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Surveillance of antimicrobial resistance and evolving microbial populations in Vermont: 2011–2018

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Abstract

Objective: This study presents trends in organism isolation and antimicrobial resistance in routine microbiology test results from acute-care hospital microbiology laboratories in Vermont.

Methods: The WHO Collaborating Centre for Surveillance of Antimicrobial Resistance captured microbiology test results from acute-care Vermont hospital laboratories to monitor geographic and temporal trends in antimicrobial resistance and emerging microbial threats with the free WHONET software.

Results: Data were provided from 12 acute care hospital laboratories from 2011 through 2018 for 318,833 isolates from 148,994 patients (70% female, 74% outpatient, and 63% urine). Significant differences ($p < 0.05$) in age, gender, and antimicrobial susceptibility results (e.g. *Escherichia coli* and levofloxacin) between outpatient and inpatient isolates were identified with temporal increases in certain species (e.g. *Aerococcus urinae*) and resistance (e.g. *Streptococcus pneumoniae* and erythromycin). The use of multi-resistance phenotypes demonstrated significant heterogeneity ($p < 0.05$) in MRSA strains between facilities, for example *Staphylococcus aureus* resistant to six priority antimicrobials were found in no critical access hospitals (fewer than 25 inpatient beds) but in all non-critical access hospitals.

Conclusions: Comprehensive electronic surveillance of antimicrobial resistance utilizing routine clinical microbiology data with free software tools offers early recognition and tracking of emerging community and healthcare resistance threats at the local and state level.

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Declaration of interest

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Keywords

Microbiology laboratory; Antimicrobial resistance; Vermont; Surveillance; WHONET

1. Introduction

The data generated by routine microbiology laboratories could and should provide a real-time window into evolving microbial populations to support the recognition and containment of emerging threats [1]. Unfortunately, traditional approaches for surveillance of antimicrobial resistance provide only annual aggregate statistics on a few priority, pre-defined pathogen/antimicrobial combinations, offering limited insights into evolving microbial populations in real-time to support containment efforts [2]

The World Health Organization Collaborating Centre for Surveillance of Antimicrobial Resistance based at the Brigham and Women's Hospital in Boston has developed, disseminated, and supported the free WHONET software for management of microbiology laboratory data since 1989, currently used to support surveillance activities in over 2,300 laboratories in more than 120 countries [3]. The files of each laboratory, stored in diverse laboratory information systems with heterogeneous data elements and structures, can be translated to inter-compatible WHONET files via the data conversion utility BacLink [4].

The collaboration with acute care hospitals in Vermont began in 2010 when the initial scope of the data collection collaboration was to assist these hospitals with facility-level data management, including monthly electronic reporting to the Centers for Disease Control and Prevention (CDC)'s National Healthcare Safety Network (NHSN) and annual preparation of hospital "antibiograms", used by pharmacists and clinicians to aid selection of appropriate antimicrobials for patient care. In 2017, the scope of the project expanded to monitoring the epidemiology of resistant microbial populations in the community and at acute care hospitals and to providing monthly alerts of new threats. The objective of this study was to describe patient, specimen, organism, and antimicrobial susceptibility data from Vermont acute care hospitals.

2. Methods

2.1 Data sources and preparation

Since 2010, the Boston-based WHO Collaborating staff have worked with clinical laboratories in Vermont to develop customized data extraction and processing plans for microbiology test results and associated patient, sample, and location details to support monthly data collection and NHSN reporting. Core data elements collected include patient identifiers, gender, date of birth, date of hospital admission, healthcare location type (inpatient, outpatient clinic, emergency department, long-term care facility), date of specimen collection, specimen type, organism identified, and antimicrobial susceptibility test results. Non-bacterial culture results including "no growth", "normal flora", and fungal isolates, were excluded from analyses.

2.2 Data analysis

Data were analyzed using WHONET 2019's "Isolate listing summary", "%RIS and test measurements", and "Resistance profile" analyses. For antimicrobial susceptibility test statistics, the first isolate per patient per species per 365-day period was selected. As a proxy definition of healthcare acquisition, we utilized WHO's classification of patient "first isolates" obtained from samples taken on hospital day 3 and later as "hospital origin", while others are classified as "community origin" [5] Linear regressions and Chi-Square calculations were performed in Microsoft Excel without adjustment for multiple comparisons.

