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The role of surveillance systems in confronting the global crisis of antibiotic-resistant bacteria

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Abstract

Purpose of Review—It is widely accepted that infection control, advanced diagnostics, and novel therapeutics are crucial to mitigate the impact of antibiotic-resistant bacteria. The role of global, national and regional surveillance systems as part of the response to the challenge posed by antibiotic resistance is not sufficiently highlighted. We provide an overview of contemporary surveillance programs, with emphasis on Gram-negative bacteria.

Recent Findings—The World Health Organization and public health agencies in Europe and the United States recently published comprehensive surveillance reports. These highlight the emergence and dissemination of carbapenem-resistant *Enterobacteriaceae* (CRE) and other multidrug resistant Gram-negative bacteria. In Israel, public health action to control CRE, especially *Klebsiella pneumoniae* carbapenemase (KPC) producing *Klebsiella pneumoniae*, has advanced together with a better understanding of its epidemiology. Surveillance models adapted to the requirements and capacities of each country are in development.

Summary—Robust surveillance systems are essential to combat antibiotic resistance, and need to emphasize a “One Health” approach. Refinements in surveillance will come from advances in bioinformatics and genomics that permit the integration of global and local information about antibiotic consumption in humans and animals, molecular mechanisms of resistance, and bacterial genotyping.

Keywords

Developing Countries; Antibiotic Resistance; Surveillance; Public Health Agencies; One-Health

Introduction

The introduction of penicillin and sulfonamides into clinical practice in the middle of the twentieth century revolutionized the treatment of bacterial infections, offering remedy for diseases that were previously lethal. This power did not rest in the hands of a few skilled

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practitioners in wealthy societies, but became widely available. It is not an exaggeration to assert that antimicrobial chemotherapy, as well as improved sanitary conditions and vaccination, largely explain trends towards longer life expectancy around the world. Antibiotic treatment and prophylaxis of bacterial infections remain essential to sustain advances in neonatal care, surgery, organ transplantation, and cancer chemotherapy. The emergence of bacteria resistant to all or most existent antibiotics, especially in the realm of Gram-negative bacteria, constitutes a crisis: a return to the pre-antimicrobial era is a real possibility in the 21st century¹.

In order to stem this crisis, a worldwide response is urgent to find and develop new agents that fill unmet therapeutic needs, to improve the use of currently available antibiotics, and to prevent and control the transmission of bacteria resistant to antibiotics². Such actions can only be guided by reliable epidemiological information about the prevalence and impact of resistant bacteria in different settings. Although antibiotic resistance is a universal public health concern, great gaps remain in our current understanding of the magnitude of the problem. Improved surveillance of antibiotic resistance in bacteria is necessary to fill those gaps³. The ultimate goal of strengthening surveillance is to formulate strategies and interventions to address the challenge of antibiotic resistance and improve the outcome of individual patients.

WHO: antibiotic resistance surveillance on a global scale

The World Health Organization (WHO) recently issued a comprehensive report on antimicrobial resistance surveillance, which intended to provide a detailed picture of the current state of surveillance globally⁴. Data from 129 member countries was sought for a selected set of nine bacteria-antibacterial drug combinations (Table 1). Overall, 114 countries provided information regarding at least one of nine bacteria-antibacterial drug combinations; only 22 countries contributed data for all nine combinations. The paucity and inconsistency in the availability of data reveals the lack of surveillance infrastructure at the national level that can be drawn upon to collect information from individual member countries. Most of the country-level data originated from the European Region and the Region of the Americas, where regional surveillance efforts have been more successful, and less so from Asia and Africa. Furthermore, data sources were biased towards bacterial infections associated with health care, at the expense of community acquired infections. Overall, the lack of a global consensus on the methodology and data collection was acknowledged as a major obstacle for effective surveillance of antibiotic-resistant bacteria.

The report features WHONET (<http://www.whonet.org>), a freely accessible software (created and maintained by J. Stelling and T.F. O'Brien) that is widely used as a common platform for antibiotic resistance data collection, management and sharing, and serves as a strategy to facilitate global surveillance of antimicrobial resistance, including low- and middle-income countries⁵.

