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THE LABYRINTH

Indiana State Department of Health Laboratories Newsletter

Influenza: an Ancient Enemy Emerging on a New Battlefield

By Nicolas Epie, Ph.D., Division Director of Virology and Serology

"Influenza," originating from the Italian word *influentia*, was so named because people once believed the waves of sudden and widespread illness could only be influenced by the moon, planets and stars [1]. We now know, however, that such illness results from a highly-communicable viral infection. Plaguing humans for centuries, influenza contributes substantially to global rates of morbidity and mortality, especially among elderly, children and immuno-compromised persons [2]. Called "La Grippe" by the French because it grasped and hooked into those infected, the 1918 Spanish flu pandemic alone, was estimated to have killed more American soldiers than those actually lost in battle during World War I [3]. We are now, though, waging a new war with this timeless foe but on a genetic-level battlefield: the emergence of antiviral resistance. Scientific data gathered from antibiotics and antifungal usage in hospitals and clinics already provided predictions regarding the occurrence of resistant viral strains resulting from the use of antiviral agents [4,5]. Unfortunately, the existence of antiviral-resistant influenza virus strains should not come as a surprise to clinical scientists, nurses or physicians [6,7].

Prior to the discovery of influenza antivirals, seasonal and pandemic influenza was mainly managed in infected patients by preventing bacterial coinfections with antibiotics, administration of oral fluids to prevent electrolytes loss, and by controlling fever [8,9]. By providing this symptomatic support, the hope was that the patient's immune system would and could effectively clear the infection. History has proven this not always to be the outcome. Fortunately, as scientists' understanding on the molecular interactions and important processes necessary to complete the viral life cycle in cells has developed, small molecules that could inhibit these viral processes were identified and tested in laboratories. It is from this understanding of these processes of influenza virus replication that the first antivirals for influenza were discovered.

Influenza virus implicated in routine human respiratory infection, is a negative-sensed virus with 8 segments; "negative-sensed", meaning human ribosomes cannot translate this viral RNA to make viral proteins, therefore making influenza naked virus, noninfectious. Segments 1, 2, and 3 encode three components of the viral polymerase, PB2, PB1, and PBA respectively; segments 4, 5, and 6 encode hemagglutinin surface protein (HA), Nucleocapsid protein (NP), and Neuraminidase (NA), respectively. The 7th segment encodes the matrix ion channel (M2) and matrix protein (M1). The nuclear export protein (NEP) is encoded on the last segment, No. 8. To date, only the neuraminidase and the ion channel M2 viral proteins have proven to be effective antiviral targets for influenza A and B.

There are two classes of antiviral agents approved for the treatment of influenza, categorized by their mechanisms of actions [10]. In one class, the antivirals inhibit acidification of the host cell endosomes by blocking the M2 ion channels protein and therefore prevent uncoating of influenza within the infected cells. This prevents the ability of the influenza genome from being transported to the cell's nucleus, where it is transcribed by its own viral RNA polymerase. This class of antivirals include Amantadine and

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Our Mission:

The Indiana State Department of Health Laboratories partners with other public health agencies to provide timely and accurate information needed for surveillance and outbreak investigations to protect and improve Hoosier health.

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Rimantadine. The second class of anti-influenza drugs includes Oseltamivir and Zanamivir, which prevent newly-assembled influenza virions from being released out of the infected host cells. They do this by inhibiting NA enzymatic action at the cell membranes and therefore, preventing new cells from becoming infected [11]. Since the mechanism of action of these two classes of antivirals is by viral protein interaction, their effectiveness is affected by replacement of amino acids resulting from genetic mutations of the viral genomic RNA. Any random mutations encoding amino acids, which are part of the drug active binding site, may confer resistance to the influenza strain by preventing binding of the antiviral agent.

Multiple point nucleotide mutations within the NA gene on the 6th segment have been identified which substitute amino acids on the NA enzyme, affecting the binding to Oseltamivir (Tamiflu). [12,13]. These mutations can be detected via primer-specific RT-PCR or by partial/whole viral genome sequencing of the segment where the mutations have been discovered to date. Since only Oseltamivir is affected by mutations on the neuraminidase gene, the M2 inhibitor class of anti-Influenza agents are not affected by any mutations found on NA.