3. Results

3.1 Patient and specimen characteristics

Data were provided from twelve of Vermont's fifteen acute care hospital laboratories. Data were available from January 2011 through December 2018 with three exceptions. Due to changes in laboratory service provision or laboratory information systems, there were data gaps from one critical access hospital (CAH) for 2014, one community hospital from 2014 through 2016, and one tertiary care medical center for 2018. Consequently, studies of temporal trends were limited to the years 2011 through 2017, excluding the two facilities with gaps in that range. Of the twelve laboratories, six were at critical access hospitals with 25 or fewer acute care inpatient beds.

Statewide, data were available for 318,833 isolates from 148,994 patients (average = 2.1 bacterial results per patient) covering hospital inpatient and outpatient locations and 15 long-term care facilities (LTCFs). Of the 148,994 patients, 74% had specimens collected in outpatient clinics, 25% in the emergency department, 12% in inpatient units, and 1% at LTCFs. The total exceeds 100% because many patients had samples collected in more than one healthcare setting. Considering only the first organism isolation per species per 365 days per patient, there were 250,893 "first isolates"; 69% were in the outpatient setting, 20% in the emergency department, 10% in inpatient units, and 1% in LTCFs. Among inpatient first isolates with a date of admission, 69% were from hospital days 1 and 2, classified by WHO's proxy definition as "community origin" infections, while 31% were obtained on hospital day 3 or later and thus classified as "hospital origin" infections. Thus, the majority of "inpatient" isolates are likely attributable to community-acquired infections.

Characteristics of the patients and specimens, overall and according to healthcare location type, are shown in Table 1. Most of the patients (70%) were female. Thirty-five percent of patients were in the 64-year-old category, while 15% were aged 18 years. Bacterial isolates were predominantly obtained from women (70%), from the outpatient setting (74%), and from urine samples (63%). Outpatient urine samples from female patients constitute (43%) of the full database.

3.2 Organism frequencies and trends

Considering only the first isolate per species per 365-day period per patient, the distribution of the ten most frequently isolated bacterial species by location type is shown in Table 2. In

both inpatient and outpatient settings, *E.coli* and *Staphylococcus aureus* comprised at least half of the bacterial isolates found. Organism proportion from inpatient isolates on the first two days of hospitalization to a large degree paralleled their occurrence in the outpatient setting, with the exceptions of Group A and Group B streptococci, which infrequently require hospitalization for adults. Samples collected on hospital day 3 or later demonstrate higher rates of isolation of organisms commonly associated with healthcare-associated infections, including *Enterococcus* spp., and *Pseudomonas aeruginosa*.

By linear regression, organisms with a statistically significant increase ($p < 0.05$, no control for multiple comparisons) in the outpatient setting over the eight years include *Aerococcus urinae*., *Helicobacter pylori*, *Peptostreptococcus* sp, and *Staphylococcus pseudintermedius*. Among inpatients, statistically significant ($p < 0.05$) increases were seen in *Klebsiella pneumoniae*, *Klebsiella aerogenes*, *Haemophilus influenzae*, and both Group A and Group B beta-hemolytic streptococci, among others.

3.3 Antibiotic susceptibility test results

Cumulative antimicrobial susceptibility test results in 2016–2017 for Gram-positive organisms (Table 3) and Gram-negative organisms (Table 4) were calculated in accordance with recommendations of the Clinical and Laboratory Standards Institute (CLSI) [6]. Priority Gram-positive findings include 28% methicillin-resistant *S. aureus* (MRSA), 5% vancomycin-resistant enterococci (VRE), 29% penicillin-non-susceptible *S. pneumoniae* (PNSP), and 13% ceftriaxone-non-susceptible *S. pneumoniae*. Using definitions proposed a consensus group coordinated by the European Centre for Disease Prevention and Control (ECDC), 34% of *S. aureus* and 12% of *E. coli* were consider to be multidrug-resistant (MDR) [7]. Regarding priority Gram-negative findings (data not presented in the manuscript tables), ampicillin alone was relatively ineffective, while susceptibility to amoxicillin/clavulanic acid exceeded 85% for the three pathogens most commonly seen in urinary tract infections (*E. coli* 89%, *K. pneumoniae* 96%, *Proteus mirabilis* 96%).

Piperacillin/tazobactam susceptibility exceeded 85% for all Gram-negative organisms studied. Susceptibility to third-generation cephalosporins was under 85% for *Acinetobacter baumannii*, *Citrobacter freundii*, and *Stenotrophomonas maltophilia*, and thus would not generally be recommended as a treatment option. Levofloxacin susceptibility remained above 85% for all except *P. mirabilis* and *P. aeruginosa*.