Europe: advanced integrated surveillance

The European Antimicrobial Resistance Surveillance Network (EARS-Net) is a multi-country surveillance network that collects routine clinical antibiotic susceptibility data from

national surveillance systems^{6, 7}. The European Centre for Disease Prevention and Control (ECDC) hosts EARS-Net since 2010. Its charge is to document the emergence and dissemination of antibiotic-resistant bacteria in Europe, and to increase awareness among the citizenry, scientists, and public health authorities. Focused scientific papers and maps, graphs and tables from yearly reports are available through a web-based data query tool. There are two other ECDC surveillance networks that operate in close association with EARS-Net: the European Surveillance of Antimicrobial Consumption Network (ESAC-Net), and the Healthcare-associated Infections Surveillance Network (HAI-Net)^{8, 9}. HAI-Net is responsible for coordinating a yearly point prevalence survey of healthcare-associated infections in acute care hospitals throughout Europe, similar to efforts conducted in the U. S. (Table 2)^{9, 10}. EARS-Net also cooperates with the European Committee on Antimicrobial Susceptibility Testing (EUCAST) to establish guidelines and quality assurance activities among member countries¹¹.

The most recent reports from EARS-Net reveals a continuous increase between 2010 and 2013 in resistance to third-generation cephalosporins in *Klebsiella pneumoniae* and *Escherichia coli* mediated by ESBLs, with co-resistance to fluoroquinolones and aminoglycosides. Carbapenem-resistant and multidrug-resistant *Pseudomonas aeruginosa* and *Acinetobacter* spp. were common. Carbapenem-resistant *K. pneumoniae* occurred in high proportions in Greece (60%), Italy (40%), and Romania (30%) but remained infrequent in the rest of European countries⁶.

The European CDC, the European Food Safety Authority (EFSA) and the European Medicines Agency (EMA) carried out an integrated analysis on the consumption of antibiotics in food-producing animals and humans, and its impact on the occurrence of antibiotic-resistant bacteria¹². In most of the surveyed countries the average consumption of antibiotics, including fluoroquinolones and cephalosporins, was lower in food-producing animals than in humans. Correlations were observed between antibiotic consumption and resistance prevalence in animals, in humans, and from animals to humans, for *Campylobacter* and *E. coli* resistant to fluoroquinolones, cephalosporins and tetracyclines. Molecular characterization of bacterial isolates from human and food-producing animals will be necessary to understand the underpinnings of those associations. These first integrated analyses demonstrate the need to refine existing surveillance systems in order to obtain more detailed information on antibiotic consumption. Similarly, more detailed information is needed on the prevalence of antibiotic-resistant bacteria in foods originating from animals and from different locations, and further understanding of the relationship between antibiotic-resistant bacteria and animal and human commensal flora.

The surveillance systems delineated above contain limited data regarding antibiotic-resistant bacteria and antibiotic consumption among children. The Antibiotic Resistance and Prescribing in European Children (ARPEC) project, created to fill that void, reveals that the profile of antibiotic resistance in bloodstream isolates from children differ from those reported by EARS-Net. This finding indicates that caution should be used when generalizing data from surveillance to special populations¹³.

Israel: from surveillance to action

The experience of Israel dealing with carbapenem-resistant *Enterobacteriaceae* illustrates how findings from surveillance efforts ultimately can lead to interventions that prevent and control the emergence of antibiotic-resistant bacteria. After the initial identification of KPC-producing *K. pneumoniae* in isolates from Tel-Aviv hospitals in 2005, a nationwide outbreak was documented in 2006. Detailed molecular characterization revealed that the outbreak was caused by the a clone of KPC-3 producing *K. pneumoniae* related to the international strain identified by multilocus sequence typing (MLST) as sequence type (ST) 258¹⁴. In 2007, the Israel Ministry of Health initiated a nationwide intervention to respond to the threat that hyperepidemic, extensively drug-resistant *K. pneumoniae* posed to Israeli hospitals and its health care system. Data played a central role in informing and monitoring the success of the interventions at individual hospitals, which included carrier isolation, patient and staff cohorting, active search for cases, and standardized procedures for microbiologic detection. Coordination and tracking of the response depended on a national network of communications that facilitated reporting and data-sharing, as well as on-site examinations of procedures at healthcare facilities. These actions achieved a 10-fold reduction in the transmission of carbapenem-resistant *Enterobacteriaceae* in the acute care setting¹⁵.

