



Molecular Surveillance Updates for TB GIMS Users: 2017 Annual Report, National WGS service, TB GIMS enhancements

Steve Kammerer, Ben Silk, Julie Self

Molecular Epidemiology Activity
Surveillance, Epidemiology, and Outbreak Investigation Branch
Division of TB Elimination

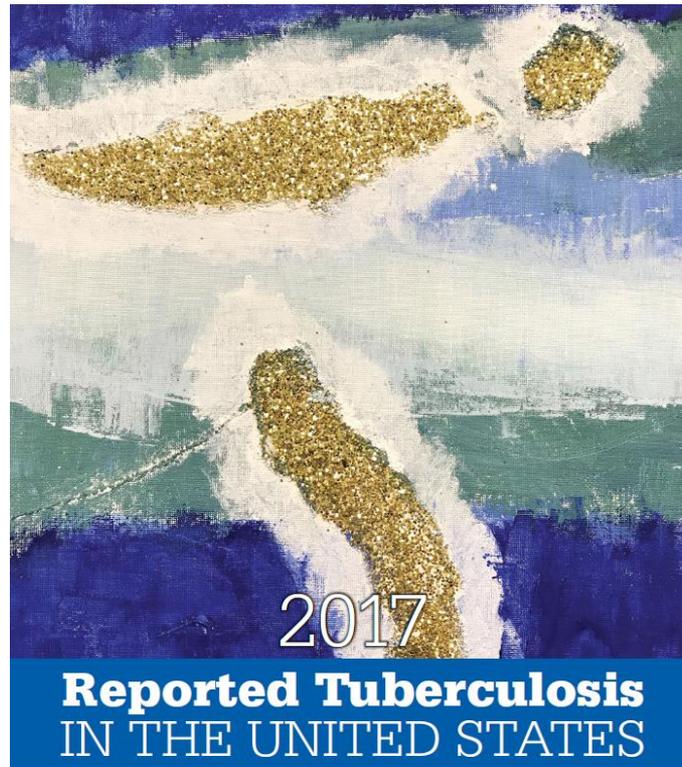
TB GIMS User Call

February 11, 2019

Housekeeping

- Instead of a roll call, please email tbgenotyping@cdc.gov and let us know you are on the call
- We are going to mute the audience until the discussion sections of the presentation
- To ask question by phone, please dial *6 after presenter unmutes the audience
- After your question is answered, please dial *6 again to mute yourself
- You may also use the chat box for questions and discussion

National Tuberculosis Genotyping Data 2017 Annual Report



Cover image: An original painting of tuberculosis bacilli by the 7-year-old daughter of CDC employee Sarah Talarico, PhD. Image courtesy of Sarah Talarico.

