AMD in Action

National Center for HIV/AIDs, Viral Hepatitis, STD and TB Prevention

FISCAL YEAR 2014

"Investments in AMD Will Transform How the U.S. Public Health System Detects and Responds to Diseases."

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Public health experts need the right tools at the right time to protect Americans from microbes that are growing more fierce and moving faster than ever among us. Advanced molecular detection (AMD) lets scientists see into microbes in ways and in detail that have never been visible before. CDC's AMD initiative is a major enhancement of CDC's current microbiology and bioinformatics capabilities to find and stop infectious disease outbreaks that threaten Americans every day.

Examples of the public health benefits of AMD include more precise and timely approaches to

- Diagnose known and emerging infections
- Detect and respond to outbreaks
- Understand and control antibiotic resistance
- Develop and target measures to protect people's health

CDC's National Center for HIV/AIDS, Hepatitis, STD and TB Prevention (NCHHSTP) is at the forefront of utilizing this new technology to transform our efforts at disease detection and response. This brochure contains some of our recent work in this exciting arena.

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Multistate Outbreak of Hepatitis A Infection Linked to Pomegranate Seeds from Turkey

In 2013, an outbreak of hepatitis A made 162 people in 10 states sick after they ate a berry blend product purchased at a national chain store.

CDC detected the outbreak on May 15. Scientists promptly applied genome sequencing and other advanced analytic methods to establish that not only were the infecting strains identical, but also belonged to an unusual hepatitis A virus genotype that is rare in the United States.

CDC completed its analysis within a week of receiving samples from the first 20 cases. This automated technology proved to be quicker, simpler and more sensitive than if the samples had been processed by previous methods. As the outbreak spread, other cases also were found to be infected by the same viral strain.

Advanced molecular detection helped CDC and the U.S. Food and Drug Administration (FDA) link this specific strain of the virus with the outbreak investigation data to identify quickly a shipment of pomegranate seeds from Turkey as the source of the outbreak. With this information FDA was able to identify the company selling the seeds and take action to ensure shipments were stopped until checked. FDA worked with pomegranate seed distributors to make sure all recipients were notified.

A public announcement about the risk related to the product was made on May 31. Local public health departments and the retail chain that sold the product vaccinated more than 10,000 people as a precaution in case someone had been exposed.

Advanced molecular detection methods helped stop this outbreak in its tracks in record time, better protecting the health of the public.

Detecting Hepatitis C

Using advanced molecular techniques for rapid identification of hepatitis C outbreaks

Hepatitis C virus is the most common chronic bloodborne infection in the United States. It causes a liver disease that can lead to serious, lifelong illness.

How do you spot an outbreak when a disease doesn't cause symptoms? This is the tough question facing Hepatitis C virus researchers.

Even though 2 to 3 million Americans and another 170 million people worldwide are infected with the virus, about 80% have no symptoms. That makes it hard to detect hepatitis C outbreaks. And without detection, the disease continues to spread.

Scientists at CDC are working hard on solutions to this problem. They have created a new way to find out if different patients are infected with the same strain of the hepatitis C virus. Using innovative experimental and analytical methods involving next generation sequencing, more accurate assays, and rapid data analysis, CDC's newly developed lab tests have the advantage of being faster, cheaper, and more accurate than ever before.

These new tools also help to link cases of hepatitis C together so that public health workers can quickly pinpoint where the infection first started and put a stop to the outbreak.