This nationwide intervention also included post-acute care facilities, recognized as an important reservoir of antibiotic-resistant bacteria, where enhancement of infection control measures led to a reduction in the prevalence of CRE¹⁶. Ongoing molecular characterization in post-acute care facilities confirms the predominance of ST258 KPC-producing *K. pneumoniae*, and has permitted the detection of other mechanisms of carbapenem resistance, namely OXA-48 and New Delhi Metallo-beta-lactamase (NDM-1), imported from neighboring countries in the Middle East¹⁷. Surveillance activities extended into the community have led to the exclusion of transmission in that setting¹⁵. The Israeli experience is a prime example of the effective translation of research into public health objectives that has improved the safety of hospitalized patients in that country.

United States: regional surveillance efforts take center stage

Since 2005, the United States Centers for Disease Control and Prevention (U. S. CDC) established the National Healthcare Safety Network (NHSN) as a system to track healthcare associated infection. NHSN now encompasses more than 13,000 hospitals and healthcare facilities. The most recent report from 2008–2013 describes significant reductions in central line-associated blood stream infections and surgical site infections, progress in methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections, and increases in catheter associated urinary tract infection¹⁸. Examination of trends locally and nationally, and point prevalence surveys, are useful to measure progress and to identify areas of concern that merit attention¹⁰. Comparison of point prevalence studies of healthcare associated infections from Europe and the U. S. highlights the challenge posed by *C. difficile* infections to patient safety in the U. S. (Table 2).

Surveillance of antibiotic resistance among bacteria causing HAIs through NHSN also describes increasing multidrug resistance and carbapenem resistance in Gram-negative

bacteria from a large proportion of facilities¹⁹. A more detailed assessment of the status of carbapenem-resistant *Enterobacteriaceae* infections in the U. S. as of 2012, was possible by supplementing information derived from NSHN with data collected through the multi-site resistant Gram-negative bacilli surveillance initiative (MuGSI), a population-based surveillance project conducted by the U. S. CDC's Emerging Infections Program (EIP), and from The Surveillance Network (TSN), an electronic surveillance database of antibiotic resistance encompassing several hundred microbiology laboratories across the country^{20, 21}. Approximately 4% of hospitals reported infections due to carbapenem-resistant *Enterobacteriaceae* and as many as 18% of long-term acute care hospitals (LTACHs). The proportion of *Klebsiella* sp. resistant to carbapenems averaged 10%, occurring mostly in patients with substantial health-care exposures²². These findings served to increase awareness and have motivated public health action to counter the dissemination of CRE in U. S. healthcare facilities²³.

Important efforts to advance surveillance of CRE and other antibiotic-resistant bacteria in the U. S. have occurred at the regional level. Statewide networks for the detection of CRE have been established in Oregon, Minnesota, Maryland and Michigan^{24–27}. In Northeast Ohio, a regional network examined the microbiological and genetic determinants of clinical outcomes in hospitalized patients with carbapenem-resistant *K. pneumoniae*; two subtypes were identified within the predominant ST258, which correspond to clades I and II, as determined by genomic analyses^{28, 29}. In the region around Chicago, Illinois, a multidrug-resistant organism surveillance network involving 25 short-stay acute care hospitals and seven LTACHs served to carry out a single-day prevalence survey demonstrating CRE in 30% of patients from LTACHs, and only in 3% of patients from acute care hospitals³⁰.

The impact of the CRE epidemic in U. S. community hospitals is revealed by data from 25 hospitals in North Carolina, South Carolina, Virginia, and Georgia that are members of the Duke Infection Control Outreach Network (DICON). The rate of CRE detection, albeit low, increased more than fivefold from 2008 (0.26 cases per 100,000 patient-days) to 2012 (1.4 cases per 100,000 patient-days). However, detection in this setting is probably hampered by slow adoption of standard microbiologic methods of CRE detection^{31, 32}.