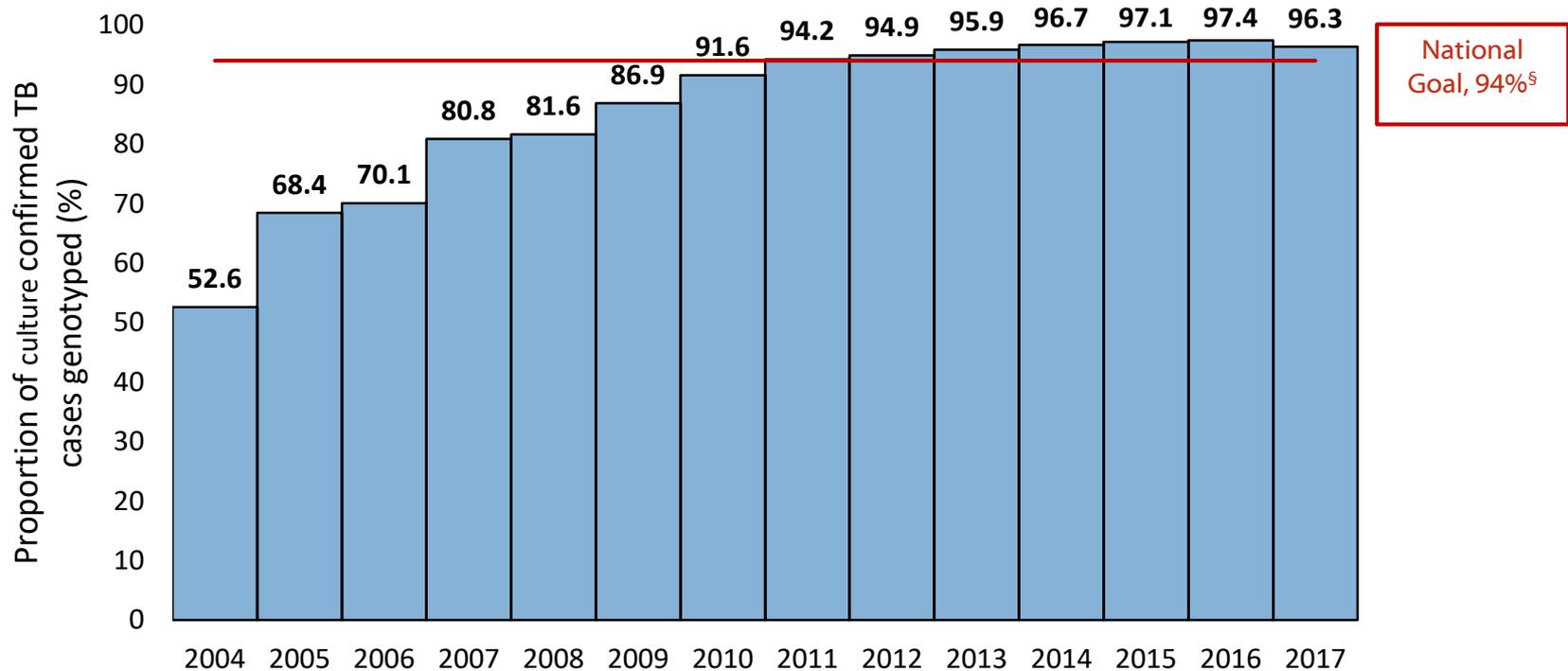


Centers for Disease
Control and Prevention
National Center for HIV/AIDS,
Viral Hepatitis, STD, and
TB Prevention

<http://www.cdc.gov/tb/statistics/reports/2017/default.htm>

GENOTYPE SURVEILLANCE COVERAGE 2004-2017

Slide 27: National Tuberculosis Genotyping Surveillance Coverage* by Year: United States†, 2004–2017



* The proportion of positive cultures with at least one genotyped isolate.

† Includes 50 states and the District of Columbia.

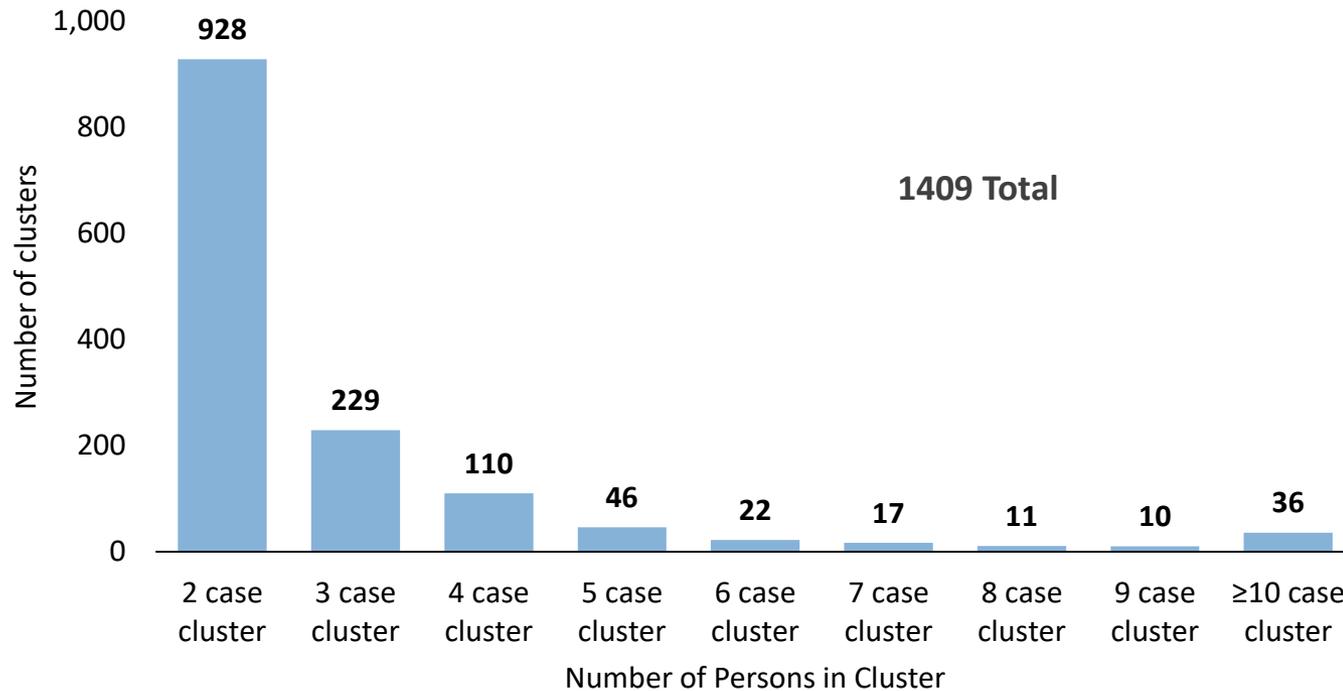
§ For the year 2020, the national goal for TB genotyping surveillance coverage will change to 100%.

