Decoding DNA to Outsmart Gonorrhea: Modern Technology Takes on Centuries-Old Bug

Like other sexually transmitted diseases (STDs), gonorrhea has been on a steady, troubling climb for the last few years – overall rates have jumped by 67% since 2013. Even more concerning is the connected and increasing threat of drug-resistant gonorrhea that has public health officials across the United States anxious to stop the common infection in its tracks. Closely monitoring for emerging resistance is critical because *Neisseria gonorrhoeae*, the bug that causes gonorrhea, has quickly developed resistance to all but one class of antibiotics. In fact, CDC's 2019 Antibiotic Resistance Threats Report found that about half of all infections are resistant to at least one antibiotic. And with few new drugs in the pipeline, ceftriaxone is the last highly effective recommended treatment available.

Now there is hope that drug-resistant gonorrhea may have met its match: scientists in the Laboratory Reference and Research Branch of CDC's Division of STD Prevention (CDC's STD lab) recently developed a new analysis tool that enhances and refines genome sequencing. Researchers hope this technology, which has helped revolutionize modern healthcare in a number of areas, will also help curtail the spread of drug-resistant gonorrhea. The new tool gives public health laboratories across the nation easy access to cutting-edge technology which decodes the DNA of gonorrhea samples, giving them insight into how individual infections are related to one another, much like finding long lost relatives through genealogical research. This critical information can help public health professionals link infections to identify clusters and, one day, could help guide patients to the most effective treatment options for their infection.

550,000 per year
estimated gonorrhea infections resistant to at least one antibiotic

1.14M per year
estimated new gonorrhea infections

>17,000 unique gonorrhea samples are contained in CDC's GC specimen bank. CDC shared ~1,000 in 2019

Centers for Disease Control and Prevention
National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention

Reining in a Dangerous Foe

How do we keep the public health concern of rising drug-resistant gonorrhea from becoming an unstoppable force? Currently, CDC's **Gonococcal Isolate Surveillance Project** (GISP) **and Strengthening the United States Response to Resistant Gonorrhea (SURGG)** ventures serve as collaborative resources for researchers and clinicians to monitor drug-resistant gonorrhea. And with the addition of CDC's powerful new tool to the arsenal, public health labs all around the country and beyond will now have the ability to analyze their own data to get a handle on what's happening with drug-resistant gonorrhea locally.

Since 2017, researchers in CDC's STD lab have used their tool – the **Drug-Resistant Gonorrhea Genome Profiler** – to help identify genes that are involved in drug-resistant gonorrhea, and now the lab is offering it to all public health laboratories to help attack this public health threat. "Classic, culture-based analyses have always been helpful in diagnosing and tracking gonorrhea. But this new tool, which sifts through data to determine which genes are involved in antimicrobial resistance, can analyze substantially more genetic data at a much faster rate. When combined with the information collected through CDC's surveillance programs, this delivers a more complete picture of how drug-resistant gonorrhea develops and where it's happening," said Dr. Matthew Schmerer, a biologist in CDC's STD lab and its principal developer.

How Does the Drug-Resistant Gonorrhea Genome Profiler Work?

The Drug-Resistant Gonorrhea Genome Profiler was designed to be user-friendly, and access is completely free. "Any public health lab scientist can use it – all it takes is simply logging on to the secure website (via CDC's Office of Advanced Molecular Detection Portal), using any laptop or desktop, inputting genome sequence data, and waiting for an analysis summary. That's it – the tool does all the work," said Schmerer.

Generated in each requesting lab's summary is a written set of clues that show what genetic markers might be affecting drug resistance in that area of the country. Most importantly, a standardized analysis of each lab's data is included, which allows for comparisons across different jurisdictions. "With the release of this new resource on a freely-accessible CDC website, it's now possible for public health labs to analyze data locally without having to send it to CDC for analysis – they can get immediate feedback to help track local gonorrhea outbreaks as they're happening," said Schmerer. Ideally, this data could then be translated and allow public health professionals to identify concerning strains of gonorrhea. Disease Intervention Specialists – community disease detectives – could then use this information to implement measures to control the spread of antibiotic resistant gonorrhea in their local community.

Schmerer says CDC's STD lab is conducting network analyses of data to bring this very vision to life in the not-too-distant future. "It's possible that rapid, comprehensive analyses provided to local labs could have better impacts on drug-resistant gonorrhea by allowing more rapid implementation of preventative measures."

What's Next?

Some labs have already tapped into the Drug-Resistant Gonorrhea Genome Profiler's powerful data analysis capabilities: public health labs in six US jurisdictions and one international jurisdiction have all used it to assess genomic data related to gonorrhea. Public health labs in other jurisdictions are also scheduled to start using it soon. The goal, says Schmerer, is getting as many public health labs on board as possible. "The more labs that access this powerful – yet simple – resource, the greater the possibility that we can halt the rise of drug resistance, and ultimately drive gonorrhea rates back down."

Learn MORE at **cdc.gov/std**

- Combating antibiotic-resistant gonorrhea
- Gonorrhea fact sheet
- What is whole genome sequencing?