The Indiana State Department of Health Laboratories (ISDHL) has the potential to perform antiviral testing using RT-PCR on the ABI 7500 with Sanger capillary sequencing using the ABI 3500, or through Next Generation Sequencing (NGS) using the Illumina Miseq pyrosequencing method. However, we presently perform only partial pyrosequencing of the NA gene using a CDC-developed method on the QIAGEN ProMark Q24 pyrosequencer. Once such sequencing is completed, the sequences are compared to strain sequences identified by the CDC, as conferring Oseltamivir resistance. Some influenza virus types with genetic changes will have on their surface neuraminidase proteins that are no longer recognized by oselta-mivir.

FIG 1. Prevention is always better than cure. You should contact your doctor and find out how you can get the flu vaccine this flu season. The above picture is taken from the CDC Public Health Image Library website (https://phil.cdc.gov/Details.aspx?pid=14221)

This ISDHL antiviral-resistance testing method initiates with influenza RNA being reverse-transcribed and then amplification PCR using NA-specific primers. Subsequently, the amplified fragment of the NA gene is sequenced on the QIAGEN Pro-MarkTM Q24 pyrosequencer. This pyrosequencing method uses the detection of pyrophosphate released from the synthesis reaction to determine nucleotide incorporation. The detection of a given position in a sequence occurs from a luciferase-generated signal from a reaction with processed pyrophosphate byproduct of nucleotide. This nucleotide incorporates into a growing chain and a substrate (Luciferin).

Antiviral susceptibility testing by sequencing of genetic markers provides valuable information to clinicians and epidemiologists in order to make the right choice in delivering patient care and investigating outbreaks. This is especially important when confronted with high risk patients for whom influenza infections may be life threatening. Presently, we only test for mutations on the NA gene; nevertheless, as advanced molecular methods become affordable to public health laboratories throughout the nation, these additional methods will be able to provide the entire genome sequence of a given influenza strain. NGSis now available at ISDHL and we hope to expand current use to include sequencing of viral genomes, such as influenza and Hepatitis C Virus. This will be in an attempt to provide to physicians and epidemiology, complete genomic information, and possibly predict the effectiveness of a given antiviral agent in circulation.

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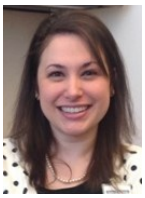
Introducing the Antibiotic Resistance Laboratory Network (ARLN)



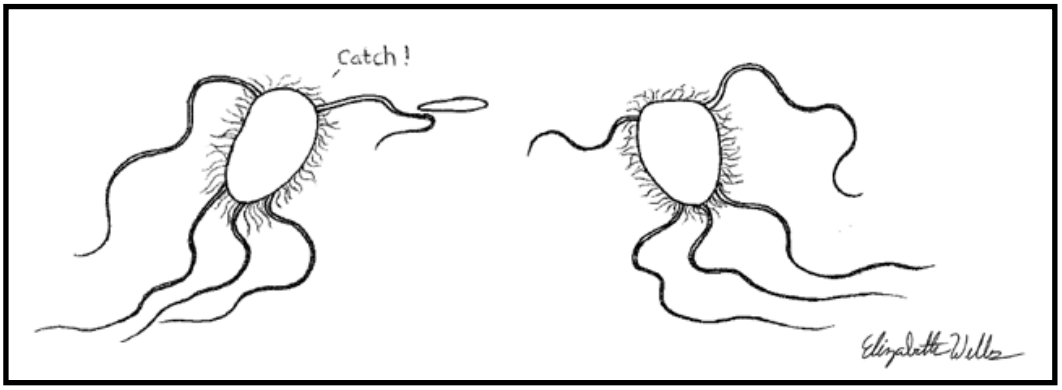
By Sara Blosser, Ph.D., Director of Clinical Microbiology, D (ABMM)

You're working the AST bench in your hospital's laboratory and you see a *Klebsiella pneumoniae* isolate from a blood culture that is resistant to ertapenem, imipenem and doripenem. Not as unusual these days as they once were, but *how* is that isolate resistant to the carbapenems?

Organisms that belong to the *Enterobacteriaceae*, a family of Gram-negative organisms that include *K. pneumoniae*, can become resistant to carbapenem antibiotics by several mechanisms. I like to think about these in two "buckets." First, the "*this is pretty bad for the patient"* bucket, and second, the "*this is bad for the patient – and every other patient in that hospital"* bucket.

