Molecular HIV Surveillance

TOWARDS NO NEW HIV INFECTIONS

Kidane Meshesha
Epidemiologic Services Unit
Division of HIV, STD & Tb Services
New Jersey Department of Health
Outline

• Background – New HIV transmissions are not declining any further
• Key Definitions
• Integrated HIV Surveillance and Prevention: PS18-1802
• Identification transmission networks - Existing and New approach
  - Understanding transmission clusters for prevention
• Integrating New Technology and Approach
Background
The Incidence of HIV is not declining

• After about 5 years of substantial declines, the number of annual new HIV infections began to level off in 2013, to about 39,000 infections per year. (HIV Surv. Suppl. Report Vol. 24, No.1  Published Feb, 2019)

• Incidence estimates- # of new infections, not diagnosis per year

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>US</td>
<td>41,000</td>
<td>40,300</td>
<td>40,000</td>
<td>38,900</td>
<td>38,100</td>
<td>39,000</td>
<td>38,700</td>
</tr>
<tr>
<td>NJ</td>
<td>1,100</td>
<td>1,000</td>
<td>1,100</td>
<td>1,000</td>
<td>1,100</td>
<td>950</td>
<td>1,000</td>
</tr>
</tbody>
</table>

• CDC estimates that the decline in new HIV infections has plateaued because effective HIV prevention and treatment are not adequately reaching those who could most benefit from them.

- African American gay and bisexual men: 9,800 (2010), 9,800 (2016)
- Latino gay and bisexual men: 6,400 (2010), 8,300 (2016)
- White gay and bisexual men: 8,000 (2010), 6,700 (2016)
- African American heterosexual women: 4,700 (2010), 4,000 (2016)
- People who inject drugs: 2,700 (2010), 1,900 (2016)
- African American heterosexual men: 2,300 (2010), 1,800 (2016)
- White heterosexual women: 1,000 (2010), 1,000 (2016)
- Latino heterosexual women: 1,200 (2010), 980 (2016)
• (In 2016), responsible for more than 80% of new HIV infections in the US
• In 2016, approximately 15% did not know they were infected >> for 38% of new transmissions

23% of people knew they were infected with HIV but were not receiving treatment and they accounted for 43% of new transmissions.

Individuals who were receiving care but not virally suppressed made up 11% of the HIV-infected population and caused 20% of new infections.
The study used both HIV sequence and partner naming data from 1342 HIV-infected persons in New York City between 2006 and 2012 to infer and compare sexual/drug-use named partner and genetic transmission networks.

Using these networks, they used genetic testing data for identifying potential transmission partners.

In 48% of cases, named partners were infected with genetically closely related viruses, compatible with but not necessarily representing or implying, direct transmission.
Gaps in reaching to all affected/exposed

Partner Services identifies/discovers ONLY 48% of transmission partners.
Key Definitions

• HIV Resistance Testing/Genotype Testing/Sequencing
  - Conducted in order to identify viral resistance to antiretroviral medications and help the HIV care provider select an appropriate treatment regimen.

• HIV Transmission Clusters
  - Identified through analysis of HIV genetic sequence data that is generated through HIV drug resistance testing.

• HIV Outbreak
  - An increase, often sudden, in the number of cases of a disease above what is normally expected in that population in that geographic area.

• Risk Network
  - All persons in the transmission cluster, plus all HIV-uninfected or HIV-unknown sexual or needle-sharing partners of persons in the identified molecular cluster or their immediate HIV-infected partners.
Strategy 3: Develop, maintain, and implement plan to respond to HIV transmission clusters and outbreaks

- Identify and investigate HIV transmission clusters and outbreaks
- Rapidly respond to and intervene in HIV transmission clusters and outbreaks
- Maintain outbreak identification and response plan
Methods to detect/identify transmission networks
Method 1: Partner Services

- Partner services data, although key, provide incomplete information about transmission networks
  - Many partners not named
  - Named partners not always located
  - Named partners often do not represent transmission partners
  - Partner services for all new diagnoses?