In examining findings for 2016–2017 with comparable results for 2011–2012 (data not presented), we noted the relative stability of susceptibility proportions in Vermont over the eight-year period with some exceptions, including the following where susceptibility dropped by more than 5%: *C. freundii* with ceftazidime (6% decrease in susceptibility), *S. maltophilia* with cefepime (9%) and gentamicin (13%), *Enterococcus* spp. with erythromycin (9%), and *S. pneumoniae* and clindamycin (9%).

The ability to monitor carbapenem resistance trends early in the time period was compromised by a significant shift in the CLSI MIC breakpoints. This was particularly evident for imipenem, where the susceptible breakpoint decreased by from 4 mcg/ml to 1 mcg/ml in June 2010 (though with variable adoption of these new breakpoints by

laboratories), especially in organisms with intrinsic decreased susceptibility like *P. mirabilis* and *M. morganii*. Because of the widespread use of limited-dilution MIC panels and delays in the adoption of updated panels and software upgrades, these organisms appeared to be 99% and 92% susceptible respectively in 2011–2012 since most results were recorded as MIC 4 mcg/ml, but with the new breakpoints, only 55% and 67%, respectively, of the isolates are now classified as susceptible reflecting a high degree of intrinsic decreased susceptibility in these organisms.

Table 5 explores in greater detail the relationship of resistance to several risk factors, with *E. coli* as an example. For each variable, the value with the greatest susceptibility is listed first with decreases in susceptibility on subsequent rows greater than or equal to 5% marked in gray. Among outpatients, isolates obtained from males were typically slightly less susceptible (by 1–4%, statistically significant, $p < 0.05$, but not clinically significant) than isolates from females for most antimicrobials but much less susceptible (by 9%, statistically significant, $p < 0.05$, and potentially impacting therapy guidelines) for levofloxacin (LVX). Little difference was noted by age except again for LVX (94% susceptible in ages 0–18 years, 92% susceptible in ages 19–64 years, and 80% susceptible in ages 65 years and older). After stratification by age, little difference in susceptibility patterns was noted by gender, suggesting that the gender-related difference is primarily related to the age of men (median age 69) versus women (median age 57) seeking medical care rather than specifically to gender. Little difference was seen between urine and non-urine isolates among both inpatients and outpatients. Notable differences were seen in comparing healthcare settings for several antibiotics, generally with susceptibility greater in outpatient isolates and lowest in intensive care unit (ICU) and LTCF isolates and isolates from hospital day 3 or later.

Table 5 also demonstrates that there was relatively little variation (<5%) among the Vermont facilities in *E. coli* susceptibility for most antimicrobials except for ceftazidime (range from 80% to 100% susceptible). Larger interlaboratory differences exceeding 20% attesting to marked heterogeneity within the state with implications for local treatment guidelines were noted for other species including *S. aureus* (OXA 56%–78%, CLI 68%–92%, ERY 38%–58%, and LVX 67%–100%), *P. aeruginosa* (TOB 77%–100%), and *P. mirabilis* (AMP 57%–90%, CIP 64%–90%, LVX 63%–96%, and SXT 60%–93%).

Table 6 displays the statewide and facility distribution of the common MRSA multi-resistance phenotypes defined by results from seven antimicrobials with good data availability (over 98%) from most facilities in the state: penicillin (PEN), oxacillin (OXA), erythromycin (ERY), gentamicin (GEN), levofloxacin (LVX), trimethoprim/sulfamethoxazole (SXT), and vancomycin (VAN). For one community hospital, ciprofloxacin was used as a proxy indicator for levofloxacin. Three facilities were excluded because of insufficient data for one antimicrobial (levofloxacin for one community hospital) or two antimicrobials (levofloxacin and gentamicin for a tertiary care medical center and a critical access hospital).

The distribution of MRSA multi-resistance phenotypes around the state was not homogeneous. Some of the more notable facility-specific findings are highlighted in gray:

CAH-5 has a predominance of relatively susceptible MRSA and when compared with other facilities; CAH-4 and CAH-5 (two facilities in close geographic proximity) were the only facilities to isolate resistance profile 10 (non-susceptible to PEN, OXA, GEN, and SXT); and acute care hospital-4 was the only facility to isolate profile 14 (non-susceptible to PEN, OXA, GEN, LVX, and SXT). All of the acute care laboratories found MRSA isolates resistant to six antimicrobials (susceptible only to VAN among the seven antimicrobials studies), while none of the CAH facilities did, where more susceptible phenotypes predominated.