In that first bucket, the one that is primarily bad for the patient, are chromosomally-mediated mechanisms of resistance. Thinking back to high school biology, chromosomes are the DNA-structures that encode the specific genetic instructions for the functioning of an organism. Chromosomes are an essential component of an organisms' genetic makeup, and not easily discarded. On the antibiotic resistance front, chromosomal mechanisms of resistance, such as AmpC production, are hard-wired into the organism's DNA – they're not going anywhere that the organism doesn't go itself.

In the second bucket, the one that really keeps me up at night, are the plasmid-mediated mechanisms of resistance. Plasmids are something we see frequently in bacteria, and bacteria are pretty smart when it comes to plasmids. We know sex is useful for the exchange of genetic information. Well, bacteria don't have sex as often as eukaryotes, so they have adapted another mechanism for genetic information exchange: plasmids. Think of them like a Frisbee. They are circular pieces of DNA that can be flung from bacteria-to-bacteria, or from bacteria-to-the-environment-to-bacteria. Put a gene that confers resistance to carbapenems on that Frisbee and you have enhanced potential for the spread of that resistance mechanism!

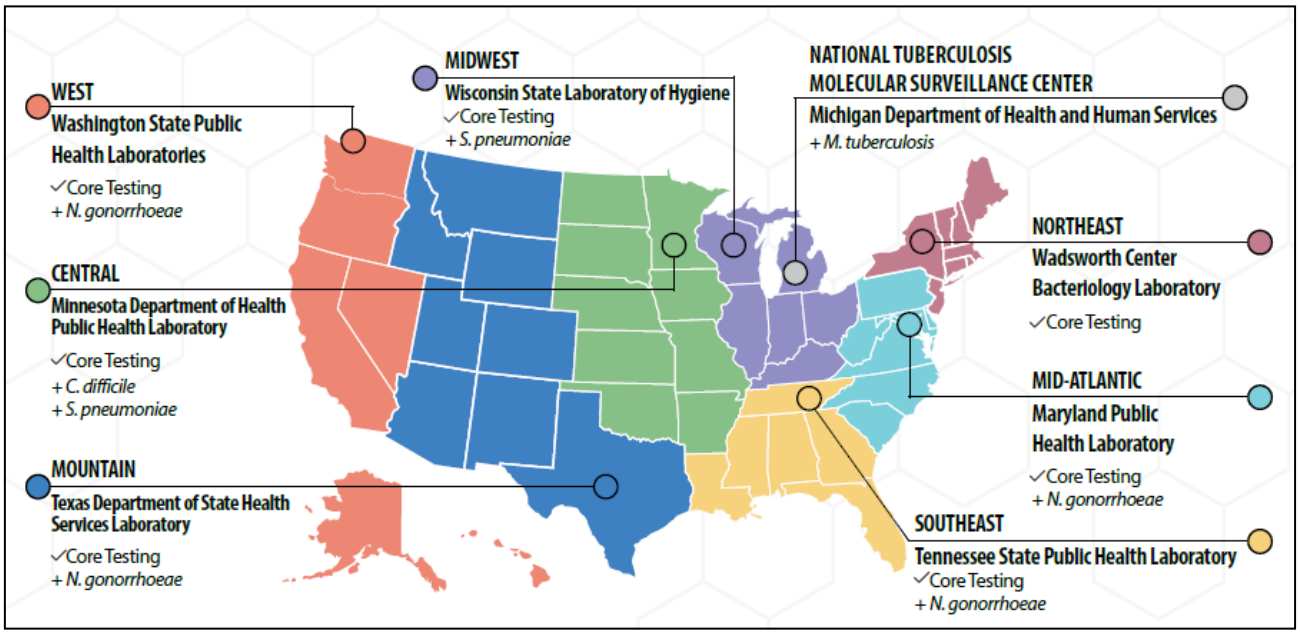


Carbapenemase genes are usually found on plasmids, which can be transferred from one bacterial cell to another.

This second category, the plasmid-mediated mechanisms of carbapenem resistance, is the focus of the ISDH Laboratories' (ISDHL) Antimicrobial Resistance program. ISDHL primarily focuses on carbapenemases, which can chew up or degrade carbapenem antibiotics. Our goal at ISDHL is to identify these mechanisms quickly, so that patients can be treated most effectively and to prevent the spread of these mechanisms within a facility. At ISDHL, we have been identifying organisms with these mechanisms, called Carbapenemase Producing-Carbapenem Resistant Enterobacteriaceae (CP-CRE), since 2013.