ARMoR program: a model from the U. S. Department of Defense

The Antimicrobial Resistance Monitoring and Research (ARMoR) program was established by the U. S. Department of Defense in 2009 as a comprehensive surveillance program including the participation of epidemiologists, bioinformaticists, microbiologists, and healthcare providers. It features centralized data gathering, taking advantage of the existing electronic medical record, as well as detailed molecular characterization of multidrug resistant organisms in a central laboratory. A fundamental aspect of the ARMoR program is the transmission of laboratory and surveillance data back to participating hospitals through periodic reports on target bacteria. Similarly, these reports are communicated to leaders and policy makers within the healthcare facilities and the organization. Although it is challenging to establish a causal effect, there has been a significant decrease in the prevalence of carbapenem-resistant *Enterobacteriaceae* after the implementation of the ARMoR program. Indeed, this program serves as a model for comprehensive programs to

combat antimicrobial resistance, to be adopted by other healthcare organizations in the U. S.³³

A national plan to strengthen surveillance

Recently, the President of the U. S. issued the National Action Plan for Combating Antibiotic-Resistant Bacteria, which features the strengthening of surveillance as a fundamental component. The plan contemplates routine reporting of antibiotic use and resistance data to NHSN by most U. S. hospitals, as well as monitoring of antibiotic use and resistance along the continuum of food production, from farms to processing plants to supermarkets. The National Action Plan also calls for the creation of a regional public health laboratory network offering genetic characterization of antibiotic resistant bacteria.

A “One-Health” approach, where the health of humans is recognized to depend on the wellbeing of animals and the conservation of the environment, is emphasized throughout the plan.³⁴ Therefore, one of the goals is to integrate data from the NHSN, EIP, and the National Antimicrobial Resistance Monitoring System for foodborne and enteric bacteria (NARMS), with data from the National Animal Health Monitoring System (NAHMS), the National Animal Health Laboratory Network (NAHLN), and the Veterinary Laboratory Investigation and Response Network (Vet-LIRN). An additional goal is to develop laboratory-based surveillance to detect and monitor antibiotic-resistance in key animal and human foodborne pathogens in collaboration with WHO and the World Organization for Animal Health.

Under-resourced countries: filling the gaps in surveillance

Important gaps in the surveillance of antibiotic-resistant bacteria are evident in developing countries. Ironically, it is often in these countries where the challenge posed by resistant bacteria is the greatest, threatening to erode the important contribution of antibiotics to the health of the population. A noteworthy example that illustrates the need and potential impact of surveillance systems in combating antibiotic resistance is provided by Viet Nam. In this Southeast Asian country with more than 90 million inhabitants, Gram-negative bacteria reach high levels of resistance (40% of ESBL-producing *Enterobacteriaceae* among hospitalized patients; presence of NDM-1 in patients and the hospital environment; and high carbapenem resistance rates in *P. aeruginosa* and *A. baumannii*). This is likely due to limited infection control and diagnostic capabilities, and to widespread overuse and misuse of antibiotics³⁵.

To respond to this challenge, an ambitious program is underway that aims to strengthen the country’s ability to implement infection control and antimicrobial stewardship programs. The Ministry of Health of Viet Nam has committed to build a surveillance program to monitor hospital antibiotic use and resistance, community antibiotic use and resistance, and antibiotic use and resistance in animals, and to provide a reference laboratory and quality assurance mechanisms for local microbiology laboratories³⁵. Additionally, Viet Nam Resistance (VINARES) is being implemented as a capacity-building initiative designed to equip sixteen hospitals with the tools to perform self-sufficient antibiotic surveillance and carry out antimicrobial stewardship. Hospitals submit monthly data on antibiotic consumption, infection control surveillance, and susceptibility of bacterial pathogens (using

WHONET); hospitals receive regular reports, which compare their performance to that of other hospitals³⁶. These objectives and framework are eminently transferable to other developing countries, and compatible with resolution 67.25 from the World Health Assembly that urged countries, especially low- and middle-income countries, to develop capacity to combat antimicrobial resistance through strengthened surveillance and laboratory capacity³⁷.