4. Discussion

4.1 Primary findings

In this work, we describe a comprehensive approach to electronic data capture from routine clinical laboratories and analysis and apply this to descriptions of microbial epidemiology in Vermont over an eight-year period. At the state level, resistance trends remained relatively stable for many key resistance pathogens, but with several exceptions noted. This relative stability at the state level stands in contrast to the heterogeneity seen between facilities, especially when multi-resistance phenotypes are considered, suggesting that automated monitoring of resistance phenotypes can improve the timely recognition, tracking, and containment of distinct MRSA strains [8].

4.2 Patient and sample characteristics

The high proportion of women (70%) can be attributed primarily to the frequency of urinary and genital tract infections in a general population, but also in part to longer life expectancy and higher rates of healthcare service utilization [9]. The high proportion of samples among young adults (modal age range of 15 to 24 years) stands in stark contrast to their low proportion of samples among hospitalized patients (modal age range of 75 to 84 years).

4.3 Organism trends

The two most common pathogens identified in all settings were *E. coli* and *S. aureus*. As expected, Group A and Group B beta-hemolytic streptococci were more common in the outpatient setting, while pathogens more commonly seen in nosocomial infections such as *P. aeruginosa* and *K. pneumoniae* were more frequent among inpatients. Patient date of admission was valuable in discriminating the epidemiology of isolates collected from hospitalized patients.

Among outpatients, statistically significant increases ($p < 0.05$) in organism isolation over time were seen in a number of species and may reflect changes in patient population coverage, sample collection and processing practices, contamination rates, as well as true increases in infection incidences. For *H. pylori*, *S. pseudintermedius*, and the anaerobe *Peptostreptococcus* spp. increased isolation also may reflect improved capacity by laboratories to isolate and speciate fastidious or difficult-to-identify pathogens. The increase in *A. urinae* is noteworthy (including one isolate from a dialysis unit) as this pathogen is increasingly recognized as an emerging cause of urinary tract infections in older patients with urological disorders [10].

4.4 Antibigrams and resistance profiles

Annual cumulative antimicrobial susceptibility test statistics are key components of facility- and statewide antimicrobial stewardship activities supporting the assessment and revision of treatment guidelines and permitting the monitoring of temporal and geographic trends. Significant differences in antibiogram findings between facilities and regions may suggest differences in patient populations served, antimicrobial use patterns, or deficiencies in hospital hygiene and infection control practices that could be explored further.

A rich view of the diversity in resistance epidemiology in the state is evident when one explores the use of multi-resistance phenotypes to categorize isolates according to the set of antimicrobials to which the organism is non-susceptible. The “typical MRSA” seen in Vermont is non-susceptible to PEN, OXA, ERY, and LVX. While this phenotype was seen in 48% of patients with MRSA at the state level, this ranged from 31% in one of the critical access hospitals to 58% in one of the acute care hospitals. Certain phenotypes were only seen in a single facility (Profile 14) or in a small geographic area of the state (Profile 10), while strains non-susceptible to six of the seven profile antimicrobials (susceptible only to VAN) were seen in all acute care hospitals, but in none of the critical access hospitals. In previous studies, we have demonstrated the use of multi-resistance phenotypes as epidemiological strain markers to improve the sensitivity, specificity, and timeliness of detection of hospital [11,12] and community [13,14] outbreaks using the free SaTScan software [15], which has been integrated within WHONET.

4.5 Comparison to other studies

A comparison of the present results with findings from other studies can offer some validation of the findings of this study and identify methodological distinctions in their approaches. Results from HealthMap ResistanceOpen [16] are derived from routine hospital antibiogram results for four priority resistant pathogens from contributing facilities nationwide, and the results for these four pathogens for Vermont were very similar to our findings: MRSA (31% in ResistanceOpen from 2014–2015 versus 28% in our study), VRE (8% versus 5%), *E. coli* resistant to third-generation cephalosporins (4% versus 4% for ceftriaxone and 34% for ceftazidime), and *K. pneumoniae* resistant to carbapenems (0% versus 0%).

The CDC Antibiotic Resistance Patient Safety Atlas (ARPSA) [17], comprising case reports of healthcare-associated infections to NHSN, takes a different approach. Reflecting this bias associated with hospital acquisition, estimates of resistance from ARPSA were higher than estimates presented here, for example 44% MRSA from 52 Vermont patients in ARPSA in 2016–2017 in comparison to 32% MRSA in 7,692 Vermont patients in this study.