In 2016, the CDC established the Antibiotic Resistant Laboratory Network (ARLN), a network of 57 laboratories (all 50 states, six major cities, and Puerto Rico) to rapidly identify CP-CREs and other emerging mechanisms of antibiotic resistance. This network provides two main benefits: first, a unified approach in identifying isolates/mechanisms and second, a network for quicker results. As every state has different challenges and needs, the regional approach allows us to respond equally, no matter the geography of an outbreak.

When a new resistance threat or outbreak is detected within a healthcare facility, state or local laboratories first assess the issue. If the needs of the threat/outbreak exceed those resources, a regional laboratory or the CDC can be mobilized to characterize isolates, support the response, and track these discoveries. Here in Indiana, we network with the Midwest Regional laboratory, which is located in Madison, Wisconsin.



ARLN Regional Laboratories and National Tuberculosis Molecular Surveillance Center (from the https://www.cdc.gov/drugresistance/pdf/About-ARLN-Map.pdf).

So what types of testing are performed at ISDHL?

- Molecular testing for the five major carbapenemases seen in the USA: KPC, NDM-1, VIM, IMP, and OXA-48-like
- Phenotypic testing for novel carbapenemases
- Antimicrobial susceptibility testing for the carbapenems and colistin
- Molecular testing for *mcr-1*, a mobile mechanism of colistin resistance
- Confirmation of *Candida* speciation, to rule-out *Candida auris*

What types of testing are performed at the regional laboratory?

- Molecular colonization testing for CP-CREs
- Detection of new and emerging threats, such as Carbapenem Resistant *Acinetobacter baumanii* (CRAB)

Fungal susceptibilities for *Candida* species

What is Molecular Colonization Testing?

If an NDM, VIM, IMP, OXA-48-like or novel CP-CRE is discovered in Indiana, the CDC would likely recommend a limited point-prevalence survey be conducted. The purpose of this colonization survey is to assess close-contacts to the confirmed patient (sometimes called an 'index patient') in order to identify and limit the spread of these mechanisms of resistance.

In consultation with the ISDH, ISDHL, and the hospital infection preventionist (IP), the ARLN regional laboratory would ship swabs and transport medium to the facility, along with instructions for collection. While waiting for the swabs, the IP and an ISDH epidemiologist will develop a line list of potential transmission.

A line list is a table that summarizes information about individuals associated with an outbreak. Each individual is listed in a row on the table, and the information specific to that patient is sorted into columns. Information that is relevant to a CP-CRE line list includes patient identifiers, demographic or clinical information, risk factors, and any known laboratory results. A line list helps to clarify who was, and who was not, at highest risk of exposure to the index patient.

Once the swabs are received, the IP, or their designee, will collect a rectal swab from the close-contacts then ship the specimens to the regional laboratory for testing. Testing takes 1-2 days; however, the regional laboratory serves several other states so results may be delayed up to a week.

(Continued on next page)

"ARLN " (continued from page 5)

The regional laboratories use the Cepheid CarbaR® or laboratory-developed tests to identify specific mechanisms of resistance. As the organism or mechanism can vary widely, each of the regional laboratories has developed a flexible algorithm for dealing with colonization testing.

If no transmission has occurred, everyone can relax – but just a little. Contact precautions should remain in place for the duration of the index patient's stay and hand hygiene should always be practiced!

If transmission has occurred, a deeper dive into the potential spread of the organism/mechanism is warranted. More point prevalence or clinical testing will likely follow.

What can you do to support the ARLN?

The goals of the ARLN are to **Detect-Respond-Prevent**; the same goals as ISDH!

Detect: If you suspect you have an organism that meets the CP-CRE definition outlined in the Indiana Communicable Disease Rule, report the finding to IP and submit the isolate to ISDHL as soon as possible, or at least within three business days.

Not sure of how to identify suspect CP-CREs? Consider taking the ISDHL's CP-CRE Workshop, offered twice a year. The dates and times of these workshops will be announced via ISDH Lab Info several weeks in advance.

Respond: While ISDHL is testing your isolate, the IP should be placing that patient into contact precautions and initiating an investigation. Questions they should be asking include: Was the patient housed in a single room or did they have roommates? Did the patient have any invasive medical procedures performed in the past few months? Did the patient have any invasive devices at the time of specimen collection? What pre-existing conditions does the patient have? Has the patient traveled outside of the United States? The results of these questions help our ISDH epidemiologists provide the best advice on the care and management of the patient as well as to better understand the potential dynamics of a case.