Indeed, they resonate with a surveillance initiative undertaken in Colombia, a middle-income country in South America. Since 2003, the Centro Internacional de Entrenamiento e Investigaciones Médicas (CIDEIM) developed a surveillance project that now comprises 23 hospitals in 10 cities, with the objective of tracking antibiotic resistance among Gram-negative bacteria. In the most recent four-year period, a total of 38,048 bacterial isolates were analyzed using WHONET, demonstrating increasing trends in the proportion of multidrug-resistant bacteria. Detailed molecular characterization of resistance determinants and strain typing of carbapenem-resistant organisms was carried out in a central laboratory, revealing in the case of carbapenem-resistant *K. pneumoniae*, the coexistence of KPC-producing and VIM (Verona integron-encoded metallo-beta-lactamase)-producing isolates³⁸. Feedback on their respective data on antibiotic resistance, molecular mechanisms and strain typing is transmitted to participating hospitals. These reports, in turn, help inform infection control and antimicrobial stewardship actions at the local level. Additionally, they provide insight into the molecular epidemiology of antibiotic-resistant Gram-negative bacteria in Colombia, and permit comparisons to be drawn at the continental and global levels^{39–41}.

Conclusion: challenges and opportunities in surveillance

This review highlights models of surveillance for antibiotic-resistant bacteria around the world (Table 3). Notwithstanding their current limitations, these surveillance schemes remain an essential complement to better diagnostics, potential vaccines, and novel antibiotics active against resistant bacteria. Furthermore, the analysis of bacterial isolates through surveillance projects yields important insights into the transmission dynamics and mechanistic underpinnings of resistance. The threat posed by the emergence and dissemination of antibiotic-resistant bacteria demands the strengthening of current regional, national and global surveillance systems.

The impact of surveillance can be improved by incorporating data on antimicrobial use and antibiotic resistance, as well as data from different components of healthcare. A “One-Health” approach, integrating multiple disciplines working locally, nationally, and globally to improve the health of people, animals, and the environment is a paradigm very well suited to surveillance schemes. Existing surveillance systems are very limited in this regard. Another crucial shortcoming of antimicrobial resistance surveillance is that data are consigned in one-time or annual reports, and do not reflect an up to date assessment of antibiotic consumption and resistance. ARTEMIS (Antimicrobial Resistance Trend Monitoring System), a pilot network of 7 European health care institutions sharing data about drug resistance and consumption using a Semantic Web-based model, provides an example of how this problem can be overcome. Queries obtained within a few seconds provide real-time information about antimicrobial resistance that is accurate, comparable to

data from EARS-Net. This or similar platforms can serve as the backbone of future multisite and multinational surveillance networks that allow rapid detection of emerging resistance to antibiotics, and guide immediate infection control and public health actions⁴². Also harnessing the power of bioinformatics, an alternative approach to monitor trends in antibiotic resistance proposes the use of automated semantic and scientometric analysis of PubMed entries. When the relationship between the introduction of novel antibiotic classes into the market and emergence of bacterial resistance was investigated, and compared with data from EARS-Net, only a partial correlation was observed between scientometric analysis and development of resistance. Nevertheless, insight was gained about the public health importance of certain resistance mechanisms⁴³.

The application of genomic tools to the characterization of antibiotic resistance determinants and strains also promise to enhance surveillance. In this regard, the outbreak of carbapenem-resistant *K. pneumoniae* that occurred in 2011 at the U.S. National Institutes of Health Clinical Center provides an illustrative example. Whole-genome sequencing gave insight into the reasons why the epidemic progressed despite initial infection control measures, by revealing unexpected transmission routes⁴⁴. In another analysis, long-read genome sequencing with full end-to-end assembly revealed that carbapenem resistance genes are located on a wide array of plasmids, with evidence of horizontal gene transfer between bacteria in the hospital environment⁴⁵.

The integrated surveillance of antibiotic resistance, thus enhanced by genomics and bioinformatics, promises to overcome some of the obstacles we encounter in understanding the emergence of resistance, and to yield more “precise” approaches to prevention, diagnostics, screening, and treatments that may preserve the benefits of antibiotics to individual patients and to society⁵.