This new system will speed up the detection of hepatitis C virus outbreaks and help public health professionals quickly and more simply control them—a great example of how cutting edge technology is helping to protect our nation's health!
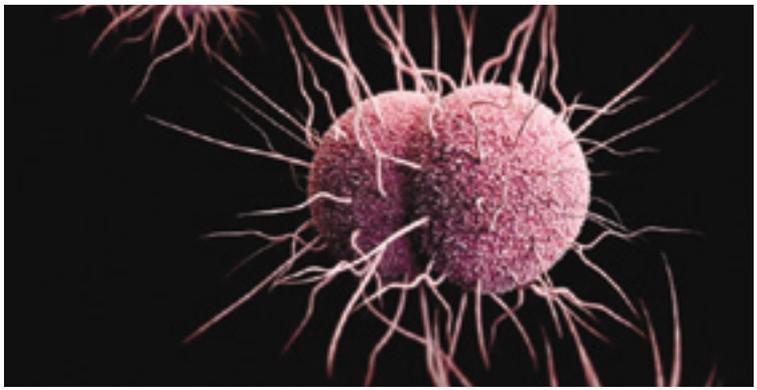
Treating the Antimicrobial-Resistant Gonorrhea Threat

Genomic sequencing of *Neisseria gonorrhoeae* to respond to the urgent threat of antimicrobial-resistant gonorrhea

Gonorrhea is increasingly resistant to the drugs prescribed to treat it, and few antibiotic options remain. Research can help unlock the potential to develop new drugs to treat gonorrhea and better tests to find out if a patient has a resistant infection.

Blindness in newborns, infertility in women, and severe scarring in the urinary tract of men—these were the outcomes of untreated gonorrhea before antibiotics revolutionized its treatment and cure.

More than 80 years ago, gonorrhea became easily treatable with a single dose of antibiotic. But over the past few decades, public health agencies have seen a growing number of gonorrhea cases that do not respond to the antibiotics that doctors traditionally have used to treat the disease. The threat of these drug-resistant strains is getting worse. If the last recommended treatment stops working, America could once again face the health problems of the early 20th century.

To fight this urgent public health threat, CDC is using the latest advances in genome sequencing techniques to unlock the DNA of the bacterium that causes gonorrhea. This information is critical to the development of new drugs to treat gonorrhea, as well as better tests to find out quickly if a patient's infection is resistant.

This cutting edge research will tell how the bacteria are changing and help scientists find better ways to prevent gonorrhea. Using these new approaches, CDC hopes to keep untreatable gonorrhea from becoming a reality.
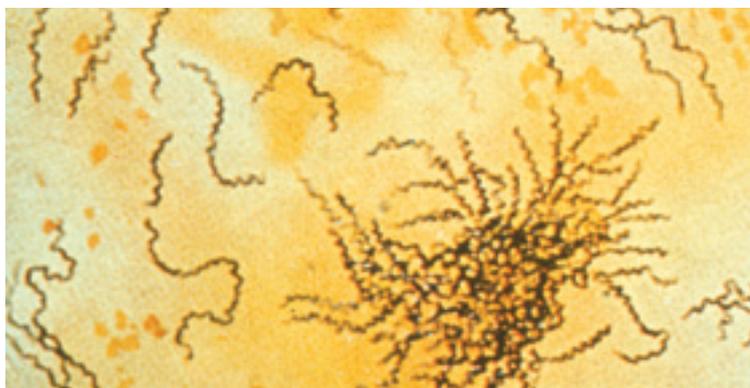
Tracking STD Transmission

Integrating data to understand better the transmission networks involved in the spread of infectious disease and drug resistance

Syphilis is one of many sexually transmitted diseases that can have very serious complications when left untreated.

HIV, other sexually transmitted diseases, hepatitis, and tuberculosis (TB) affect millions of people in the United States. These infections can be spread in many ways, including sexual contact, contact with bodily fluids of an infected person, and via air droplets. Even though scientists know that certain groups—such as gay and bisexual men and persons who inject drugs—are more likely to be affected, less is known about the connections between people that result in the spread of these infections. In addition, using epidemiological data alone may not always identify links between infected persons. Understanding these connections is critical to stopping the spread of disease.