Once the ISDHL results are back to your facility, ensure that they have been transmitted to the IP as well as the physician taking care of the patient. If the patient is positive for a CP-CRE, they should remain in contact precautions for the remainder of their stay (acute care and long-term acute care facilities). In a long-term care facility, the patient should remain in contact precautions as indicated by their functional and clinical status. The CDC's CRE Toolkit (https://www.cdc.gov/hai/pdfs/cre/CRE-guidance-508.pdf) is a great resource for these types of decisions.

Prevent: This is the hardest piece. Hand hygiene, we hear about it constantly, but it is one of the key pieces to preventing transmission within a facility. Wear appropriate PPE all the time. Consider implementing colonization screening within your facility. These organisms hide out in the GI tract; they can go undetected until they start to cause disease. With the high mortality rate (40-50% in invasive cases!) attributed to these organisms, prevention is our best defense. Knowing the colonization status of patients, and isolating appropriately, is the best way to prevent spread.

Interested in Doing More?

Consider submitting carbapenem-resistant Pseudomonas aeruginosa to the ISDHL for additional testing. Isolates should be from a clinical source, and resistant to imipenem, doripenem or meropenem with an MIC of ≥ 8 µg/mL.

Consider becoming an ESBL or Carbapenem-Resistant Acinetobacter baumanii pilot site. This site would work directly with the ARLN regional laboratory to establish a baseline surveillance program for certain mechanisms of resistance.

Consider becoming a CP-CRE Special Projects Pilot Site. We're looking for two sites to participate in a four-month pilot with ISDHL and the CDC.

Contact Dr. Sara Blosser, sblosser@isdh.in.gov or 317-921-5894 for more information on any of these opportunities.

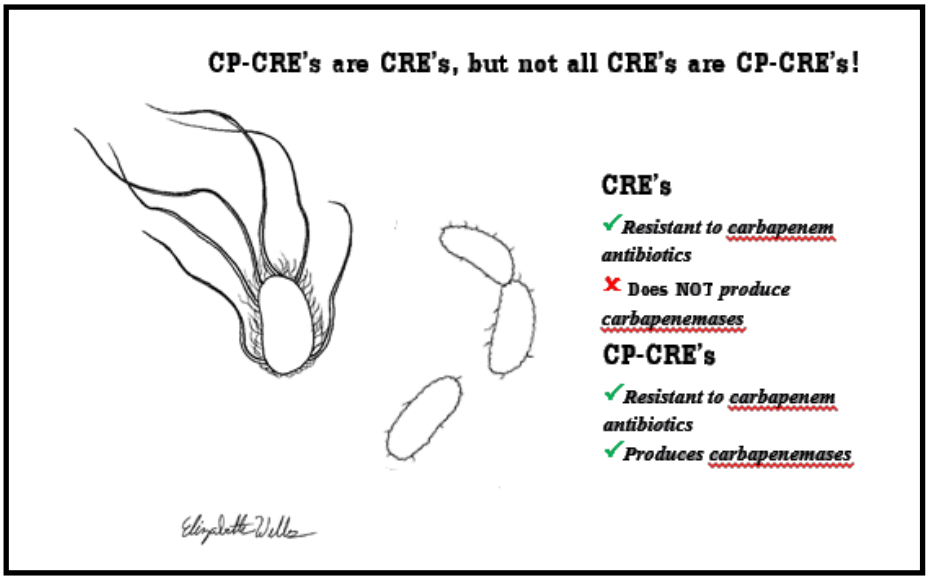
ISDH Laboratories Conducts CP-CRE Workshop for Indiana Labs

By Shelley Matheson

The Indiana State Department of Health (ISDH) Laboratories conducted "A Hands-on Workshop for Indiana Laboratories: Carbapenemase-producing Carbapenem-resistant Enterobacteriaceae (CP-CRE)" at ISDH Laboratories on September 8, 2017. Nine laboratorians were present from nine different Indiana hospitals. This workshop provided an overview of Carbapenemase-producing Carbapenem-resistant Enterobacteriaceae, as well as classification of organisms and current Indiana surveillance efforts. Upcoming Indiana Communicable Disease Rule changes and methods to screen for patient colonization were discussed. Laboratory exercises demonstrated the interpretation of the Modified Hodge Test (MHT), the modified carbapenem inactivation method (mCIM), the Metallo Beta Lactamase (MBL) E-test, and the CarbaNP test. Laboratories were provided with a CarbaNP kit to take back to their laboratories.