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Conflicts of interest

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Key points

- Bacterial resistance to antibiotics is a major global health threat. Systematic, comprehensive surveillance is essential to determine the magnitude of the problem, and inform local, regional, national and global interventions to address the challenge of resistance.
- The framework of antibiotic-resistance surveillance needs to be adjusted to meet the mission and capacity of supranational, national and regional public health agencies, the resources of healthcare facilities from wealthy and emerging economies, and the objectives of researchers and healthcare providers.
- Advances in bioinformatics and genomics will render surveillance of bacterial resistance to antibiotics more effective at preventing and controlling infections, revealing insights into the underpinnings of antibiotic resistance, and improving the outcomes of patients.

Table 1

Bacteria – antibiotic resistance combinations included in the WHO Antimicrobial Resistance Report on Surveillance, 2014 (4).

Bacteria	Resistance/decreased susceptibility to:	Number of countries providing data (N=194)	Range of reported resistance:
<i>Escherichia coli</i>	3 rd generation cephalosporins	84	0 – 82
	Fluoroquinolones	90	3 – 96
<i>Klebsiellapneumoniae</i>	3 rd generation cephalosporins	85	2 – 82
	Carbapenems	69	0 – 68
<i>Staphylococcus aureus</i>	Methicillin (i.e MRSA)	83	0.3 – 90
<i>Streptococcus pneumoniae</i>	Penicillin	66	0 – 73
Nontyphoideal <i>Salmonella</i>	Fluoroquinolones	66	0 – 96
<i>Shigella</i> species	Fluoroquinolones	34	0 – 47
<i>Neisseria gonorrhoeae</i>	3 rd generation cephalosporins	42	0 – 36

Table 2

Organisms isolated in select hospital acquired infections in point prevalence studies carried by the European Healthcare-acquired Infections Network (HAI-Net) and the U. S. National Healthcare Safety Network (NHSN)(9, 10).

		All HAIs, Number	All HAIs, %	Rank	Pneumonia/lower respiratory tract, %	Surgical site infections, %	Urinary tract infections, %	Bloodstream infections, %	Gastrointestinal tract infections, %
Number of HAIs, all	HAI-Net	15000	100		23.4 (n=3516)	19.6 (n=2941)	19 (n=2848)	10.6 (n=1585)	7.6 (n=1134)
	NHSN	504	100		21.8 (n=110)	21.8 (n=110)	12.9 (n=65)	9.9 (n=50)	17.1 (n=86)
<i>Clostridium difficile</i>	HAI-Net	548	5.4	8	0	0.1	0	0	61.3
	NHSN	61	12.1	1	0	0	0	0	70.9
<i>Staphylococcus aureus</i>	HAI-Net	1243	12.3	2	12.6	17.9	1.8	15.9	0.8
	NHSN	54	10.7	2	16.4	15.5	3.1	14	1.2
<i>Coagulase-neg. staphylococci</i>	HAI-Net	752	7.5	6	1.7	9.6	1.4	18.5	1.7
	NHSN	24	4.8	9	0	6.4	1.5	18	0
<i>Enterococcus spp.</i>	HAI-Net	969	9.6	3	2.2	14.5	12.5	8.2	7.5
	NHSN	44	8.7	5	1.8	14.5	16.9	12	5.8
<i>Streptococcus spp.</i>	HAI-Net	246	2.4	12	2.7	3.6	0.7	2.8	1.0
	NHSN	25	5	8	6.4	7.3	3.1	4	2.3
<i>Citrobacter spp.</i>	HAI-Net	91	0.9	15	0.8	1.1	1.4	0.4	0.6
	NHSN	6	1.2	15	1.8	0.9	1.5	0	0
<i>Enterobacter spp.</i>	HAI-Net	422	4.2	9	5.0	5.4	3.9	3.4	2.2
	NHSN	16	3.2	10	2.7	4.5	3.1	4	0
<i>Escherichia coli</i>	HAI-Net	1601	15.9	1	8.8	14.0	36.2	11.0	5.6
	NHSN	47	9.3	4	2.7	12.7	27.7	10	1.2
<i>Klebsiella spp.</i>	HAI-Net	872	8.7	5	11.4	6.0	12.0	9.8	3.9
	NHSN	50	9.9	3	11.8	13.6	23.1	8	1.2
<i>Proteus spp.</i>	HAI-Net	380	3.8	10	2.4	3.6	7.9	2.0	0.3
	NHSN	8	1.6	11	0.9	4.5	1.5	0	0
<i>Serratia spp.</i>	HAI-Net	115	1.1	13	2.6	0.7	0.6	1.6	0.3
	NHSN	6	1.2	15	1.8	0	3.1	0	0
<i>Acinetobacter spp.</i>	HAI-Net	366	3.6	11	8.7	2.9	1.5	4.1	0.3
	NHSN	8	1.2	11	3.6	1.8	0	0	0
<i>Pseudomonas aeruginosa</i>	HAI-Net	901	8.9	4	17.4	7.6	8.4	6.1	2.5
	NHSN	36	7.1	6	12.7	6.4	10.8	4	1.2
<i>Stenotrophomonas maltophilia</i>	HAI-Net	100	1.0	14	3.2	0.6	0.0	1.0	0.6
	NHSN	8	1.6	11	5.5	0	3.1	0	0
<i>Candida spp.</i>	HAI-Net	610	6.1	7	7.8	3.9	6.2	7.4	4.3
	NHSN	32	6.3	7	3.6	2.7	4.6	22	3.5