Table 26: Top 5 Most Frequently Reported GENTypes, 2015-2017

GENType	PCRType	No. of TB cases (%)	No. of Reporting Areas with GENType
G00012	PCR00002	181 (0.9)	28
G00010	PCR00002	163 (0.8)	20
G00016	PCR00041	144 (0.7)	23
G05056	PCR00041	114 (0.5)	23
G00017	PCR00803	76 (0.4)	18

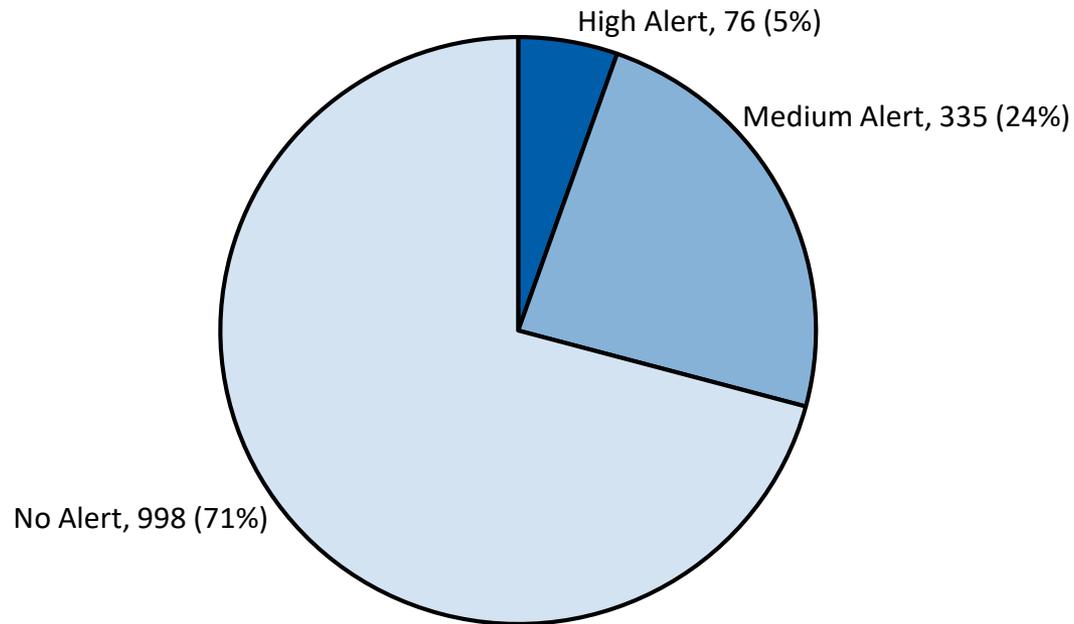
**COUNTY-BASED GENTYPE CLUSTERS
2015-2017**

Slide 28: Number of County-based Tuberculosis Genotype Clusters* by Cluster Size, United States, 2015–2017



*Genotype cluster is defined as two or more cases with matching spoligotype and 24-locus MIRU-VNTR (GENType) within a county during the specified 3-year time period.