Dr. Sara Blosser, ISDH Laboratories Clinical Microbiology Division Director, described the difference between CRE and CP-CRE, as well as surveillance efforts surrounding CP-CRE in Indiana. In addition, she gave an overview of the CarbaNP test, as well as other methods for CP-CRE detection. With the assistance of Jon Radosevic (Supervisor, Reference Bacteriology) and Kelly Tippman (Microbiologist), the hands-on portion of the workshop was well-received. Participants were allowed to set up and read a Carba NP test, and interpret the MHT, MBL E-test and mCIM. In addition, Henry Fu, Applied Systems Analyst at ISDH Laboratories, described and demonstrated the use of LimsNet when submitting a specimen suspected of CP-CRE. A pre- and post-test were given to attendees to demonstrate a percent increase in learning. A 31% increase in learning was demonstrated.

Thus far, five CP-CRE trainings have been held at ISDH Laboratories since 2015, and the ISDH Outreach and Training Team plan to continue these trainings in 2018. During the five trainings already provided, more than sixty clinical laboratorians have been trained on how to properly test for and submit potential CP-CRE's. Information gathered from course evaluations indicated 100% of attendees either agree or strongly agree the training was well-structured and organized, hands-on exercises were plausible and realistic, presentations were helpful, the presenters were knowledgeable about the material, and participation was appropriate for those who attended. Comments received on course evaluations included "Dr. Blosser's knowledge is incredible! I wish I had recorded the presentation to bring home! Thank you so much!" Another one stated, "This training and the hands-on workshop was an invaluable experience."



NARMS
(National Antimicrobial Resistance Monitoring System)

By Ryan Gentry, M.S.

Two million people each year in the U.S. become infected with bacteria resistant to antibiotics. Over 400,000 of these infections are estimated to come from common foodborne pathogens, such as Salmonella and Campylobacter, according to a 2013 CDC report on antibiotic resistance threats. Antibiotics have been used for over 60 years to control infections and improve growth in food-producing animals. In 2011, the FDA reported that in the United States, more kilograms of antibiotics are sold for food-producing animals than for people. Any usage of antibiotics can lead to resistance, and resistant bacteria are more common in places where antibiotics are frequently used. Contamination of meat during slaughtering and processing can lead to you getting exposed to foodborne pathogens, some of which may be resistant to antibiotics. This is not the only route. Exposure to animal feces (directly or through contamination of irrigation water or soil) can spread resistant bacteria to fruits and vegetables you eat. So eating a vegetarian diet does not make you immune; anyone can become infected with antibiotic-resistant bacteria.

The good news is efforts to prevent foodborne and other enteric infections help to reduce both antibiotic-resistant infections and antibiotic-susceptible infections. Those infections by themselves cause 48 million illnesses, 128,000 hospitalizations, and, sadly, 3,000 deaths each year from eating contaminated food. Most enteric infections are self-limiting and antibiotics are only needed to treat severe cases. However, without antibiotics to treat these cases, the illnesses may be prolonged or become more severe, resulting in dire outcomes for the individual. By monitoring antibiotic resistance patterns in these bacteria, we can better understand their transmission and detect emerging trends of resistance to develop better prevention strategies.

Last year the National Antimicrobial Resistance Monitoring System, or NARMS, celebrated its 20th anniversary. I am willing to bet few outside of the public health community have ever heard of NARMS. Established in 1996, NARMS is a collaborative program of state and local public health departments and universities, the U.S. Food and Drug Administration (FDA), the Centers for Disease Control and Prevention (CDC), and the U.S. Department of Agriculture (USDA). Developed as a national public health system to track antibiotic resistance trends in enteric bacteria that are found in ill people, retail meats, and food-producing animals in the U.S, the system collects data from isolates of Salmonella, Campylobacter, and other bacteria transmitted commonly through food. Surveillance data from NARMS collaborators is used to combat antibiotic resistance through regulations, policies, and public health recommendations promoting antibiotic stewardship.