A number of publications have explored the use of additional metrics for monitoring resistance to multiple agents using ECDC consensus guidelines or other definitions for recognizing multidrug-resistant (MDR, examples provided earlier in Results), extensively drug-resistant (XDR), and pandrug-resistant (PDR) [18], though reliable application of the XDR and PDR definitions requires testing of a full complement of defined antimicrobials, beyond the scope of routine clinical diagnostics. Newer concepts of usual drug resistance

(UDR) [19] and difficult-to-treat resistance (DTR) [20] have been proposed with more practical application to the assessment of available therapeutic options and to the design of clinical trials for multiresistant pathogens, though precise definitions may vary depending on the pathogen, clinical scenario, and geographic setting.

4.6 Strengths and limitations

The diagnostic microbiology laboratories of the world offer a richly detailed real-time window into the appearance and dissemination of evolving microbial populations. Yet traditional surveillance strategies typically rely only on annual aggregate statistics of a few key indicators to support treatment guideline revisions on case-reporting of priority threats, missing the opportunity to detect and respond to a range of emerging community and healthcare-associated threats in real time.

There are a number of limitations to highlight when relying on routine diagnostic laboratory data. One must remain cognizant of potential biases due to the decision of patients to seek healthcare, the decision of a healthcare provider to take a clinical sample, laboratory processes for sample processing and reporting, and the quality of laboratory test performance. Generally, little clinical information on patient disease, prior therapy, or clinical outcome is available, and there may be important differences in the completeness, quality, and representativeness of results between facilities. Such differences must be acknowledged when interpreting findings and developing treatment guidelines and interventions. Yet despite these limitations, routine clinical data already exist as a freely available information resource that is underutilized for recognition of novel threats, emerging trends, and the real-time tracking and containment of emerging infections.

4.7 Conclusions

This study explores the potential insights offered by the systematic collection and analysis of routine clinical laboratory data in one U.S. state. Linking resistance data to community and healthcare antimicrobial use patterns and infection prevention interventions would further inform the causative relationship among these and their impact on trends observed. Facility and regional differences in resistance rates need to be fed back in a timely manner to policy makers, antimicrobial stewardship committees, infection preventionists, microbiologists, and state epidemiologists to inform local treatment and resistance containment interventions to intercept and contain microbial threats and to assess their impact.

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Key issues

- Antimicrobial resistance is an emerging public health threat imposing significant health and economic burdens on patients and healthcare facilities. Routine clinical microbiology laboratory data provide a rich source of real-time data for monitoring and responding to emerging antimicrobial issues, but remains largely untapped for purposes of epidemiological surveillance.
- WHONET and its data capture module BacLink are free softwares distributed by the WHO Collaborating Centre for Surveillance of Antimicrobial Resistance to support the capture, analysis, and sharing of existing microbiology laboratory data.
- This paper presents demographic and temporal trends in microbial isolates and antimicrobial resistance in Vermont populations with data extracted from the microbiology laboratories of twelve acute care facilities in Vermont.
- Among outpatients over the eight-year period, there was a statistically significant increase ($p < 0.05$) in the number of patients with *A. urinae*, *H. pylori*, *Peptostreptococcus* spp., and *S. pseudintermedius* among others. Among inpatients, statistically significant increases ($p < 0.05$) were seen in *K. pneumoniae*, *K. aerogenes*, *H. influenzae*, and both Group A and Group B beta-hemolytic streptococci, among others. In some cases, these increases are likely due to true increases in infection rates, while in others, the increases are likely due to improved capabilities for microbial speciation or changes in specimen processing practices.
- We noted the relative stability of susceptibility proportions in Vermont at the state level over the eight-year period for most of organisms of routine clinical importance but with a number of exceptions where susceptibility dropped by more than 5%: *C. freundii* with ceftazidime (6% decrease in susceptibility), *S. maltophilia* with cefepime (9%) and gentamicin (13%), *Enterococcus* spp. with erythromycin (9%), and *S. pneumoniae* and clindamycin (9%)
- Antimicrobial multi-resistance test results are valuable phenotypic markers for improving the timely recognition and monitoring of distinct microbial strains. For example, isolates of *S. aureus* resistant to a core set of seven antimicrobials were seen in none of the critical access hospitals (25 inpatient beds) but in all of the non-critical access hospitals.
- WHONET supports surveillance of infectious diseases and antimicrobial resistance in over 2,300 microbiology laboratories in over 120 countries, so the data management and interpretation strategies elaborated within this paper have broad applicability for healthcare facilities.

Table 1.

Patient and sample characteristics from twelve Vermont hospital laboratories, 2011–2018. Numbers indicate the number of patients followed in parentheses by the percentage of patients.