Slide 29: Tuberculosis Genotype Clusters by TB GIMS* Alert Levels[†], United States, 2015–2017



*Tuberculosis Genotyping Information Management System

[†]Alert level is determined by the log likelihood ratio statistic (LLR) for a given cluster, identifying higher than expected geospatial concentrations for a TB genotype cluster in a specific county, compared to the national distribution of that genotype; TB GIMS generates alert level notifications based on this statistic: “No alert” is indicated if LLR is between $0 < LLR < 5$, “medium” is for LLR of $5 < LLR < 10$ and “high” alert is for clusters with $LLR \geq 10$.

Table 24: Select Characteristics of Cases in GENType Clusters by Alert Status, 2015-2017

Case Characteristics	Cases in Non-Alerted clusters (LLR<5) (2,473 cases in 998 clusters)	Cases in High Alert clusters (LLR ≥10) (750 cases in 76 clusters)
U.S.-Born	869 (35%)	646 (86%)
Non-U.S.–Born	1,598 (65%)	103 (14%)
Homeless within past year	195 (8%)	164 (22%)
Excess alcohol use within past year	329 (13%)	240 (32%)
Non-injecting drug use within past year	260 (11%)	194 (26%)
Injecting drug use within past year	42 (2%)	30 (4%)
Correctional facility at time of diagnosis	94 (4%)	53 (7%)
HIV positive status	135 (5%)	64 (9%)

**ESTIMATES OF RECENT TRANSMISSION
2016-2017**

Estimating Recent Transmission

- In 2015, CDC scientists developed and published a genotype-based method to estimate the proportions of cases attributed to recent transmission.
- The method was field-validated using data collected by local health departments
- For the second year, the annual report provides aggregated estimates of recent transmission using this method.

Recent Transmission References



American Journal of Epidemiology

Published by Oxford University Press on behalf of the Johns Hopkins Bloomberg School of Public Health 2015. This work is written by (a) US Government employee(s) and is in the public domain in the US.

DOI: 10.1093/aje/kwv121

Practice of Epidemiology

A Field-Validated Approach Using Surveillance and Genotyping Data to Estimate Tuberculosis Attributable to Recent Transmission in the United States

Anne Marie France*, Juliana Grant, J. Steve Kammerer, and Thomas R. Navin

* Correspondence to Dr. Anne Marie France, Division of Tuberculosis Elimination, Centers for Disease Control and Prevention, 1600 Clifton Road NE, Mail Stop E-10, Atlanta, GA 30329 (e-mail: afrance@cdc.gov).

Initially submitted September 16, 2014; accepted for publication April 27, 2015.

RESEARCH ARTICLE

Recent Transmission of Tuberculosis — United States, 2011–2014

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Division of Tuberculosis Elimination, Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America

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click for updates

Recent Transmission Content

- Overview/Notes on Recent Transmission (Pages 82-83)
- Figure 1 (Page 84): Estimated Cases Attributed to Recent Transmission of Tuberculosis, United States, 2016-2017
- Figure 2 (Page 85): Estimated Percentage of Extensive Recent Transmission of Tuberculosis in Counties with ≥ 10 Genotyped Cases, United States, 2016-2017

- Table 57 (Page 86): Counts and Percentages of Tuberculosis Cases Estimated to be Attributed to Recent Transmission and Extensive Recent Transmission: Reporting Areas, 2016–2017

Recent Transmission Content (2)

- Table 58 (Page 87): Counts and Percentages of Tuberculosis Cases Estimated to be Attributed to Recent Transmission and Extensive Recent Transmission: Counties with >5 Percent Estimated Extensive Recent Transmission, 2016–2017
- Table 59 (Page 88): Characteristics of Tuberculosis Cases Estimated to be Attributed to Recent Transmission and Extensive Recent Transmission: United States, 2016-2017