The aggregate human data collected by CDC NARMS is gathered from a network of state and local public health laboratories across the country that submit Salmonella, Campylobacter, Shigella, E. coli O157, and Vibrio (other than V. cholerae) isolates from clinical specimens from humans to CDC NARMS for antimicrobial susceptibility testing. The Indiana State Department of Health Laboratories (ISDHL) has contributed over a thousand isolates to the NARMS program since 2003 when the surveillance system was expanded to all fifty states. Funding from the CDC through the Epidemiology and Laboratory Capacity for Infectious Diseases (ELC) Cooperative Agreement helps support the cost of providing isolates. This funding is also essential in providing the next big leap for tracking antibiotic resistance trends: whole genome sequencing (WGS) of enteric bacteria. WGS provides faster more accurate detection of antimicrobial-resistant bacteria using the network of state and local public health laboratories participating in the CDC NARMS.

To lower your risk of becoming infected by an enteric bacteria resistant to antibiotics, you can follow the same food safety tips for avoiding foodborne illnesses in general:

CLEAN. Wash your hands and surfaces often.

SEPARATE. Don't cross-contaminate.

COOK. Cook to the right temperature.

CHILL. Keep your refrigerator below 40°F and refrigerate foods properly.

http://www.fightbac.org

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FDA NARMS www.fda.gov/AnimalVeterinary/SafetyHealth/AntimicrobialResistance/NationalAntimicrobialResistanceMonitoringSystem

CDC NARMS

www.cdc.gov/narms

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FDA Summary Report on Antimicrobials Sold or Distributed for Use in Food-Producing Animals, 2011.

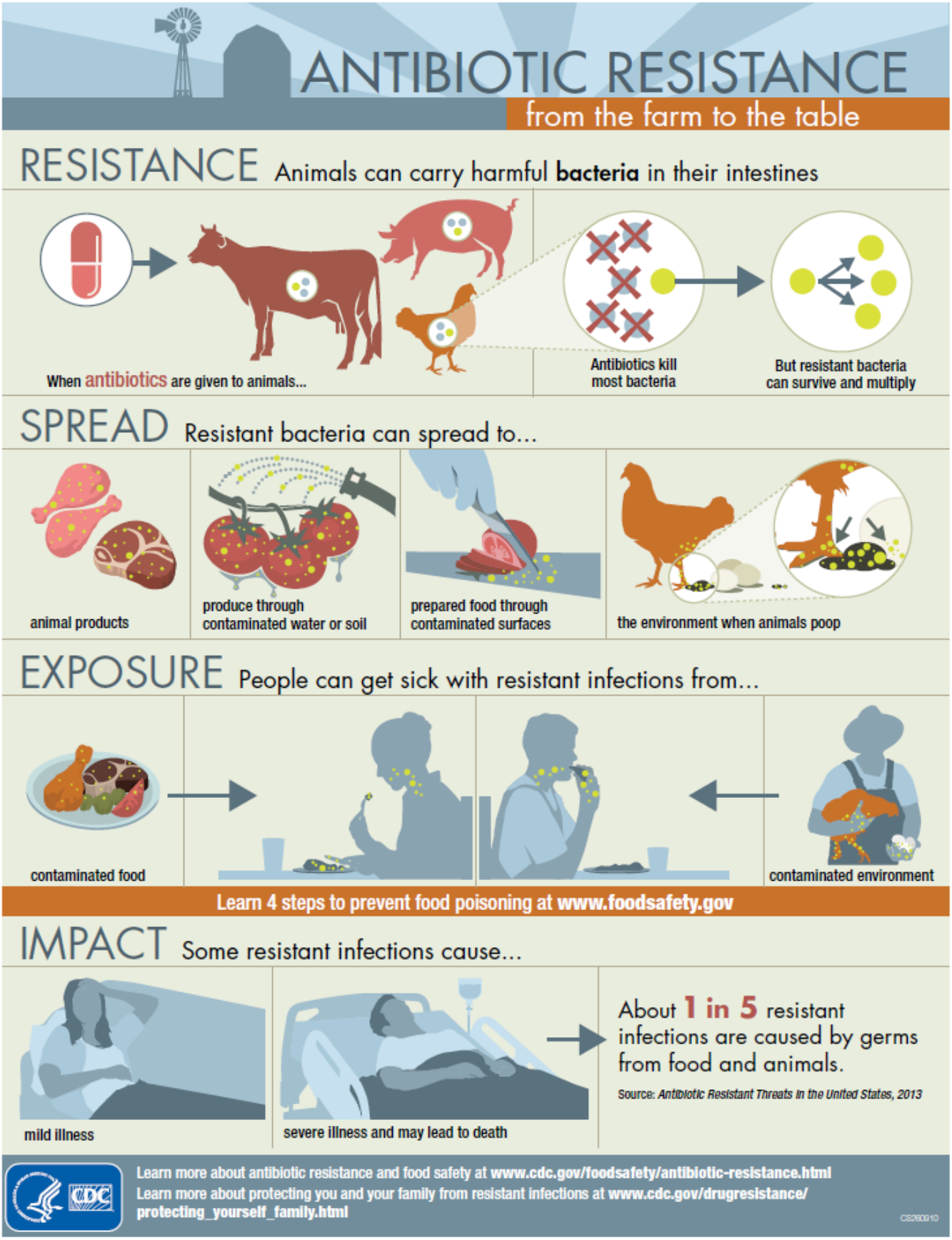
http://www.fda.gov/downloads/ForIndustry/UserFees/AnimalDrugUserFeeActADUFA/UCM338170.pdf

