. Population areas clustered by positive/negative trend, and by dominant periods of 8- < 19mo, 19- < 38mo, and 38-71mo.
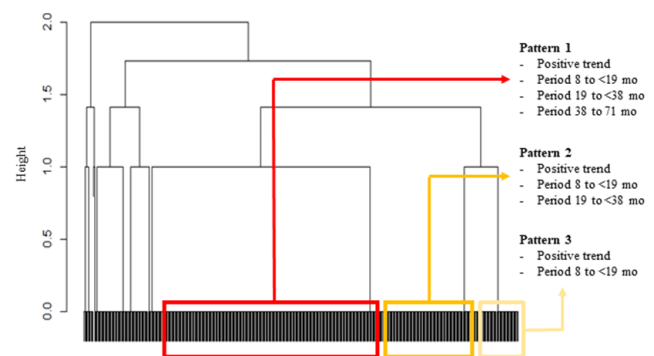
Figure 2. Spatial distribution of the three main identified temporal patterns in pertussis incidence in the United States, from 2000 to 2017.
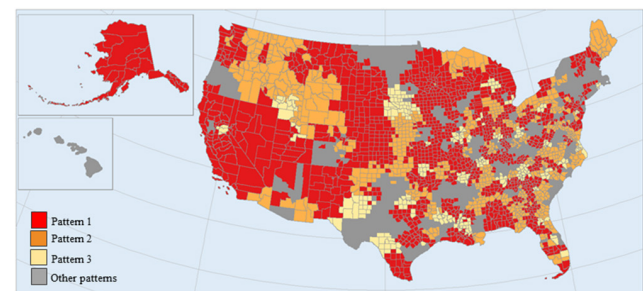
Disclosures. All authors: No reported disclosures.

1608. Use of Selective Reporting of Antimicrobial Susceptibilities and Its Impact on Antimicrobial Resistance Surveillance—National Healthcare Safety Network, 2017–2018

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Background. Selective reporting (SR), recommended by the 2016 IDSA/SHEA antimicrobial stewardship guidelines, is a strategy to guide prescribing decisions by limiting the antimicrobial susceptibility testing (AST) results available to prescribers. Yet, SR carries risks that cumulative antibiograms reflect only partial AST results. The Clinical Laboratory Standards Institute (CLSI) M100 performance standards stipulate that AST results should be routinely reported for some antimicrobials (Group A agents) while SR is appropriate for other antimicrobials (Group B agents). We assessed the extent of SR use and its impact on national antimicrobial resistance (AR) surveillance.

Methods. We used Enterobacteriaceae (EB) and *Staphylococcus aureus* (SA) blood culture AST results that hospitals reported for group A and B agents to the CDC's National Healthcare Safety Network's AR option from 2017 through 2018. Routine reporting for an organism-agent combination was defined as results reported for ≥ 90% isolates for the hospital's most frequently reported agents. SR was defined as a shortfall of > 20% in results reported for an agent compared with a routinely reported agent in a hospital that reported ≥ 30 isolates. We compared hospital antibiograms