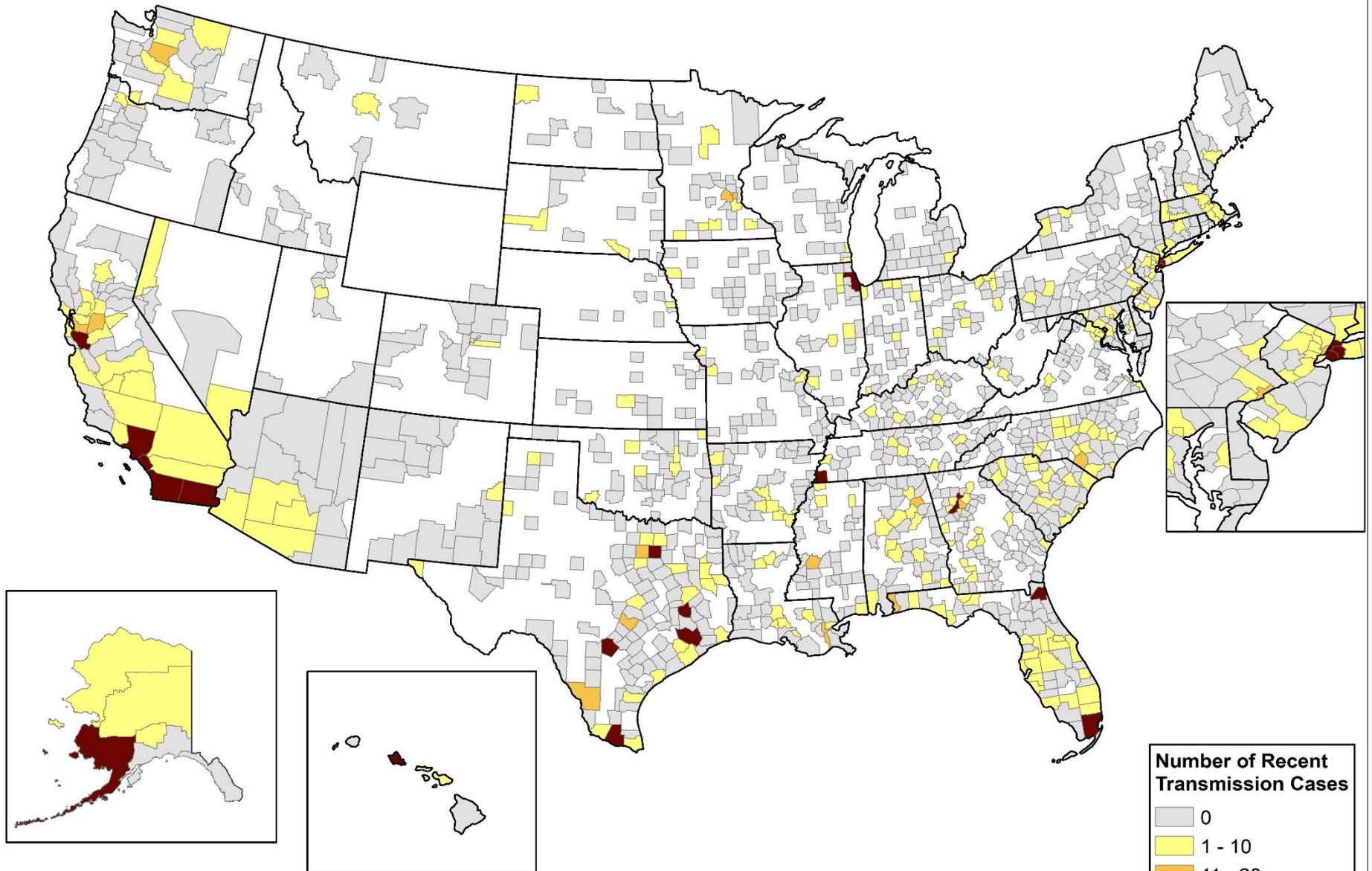
Limitations of Recent Transmission Estimates

- Applied to culture-confirmed, genotyped cases (~75% of cases)
 - Pediatric cases likely due to transmission are underestimated in the estimates
- Recent transmission may be overestimated in areas with common genotypes or in relatively closed populations/remote areas in which prevalent genotypes have dominated for many years
- The molecular resolution of genotyping method affects the estimates (e.g., diversity may be greater than represented by MIRU24 in cases reported by areas bordering Mexico)
- Recent transmission may be underestimated in situations in which related cases have genotypes with a single locus variant.