  PS alone: Incomplete for high-impact prevention efforts

- PS provides very useful “Social Network Analysis” which enriches the cluster data – will be included in cluster investigation and response
Method 2: Time-Space Analysis

- Identify populations with increased diagnoses in a particular geographic area or population as soon as possible
- Give particular attention to situations that might be associated with very recent and rapid transmission or severe consequences, Useful in areas with low prevalence of HIV (like many rural communities)
  e.g. IDU’s in Scott County, Indiana
- May represent recent and rapid transmission
- Could also reflect an increase in testing that has diagnosed people with longstanding infection
- Currently, analysis is by county.
Method 3: Molecular Surveillance

• The Gold Standard for identifying transmission partners
• Collection and pairwise comparison of viral sequence data collected from HIV Genotype/resistance testing
  - identifies recent transmission events
  - detects and tracks the growth of the transmission cluster
  - identify members of the cluster and characterize risk profiles
  - provides the tools for prevention
    >> customized prevention strategies
    >> pin-pointed intervention to contain the outbreak
What Data Do We Use to Find These Networks?

- As part of HIV care, health care providers order testing to learn what treatments will work best for a person’s HIV strain
  - Called drug resistance /genotype testing
  - This testing involves determining the genetic sequence of the virus (NOT the person)
- We sometimes call this ‘molecular data’
  - Intermediate products of genotype testing systems
  - Not reported out to ordering provider
- 'CCTCAGATCACTCTTTTGGAACGACCCCTCGTCACAAATAAGGATAGGAGG
  CAACTAAAGGAAGCTCTATTAGATAACAGGAGCAGATACAGTAGTAGAGAA
  GAAATGAGCTTACCAGGAAAATGGAAAACCAAAAATGATAGGAGGAATGG
  AGGTGGATCAAAAGTAAGCAGTAGTACATAATACATATAGAATAATCTGGGA
  TATAAAAGCTATAGGTACAGTAGTATTAGTAGGACCACACCTGTCAACATAATGG
  AAGA ..........
Identifying Transmission Networks

- Use local installation of HIV-Trace, developed by University of California, San Diego
- Perform pairwise comparisons of all sequences to calculate genetic distance
- Identify pairs of sequences below a given genetic distance threshold

indicates underlying transmission link (without directionality)

Infer a transmission network
Hypothetical Molecular cluster and corresponding underlying transmission cluster and risk network

- a. Hypothetical molecular cluster identified through sequence analysis
- b. Hypothetical underlying transmission cluster
- c. Hypothetical underlying risk network

Legend: Circles represent persons with HIV infection or persons at high risk of HIV infection; lines represent sexual or risk relationships between persons.

- HIV-infected, diagnosed, in care
- HIV-infected, diagnosed without a sequence
- HIV-infected, not diagnosed
- HIV-uninfected, at risk

HIV surveillance data cannot reveal which cases are directly related by transmission or determine the direction of transmission.
Molecular Epidemiology and HIV

- Analysis: compares nucleotide sequences to determine relatedness

We can infer a direct OR indirect epidemiologic link.
We cannot infer directionality.
A transmission cluster represents a subset of an underlying risk network.

- Can include persons with diagnosed HIV infection who:
  - Entered HIV care
  - Had HIV drug resistance testing
  - Had HIV genetic sequences transmitted to surveillance program

- Can also include:
  - Persons with undiagnosed HIV infection
  - Persons with diagnosed HIV infection who do not have a sequence available

- Can also include (Finding the contours of the network):
  - Persons who are not HIV-infected but may be at risk for infection
What is Molecular Surveillance now...

It is about the Detection of Transmission Clusters as they start and grow.

It is a Near Real-time transmission identification tool in order to interrupt further transmissions and outbreaks.

Helps to Understand transmission dynamics which is critical to both screening and intervention programs.
Integrating New Technology and Approach

>>>>>> additional tool in the tool box
Key Elements to Collection and Use of HIV Nucleotide Sequences - 1

1. Establish the Infrastructure, Systems and Processes needed to conduct Molecular HIV Surveillance to guide Public Health Action

- Collaborate with laboratories to electronically collect HIV sequence data
  • Collect all HIV sequences generated as part of HIV care (i.e., initial and subsequent, regardless of time from HIV diagnosis)

- Integrate HIV nucleotide sequence collection into existing electronic laboratory reporting (ELR) processes >>> working with the ELR team in Communicable Dis.

