Introduction to TB Genotyping Information Management System (TB GIMS)

Molecular Epidemiology Activity
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Agenda

- What is genotyping?
- Genotype nomenclature
- NTGS methods
- Overview of TB GIMS
- TB GIMS data flow
- TB GIMS User roles
- Applying genotyping using TB GIMS
**What is TB Genotyping?**

- Examines tiny DNA variations to determine genetic relatedness of TB strains from different patients
- Only performed with culture-positive cases

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**Genotypes and Transmission**

- Genotyping helps us understand transmission relationships among cases
- We expect genotypes from related cases to match
**Genotype cluster**
- Two or more patients with matching TB genotypes are considered part of a genotype cluster
  - Usually restricted by place and time
- Patients in a genotype cluster are more likely to be in the same chain of transmission
- Transmission among patients in a genotype cluster may not be
  - Recent
  - Direct

**National TB Genotyping Service (NTGS)**
- Started in 2004
- States voluntarily submit TB isolates for genotyping
- Genotype one isolate from every culture-positive TB patient in the United States
  - “Universal Genotyping”
- In 2015, 96% of culture-positive TB patients in the U.S. had a TB genotype result
NTGS Genotyping Methods

- Two Polymerase Chain Reaction (PCR) methods
  - **Spacer oligonucleotide typing (Spoligotype)**
    - Spoligotype: 77777477760771
  - **Mycobacterial Interspersed Repetitive Units (MIRU)**
    - MIRU: 232234253322
    - MIRU2: 334564611872

Genotyping Laboratories

- Michigan: MIRU+ MIRU2
- CDC lab: Spoligotyping
Definition for Tuberculosis Genotyping in the United States

Spoligotype: 000000000003771
Initial 12-locus MIRU-VNTR\(^1\)
MIRU: 223325173533

PCRTypet: PCR00002
Additional 12-locus
+ MIRU-VNTR (MIRU2)
MIRU2:444534423428\(^2\)

GENType: G00010

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1 Mycobacterial interspersed repetitive unit–variable number tandem repeat
2 The complete set of 24 loci is referred to as 24-locus MIRU-VNTR and is used for GENType designation for genotype in the U.S.

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TB Genotyping Information Management System (TB GIMS)

- Launched March 2010
- Secure web-based application
- Designed to improve dissemination, management, and application of genotyping data
- As of May 2016, TB GIMS contains genotype results for over 100,000 patients
**TB GIMS Functions**

- Receive and update genotyping results from genotyping laboratories
- Link genotype results from NTGS to patient-level surveillance data from National TB Surveillance System (NTSS)
- View national, state, and local maps of cases in a genotype cluster
- Examine and compare demographic, clinical and risk characteristics of patients in genotype clusters
- Tools for outbreak detection

**TB GIMS Data Flow**

- **State Laboratory** → **Genotyping Lab**
  - Ship isolates
- **TB GIMS**
  - Link isolate to NTSS data
  - Create isolate records
- **TB Program**
  - NTSS surveillance data
- **CDC / NTSS**
  - Update Surveillance
### State Laboratory Super User

- **Primary responsibility is to ensure that isolates are genotyped**
- **Create, submit, and edit isolate records**
- **Search for genotype results**
- **Request additional testing**

### TB Program Super User

- **Primary responsibility is data management**
  - Link genotype results to patient records
  - Manage patient records with multiple genotype results
- **Access, search, and export genotype and patient records**
- **Request additional testing**
TB Lab and Program Super User

- For states with 1 or 2 TB GIMS Super Users who perform both Lab and Program functions
- Primary responsibility is to ensure that isolates are genotyped and linked with surveillance records
- Create, submit, edit, link and manage all TB GIMS records
- Request additional testing

Program Standard User

- Primary users of genotyping data
- Access, search, and export genotype and patient results
All Users

- Cluster snapshots
- Watch List
- Generate reports and maps by PCRTYPE/GENTYPE
  - Epidemic curves
  - Surveillance summary report
  - National distribution of genotypes
  - Lists of county-level alerts
  - National, state, and local maps
- TB GIMS Directory

Applying Genotyping Using TB GIMS

- Patient Level
  - Distinguish relapse from new infection
  - Detect false-positive cultures
Applying Genotyping Using TB GIMS

- **Patient Level**
  - Distinguish relapse from new infection
  - Detect false-positive cultures
  - Confirm known epidemiologic links
  - Find unknown epidemiologic links

- **Population Level**
  - Detect outbreaks
  - Define scope of outbreaks
  - Monitor outbreaks over time