NARMS Now: Human Data

wwwn.cdc.gov/narmsnow/

CDC Food Safety

www.cdc.gov/foodsafety


ANTIBIOTIC RESISTANCE
from the farm to the table
RESISTANCE Animals can carry harmful bacteria in their intestines
When antibiotics are given to animals...
Antibiotics kill most bacteria
But resistant bacteria can survive and multiply
SPREAD Resistant bacteria can spread to...
animal products
produce through contaminated water or soil
prepared food through contaminated surfaces
the environment when animals poop
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contaminated environment
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IMPACT Some resistant infections cause...
mild illness
severe illness and may lead to death
About 1 in 5 resistant infections are caused by germs from food and animals.
Source: Antibiotic Resistant Threats in the United States, 2013
Learn more about antibiotic resistance and food safety at www.cdc.gov/foodsafety/antibiotic-resistance.html
Learn more about protecting you and your family from resistant infections at www.cdc.gov/drugresistance/protecting_yourself_family.html
CS260010

Employee Spotlight: Brian Pope

We at the ISDHL very proud of all of our staff members and want our readers to get to know some of our super-star staff! As interviewed by Dr. Nicolas Epie (NE), Division Director of Virology, we would like to introduce you to our Virology Supervisor, Brian Pope (BP):

NE: Please give a brief background of yourself.

BP: I am a native of Indiana, where I have lived all my life. I joined ISDHL in 2014 when I took a position as a Microbiologist II in the Virology and Biothreat Laboratory. In this position, I performed my job efficiently and gained the respect of both colleagues and my supervisors. The position also gave me the experience needed to succeed and excel as a public health scientist. I did not join the laboratory fresh out of college. Prior to taking the position at ISDHL, I held previous positions as research technician and biologist at Indiana University and Advanced Testing Laboratories, respectively, from 2009 to 2013.

NE: What are you doing now?

BP: I am the virology supervisor in the Virology Division of ISDHL. I supervise the laboratory responsible for clinical virology testing for the state of Indiana. The Virology Laboratory is responsible for testing influenza, other respiratory viruses, and other viral diseases caused by mosquitoes like Zika, Dengue and West Nile Virus. I also supervise the testing of herpes, measles, mumps and other viruses of public health importance. My laboratory uses both molecular methods such as Polymerase Chain Reaction (PCR) and nucleic acid sequencing, as well as viral isolation methods for clinical diagnostic testing of these viruses.

NE: Please give me some highlights of your job.

BP: I was a member of the team that tested for MERS-CoV in May 2014 (that was "May The 4th be with you" day in 2014!), followed by Enterovirus-D 68 in August 2014, and then Ebola testing (even spending late nights at the laboratory). During my time at ISDHL, I have seen a few influenza seasons, "turkey flu testing in southern Indiana, mumps outbreaks at local colleges and in the community, the Zika virus, biothreat odd cases and white powders, and then, the day-to-day testing or supervising and assisting with testing now-a-days. As each outbreak have come and passed, I have started to appreciate those negative results a lot more. Presently, I've become more and more adept at paperwork and I get to supervise a wonderful team who has fully allowed me to grow into a supervisor. I appreciate their help every day and feel lucky that I was able to have a supportive team, fellow coworkers, and senior management. Also … playing board games during lunch, when able.

NE: Can you tell what your future plans are?

BP: Long term? I enjoy the laboratory, so long as I'm able to perform or assist science in some manner or another; I'm happy. Short term? Just bought a house with Audrey, so … paying the mortgage and making sure the dog is as comfortable as possible. Otherwise, it's planning the next vacation. Anywhere I can go scuba diving is fine with me.

About The LAByrinth

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