- Collect antiretroviral (ARV) use history data for newly diagnosed persons
  • Outcome standard: ≥70% of persons newly diagnosed with an initial sequence have ARV use data
2. Maintain legal authority to collect HIV sequences
   - NJ current laboratory reporting law stipulates the reporting of ‘all tests indicative of HIV’.
   - Updating the language to include all ‘Genotype’ tests is underway.
   - Also included are all CD4 Counts and Viral loads:
     (Incidence estimate, assess continuum of care and support Data-to-care activities)

     Section 2C:34-5 - Diseased person committing an act of sexual penetration
     - need to assess concerns about criminal exposure laws and the potential use of cluster data as part of criminal proceedings.
     - assess these statues potential impact on HIV Prevention efforts.
     - ensure information about transmission clusters should be used only for public health purposes.
Key Elements to Collection and Use of HIV Nucleotide Sequences - 3

- **4. HIV Outbreak Response Plan**
  - also referred as **HIV Cluster Detection, Investigation and Response Plan**
  - under development - needs your input
  - has three parts: Detection, Investigation and Response
  - has to define the threshold for an Outbreak
  - who will declare an outbreak, command and communication strategy
  - additional Federal and State resources

- **5. Protecting cluster data**
  - Appropriate handling of cluster data and considerations regarding appropriate uses of data and communication about data
  - Maintain security and confidentiality guidelines – **update as necessary**
  - Standard surveillance protections: Stored securely, Access limited
  - **Additional sensitivities around cluster data**

  Directionality: minimize use of data on specific linkages
We Can End HIV

• Exciting time in HIV treatment and prevention: can detect infection, and networks of infection, earlier than ever – preventing new transmissions and better clinical outcomes.
• CDC and the Dept. of Health are committed to
  – Using both traditional public health tools and the new tools in our toolbox to end HIV
  – Responsible use of the data is at the core of all programs/activities
  – By using this data we can effectively reach and serve more people with or at risk for HIV
  – Hearing concerns and working with the community to address them
Renewed commitments

• State
  - Governor Murphy's declaration to end the epidemic by 2025
  - Details forthcoming …
• Federal
  - President’s new plan to end HIV epidemic by 2030
  - The initiative aims to reduce new HIV infections by 75% in the next five years and by 90% in the next 10 years, "averting more than 250,000 HIV infections in that span
  - The initiative will target federal resources to the 48 highest burden counties, Washington DC, San Juan - Puerto Rico, and 7 states with substantial rural HIV burden
  - Includes Essex (24th) and Hudson (46th) in the total number of HIV diagnosis by county/cities for 2016 and 2017 combined.
  - Molecular HIV Surveillance to detect transmission clusters and outbreaks is at its Core
  - Expect to hear more in the coming weeks/months
Ending the HIV Epidemic: A Plan for America

HHS is proposing a once-in-a-generation opportunity to eliminate new HIV infections in our nation. The multi-year program will infuse 48 counties, Washington, D.C., San Juan, Puerto Rico, as well as 7 states that have a substantial rural HIV burden with the additional expertise, technology, and resources needed to end the HIV epidemic in the United States. Our four strategies – diagnose, treat, protect, and respond – will be implemented across the entire U.S. within 10 years.

**GOAL:**

Our goal is ambitious and the pathway is clear – employ strategic practices in the places focused on the right people to:

- **75%** reduction in new HIV infections in 5 years and at least **90%** reduction in 10 years.
- **Diagnose** all people with HIV as early as possible after infection.
- **Treat** the infection rapidly and effectively to achieve sustained viral suppression.
- **Protect** people at risk for HIV using potent and proven prevention interventions, including PrEP, a medication that can prevent HIV infections.
- **Respond** rapidly to detect and respond to growing HIV clusters and prevent new HIV infections.
- **HIV HealthForce** will establish elimination teams committed to the success of the Initiative in each jurisdiction.
Questions | Concerns | Engagement | Discussion

Thank You