Variable	All locations	Outpatient	Emergency	Inpatient	LTCF
Location type	148,994 (100%)	110,422 (74%)	37,387 (25%)	18,558 (12%)	1,660 (1%)
Gender					
Female	104,143 (70%)	80,835 (73%)	24,466 (66%)	10,681 (59%)	1,190 (73%)
Male	43,986 (30%)	29,310 (27%)	12,876 (34%)	7,457 (41%)	471 (27%)
Age group					
0–18	22,327 (15%)	18,118 (16%)	4,317 (12%)	1,054 (6%)	2 (0%)
19–49	48,493 (33%)	35,987 (33%)	12,637 (34%)	3,655 (20%)	28 (2%)
50–64	28,759 (19%)	21,398 (19%)	6,475 (17%)	3,817 (21%)	92 (6%)
65	51,402 (35%)	36,647 (33%)	14,296 (38%)	9,679 (53%)	1,541 (93%)
Specimen type					
Blood	8,863 (6%)	1,704 (2%)	5,392 (8%)	2,271 (12%)	19 (1%)
Genital	5,627 (4%)	4,431 (4%)	195 (2%)	706 (4%)	9 (1%)
Respiratory	21,888 (15%)	15,900 (14%)	3,743 (13%)	3,380 (18%)	34 (2%)
Soft tissue	31,849 (21%)	21,463 (19%)	7,375 (17%)	4,808 (26%)	278 (17%)
Stool	1,789 (1%)	1,081 (1%)	482 (2%)	289 (2%)	3 (0.2%)
Urine	94,120 (63%)	70,924 (64%)	23,626 (47%)	8,807 (38%)	1,434 (86%)
Unknown	5,681 (4%)	3,590 (3%)	807 (6%)	1,060 (1%)	24 (1%)

LTCF = Long-term Care Facility.

Table 2.

Distribution of the 10 most common bacterial species by location type and inpatient hospital day, 2011–2018. Numbers indicate the number of patients followed in parentheses by the percentage of patients.

Organism	Location type					Inpatient hospital day		
	All locations	Outpatient	Emergency	Inpatient	LTICF	HD 1&2	HD 3	
<i>Escherichia coli</i>	67,599 (45%)	50,380 (46%)	15,999 (43%)	5,768 (31%)	737 (44%)	2,142 (29%)	729 (23%)	
<i>Staphylococcus aureus</i>	29,496 (20%)	20,082 (18%)	6,747 (18%)	4,476 (24%)	300 (18%)	1,546 (21%)	801 (25%)	
<i>Staphylococcus, coagulase negative</i>	13,099 (9%)	8,238 (8%)	3,317 (9%)	1,629 (9%)	91 (5%)	1,093 (15%)	419 (13%)	
<i>Klebsiella pneumoniae</i>	12,419 (8%)	8,342 (8%)	2,948 (8%)	1,751 (9%)	308 (19%)	670 (9%)	251 (12%)	
<i>Enterococcus</i> sp.	12,264 (8%)	7,993 (7%)	2,345 (6%)	2,276 (12%)	352 (21%)	658 (9%)	391 (9%)	
<i>Streptococcus agalactiae</i> (Group B)	7,494 (5%)	5,778 (5%)	1,185 (3%)	751 (4%)	66 (4%)	308 (4%)	94 (3%)	
<i>Streptococcus pyogenes</i> (Group A)	7,462 (5%)	5,503 (5%)	1,751 (5%)	301 (2%)	2 (0%)	131 (2%)	16 (0%)	
<i>Pseudomonas aeruginosa</i>	5,911 (4%)	3,852 (3%)	1,254 (3%)	1,435 (8%)	181 (11%)	464 (6%)	284 (9%)	
<i>Proteus mirabilis</i>	4,767 (3%)	3,358 (3%)	1,033 (3%)	579 (3%)	229 (14%)	210 (3%)	98 (3%)	
<i>Enterobacter cloacae</i>	3,205 (2%)	2,093 (2%)	652 (2%)	523 (3%)	67 (4%)	154 (2%)	98 (3%)	

HD = Hospital Day.

Cumulative antimicrobial susceptibility test results for common Gram-positive cocci, 2016–2017. Numbers in the antibiotic columns reflect the percent susceptible.

Table 3.