Table 3

Features of Selected Surveillance Programs for Antibiotic-Resistant Bacteria

Name of program	Sponsoring institution	Description
WHO Antimicrobial Resistance Surveillance	World Health Organization	Information about nine bacteria-antibiotic combinations from 114 countries. Most of the data reported from the Regions of the Americas and Europe.
EARS-Net (European Antimicrobial Resistance Surveillance Network)	European Centre for Disease Prevention and Control (ECDC)	European-wide network of national laboratory-based surveillance systems reporting on seven bacterial pathogens. Yearly reports and interactive database with tables, graphs and maps.
ESAC-Net (European Surveillance of Antimicrobial Consumption Network)	ECDC	Europe-wide network providing data on antimicrobial consumption in the community and in hospitals. Yearly reports and interactive database with maps, graphs and tables.
HAI-Net (Healthcare-associated Infection Surveillance Network)	ECDC	European-wide network coordinating point-prevalence survey of surgical site infections, hospital acquired infections, and antimicrobial use in acute care hospitals (including intensive care) and long-term care facilities.
ARPEC (Antibiotic Resistance and Prescribing in European Children)	European Commission, Executive Agency for Health and Consumers, ECDC	Data on antibiotic prescribing in primary care and hospitals, and resistant bacteria; compilation of antibiotic prescribing guidelines for children in Europe.
NHSN (National Healthcare Safety Network)	U. S. Centers for Disease Control and Prevention (U. S. CDC)	Healthcare infection tracking system of the U. S. Identifies problems by facility, states and nationwide. Serves as benchmark of infection control. Annual reports on device associated infections and regular antibiotic resistance reports (last in 2013).
EIP (Emerging Infections Program)	U. S. CDC	Network of 10 state health departments and local collaborators. Conducts active population based laboratory surveillance for: 1) invasive bacterial disease such as pneumococcus and meningococcus (ABCs); 2) to monitor the incidence of foodborne diseases (FoodNet); and 3) healthcare associated infections (HAIC).
NARMS (National Antimicrobial Resistance Monitoring System)	U. S. CDC, U. S. Food and Drug Administration and U. S. Department of Agriculture	Interagency partnership providing nationwide human surveillance of antibiotic resistance in foodborne and enteric bacteria (Campylobacter, Salmonella, Shigella, Escherichia coli O157). Yearly reports.
ARMoR (Antimicrobial Resistance Monitoring and Research)	U. S. Department of Defense	Network of epidemiologists, microbiologists, infection control and information technology specialists within Department of Defense healthcare system. Collects antibiotic resistance data, conducts molecular characterization of bacteria, and implements infection control.
VINARES (Viet Nam Resistance)	Oxford University Clinical Research Unit, Viet Nam	Sixteen participating hospitals from Viet Nam. Data on healthcare associated infections (PPS), antibiotic consumption, treatment guidelines, surveillance database (WHONET), reference laboratory and quality assurance.