CDC scientists are using genetic information (sequence data, including next generation sequencing) for the viruses and bacteria that cause these diseases, together with demographic, geographic, and clinical data from infected persons—such as risk group, age, location, and health status—to understand more about how infected people are connected. Combined, this information helps scientists to identify more precisely how these diseases are spreading so that outbreaks can be stopped.

These new tools help CDC characterize transmission networks more quickly and easily to better target rapid responses to stop the spread of infection.

By improving the tools that are currently available, CDC can learn how diseases are spreading. With this knowledge, scientists can focus additional prevention tools to help protect health and reduce infections.
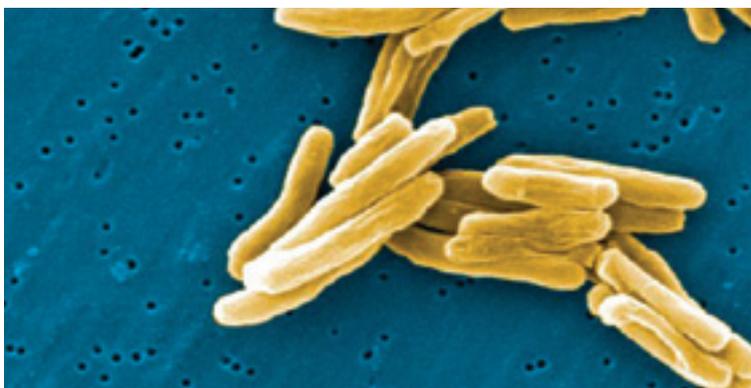
Accurately Detecting TB Outbreaks

Using genome sequencing to improve tuberculosis outbreak detection and investigation effectiveness

An outbreak investigation aims to stop transmission of TB. This public health intervention involves rapidly identifying and treating all infectious persons.

Outbreaks of tuberculosis continue to challenge public health professionals. Traditional laboratory methods include using genotyping to find outbreaks that may be hidden. Genotyping helps determine differences in the genetic makeup of an organism. But this tool also can indicate an outbreak where there isn't one, especially for genotypes that are common in the population. This slows the process of identifying and controlling an outbreak when it occurs. It also consumes resources without leading to an effective solution.

CDC scientists studying TB are evaluating whether genome sequencing will increase the accuracy of outbreak detection. To do this, they are conducting genome sequencing for all suspected large TB outbreaks identified through genotyping. They will compare the sequence data to epidemiologic data to determine how the infection has spread and which cases are linked.

If genome sequencing does result in a more accurate detection of TB outbreaks, public health officials can use scarce resources more efficiently. As well, field investigations would be more precise in finding out how the infection has spread and which locations are most important to an outbreak. This will ensure interventions have the greatest impact and protect people's health even better.

In 2014, CDC used AMD methods to help local and state health departments investigate 20 clusters of tuberculosis. The addition of AMD methods improved the accuracy of outbreak investigations. This partnership gave local and state health departments the information they needed to take action and focus intervention resources.

Better Tuberculosis Surveillance

Transforming tuberculosis surveillance to whole genome sequencing data

In the United States, genotyping surveillance of TB is done mainly to discover the hidden spread of this disease. Scientists do this by finding cases caused by the same strain of the bacteria. TB that spreads from one person to another will have the same genetic make-up when isolated in the laboratory and compared.

Traditional laboratory methods may identify isolates as being the same when they are not. False matches can slow down the work of local public health professionals and result in additional costs when public health interventions are started and then found to be unnecessary.

CDC is exploring genomic surveillance of TB using whole genome sequencing. Using this approach lets CDC scientists examine about 90% of the TB genome, instead of the current less than 1%. Instead of estimating the identity of isolates, whole genome sequencing will measure the genetic differences between isolates.

CDC expects that the data generated through genomic surveillance will provide more accurate information more quickly to public health officials. This will allow them to find potential outbreaks and respond to them rapidly. At the same time, genomic surveillance will be more cost efficient by focusing investigations on cases that are truly linked.

NOTES

Fiscal Year 2014 AMD Projects

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