Organism	Patients	Beta-lactam agents				Ribosomal agents				Other			
		PEN	OXA	CRO	CLI	ERY	GEN	TCY	LVX	NIT	SXT	VAN	
<i>Enterococcus</i> spp.	3,316	94	2	5	4	15	78 [/]	34	74	94	77	95	
<i>Staphylococcus aureus</i>	7,692	20	72		84	52	99	95	80	100	97	100	
<i>Staphylococcus</i> , coagulase negative	3,117	26	66		75	50	95		79	99	79	100	
<i>Streptococcus pneumoniae</i>	480	71 ²		87 ²	80	59			98		82	100	

PEN = Penicillin G, OXA = Oxacillin, CRO = Ceftriaxone, CLI = Clindamycin, ERY = Erythromycin, GEN = Gentamicin, TCY = Tetracycline, LVX = Levofloxacin, NIT = Nitrofurantoin, SXT = Trimethoprim/Sulfamethoxazole, VAN = Vancomycin. Antibiotics to which the species has intrinsic resistance are indicated in gray.

¹ Gentamicin results presented for enterococci were derived from testing with high concentrations of gentamicin.

² For *S. pneumoniae*, the CLSI meningitis breakpoints were utilized for PEN and CRO. CLSI = Clinical and Laboratory Standards Institute.

Table 4.

Cumulative antimicrobial susceptibility test results for common Gram-negative bacilli, 2016–2017. Numbers in the antibiotic columns reflect the percent susceptible.

Organism	Patients	Beta-lactam antimicrobials													
		Penicillins				Cephalosporins				Carbapenems				Aminoglycosides	
		AMP	AMC	TZP	CAZ	CRO	FEP	ETP	IPM	MEM	GEN	AMK	LVX	NIT	SXT
<i>Enterobacteriaceae</i>															
<i>Escherichia coli</i>	21,902	65	89	98	97	96	98	100	100	100	95	100	87	98	85
<i>Proteus mirabilis</i>	1,491	86	96	100	99	99	100	100		100	94	100	78	0	84
<i>Citrobacter freundii</i>	575	33	37	90	82	84	98	99	98	100	97	100	96	95	90
<i>Enterobacter cloacae</i>	937	12	10	88	87	85	98	97	97	100	99	100	99	43	94
<i>Klebsiella pneumoniae</i>	3,835	3	96	97	97	97	98	100	100	100	99	100	95	40	92
<i>Morganella morganii</i>	318	2	4	100	88	95	99	99		100	95	100	93	0	89
<i>Serratia marcescens</i>	369	6	6	93	94	94	100	100	100	100	100	99	96	0	99
Nonfermenting Gram-negative organisms															
<i>Acinetobacter baumannii</i>	104	7	68	87	84	30	89	3	100	97	95	100	93	3	89
<i>Pseudomonas aeruginosa</i>	1,730	1	2	91	94	10	94	0	92	92	93	97	82	0	8
<i>Stenotrophomonas maltophilia</i>	258	0	0		56	0	5	5	0	0	19	0	91	0	90

AMP = Ampicillin, AMC = Amoxicillin/Clavulanic acid, TZP = Piperacillin/Tazobactam, CAZ = Ceftazidime, CRO = Ceftriaxone, FEP = Cefepime, ETP = Ertapenem, IPM = Imipenem, MEM = Meropenem, GEN = Amikacin, AMK = Amikacin, LVX = Levofloxacin, NIT = Nitrofurantoin, SXT = Trimethoprim/Sulfamethoxazole. Antibiotics to which the species has intrinsic resistance are indicated in gray.

Table 5. Antimicrobial susceptibility test results for *E. coli* for 2016–2017 by patient and sample characteristics.

Variable	Patients (%)	Penicillins			Cephalosporins			Carbapenems			Aminoglycosides			Other		
		AMP	AMC	TZP	CAZ	CRO	FEP	ETP	IPM	MEM	GEN	AMK	LVX	SXT	NIT	
Statewide	21,902 (100%)	65	89	98	97	96	98	100	100	100	95	100	87	85	98	
Gender																
Female	17,148 (88%)	65	89	98	97	96	99	100	100	100	95	100	88	85	98	
Male	2,449 (12%)	61	86	97	95	94	96	100	100	100	94	100	79	84	97	
Age (years)																
0–18	1,725 (8%)	64	93	98	99	98	100	100	100	100	95	100	94	86	99	
19–49	6,532 (32%)	65	92	98	98	98	100	100	100	100	95	100	94	85	98	
50–64	4,010 (19%)	66	87	98	96	96	99	100	100	100	95	100	90	86	97	
65	8,368 (41%)	64	87	97	96	94	97	100	100	100	94	100	80	84	97	
Location type																
Outpatient	14,881 (74%)	65	89	98	97	96	98	100	100	100	95	100	87	85	98	
Emergency	3,550 (18%)	63	90	98	98	96	99	100	100	100	95	100	87	83	97	
LTCF	134 (1%)	38	69	92	84	75	92	100	100	100	84		49	69	94	
Inpatients	1,549 (8%)	59	87	96	96	93	96	100	100	100	93	100	72	84	98	
Hospital days 1 and 2	1,293	58	88	96	96	93	97	100	100	100	93	100	78	83	99	
Hospital days 3	655	58	80	94	96	94	95	100	100	100	94	100	71	83	99	
Intensive care unit	102	61		95	67	89	89	100	100	100	89	100	70	88	95	
Specimen type																
Urine	20,571 (92%)	65	89	98	97	96	98	100	100	100	94	100	87	84	98	
Other	1,825 (8%)	61	87	96	96	94	97	100	100	100	94	100	82	84	98	
Laboratory																
Maximum		69	90	99	100	97	100	100	100	100	96	100	92	89	98	
Median		65	89	98	97	97	99	100	100	100	95	100	91	84	98	
Minimum		62	89	97	80	95	96	100	100	98	93	100	87	84	96	

Rows with the highest proportions susceptible are presented first for each variable, and values with susceptibility proportions 5% below the first value for each variable are highlighted in gray.

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AMP = Ampicillin, AMC = Amoxicillin/Clavulanic acid, TZP = Piperacillin/Tazobactam, CAZ = Cefazidime, CRO = Ceftriaxone, FEP = Cefepime, ETP = Ertapenem, IPM = Imipenem, MEM = Meropenem, GEN = Amikacin, AMK = Amikacin, LVX = Levofloxacin, NIT = Nitrofurantoin, SXT = Trimethoprim/Sulfamethoxazole. Antibiotics to which the species has intrinsic resistance are indicated in gray. LTCF = Long-term Care Facility.

Table 6.

Distribution of MRSA multi-resistance profile by facility, 2011–2018. The values indicate the percentage of isolates within each facility with a given resistance profile.

Profile Number	Resistance profile	Number of nonsusceptible results	Acute-Care Hospitals				Critical Access Hospitals				
			Acute-1	Acute-2	Acute-3	Acute-4	CAH-1	CAH-2	CAH-3	CAH-4	CAH-5
1	PEN OXA	2	6%	7%	8%	7%	6%	5%	6%	6%	14% ↑
2	PEN OXA ERY	3	28%	33%	38%	32%	28%	33%	40%	42%	51% ↑
3	PEN OXA GEN	3	0.2%	0.2%	1%	1%	0.2%	0.2%	0.2%	0.2%	0.3%
4	PEN OXA LVX	3	3%	3%	4%	7%	4%	3%	6%	12% ↑	2%
5	PEN OXA SXT	3	0.3%	0.1%	0.1%	0.1%	1%	0.4%	0.4%	0.4%	0.4%
6	PEN OXA ERY GEN	4	0.1%	0.1%	0.1%	3% ↑	0.1%	2%	0.2%	0.2%	0.2%
7	PEN OXA ERY LVX	4	58% ↑	53%	46%	39%	56%	49%	44%	37%	31%
8	PEN OXA ERY SXT	4	0.3%	0.3%	1%	1%	1%	2%	1%	1%	1%
9	PEN OXA GEN LVX	4	0.1%	0.1%	1%	1%	0.2%	0.2%	0.2%	0.2%	0.2%
10	PEN OXA GEN SXT	4	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%
11	PEN OXA LVX SXT	4	1%	1%	1%	0.2%	1%	1%	1%	1%	1%
12	PEN OXA ERY GEN LVX	5	0.3% ↓	0.3%	1%	7% ↑	1%	3%	1%	1%	1%
13	PEN OXA ERY LVX SXT	5	2%	3%	2%	2%	3%	3%	1%	2%	2%
14	PEN OXA GEN LVX SXT	5	0.0%	0.0%	0.0%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%
15	PEN OXA ERY GEN LVX SXT	6	1%	0.2%	0.4%	1%	1%	1%	1%	1%	1%

Isolates are non-susceptible to the antimicrobials indicated. PEN = penicillin G, OXA = oxacillin, ERY = erythromycin, GEN = gentamicin, LVX = levofloxacin, SXT = trimethoprim/sulfamethoxazole, and VAN = vancomycin. The total Chi-square associated with this table is 665. Values in gray have a Chi-square contribution exceeding 20. Proportions which exceed expectations are indicated by ↑, while proportions below expectations are indicated by ↓. Acute = Acute-Care Hospital, CAH = Critical Access Hospital.