Recent Transmission Estimates

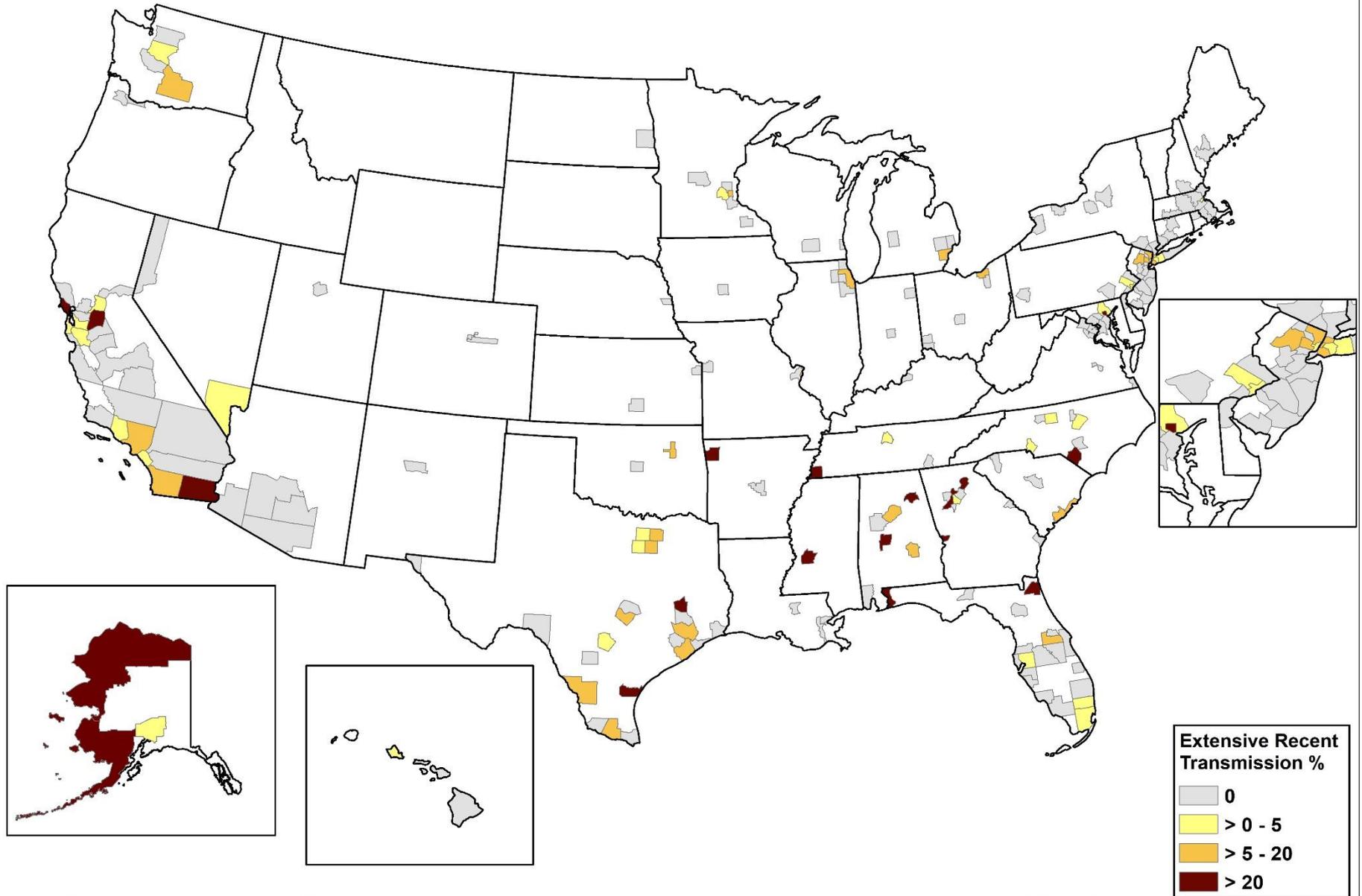
- CDC attributes 13.1% of genotyped cases in the U.S. during 2016–2017 to recent transmission.
- CDC attributes 4.6% of genotyped cases in the U.S. during 2016-2017 to extensive recent transmission
- Recent transmission estimates by reporting area range from 0% to 42%; extensive recent transmission estimates range from 0% to 24.4%
- Recent transmission estimates higher among:
 - U.S.-born persons
 - Am Indian/AK native, Native HI/Pacif Islander, non-Hispanic Blacks
 - Persons reporting homelessness, substance use, correctional residence

Figure 1. Estimated Cases Attributed to Recent Transmission of Tuberculosis, United States, 2016–2017*



*Counties shaded white had no genotyped cases that could be evaluated for recent transmission during 2016-2017.

Figure 2. Estimated Percentage of Extensive Recent Transmission of Tuberculosis in Counties with 10 or More Genotyped Cases, United States, 2016–2017*



*Counties shaded white had <10 genotyped cases that could be evaluated for recent transmission during 2016-2017.

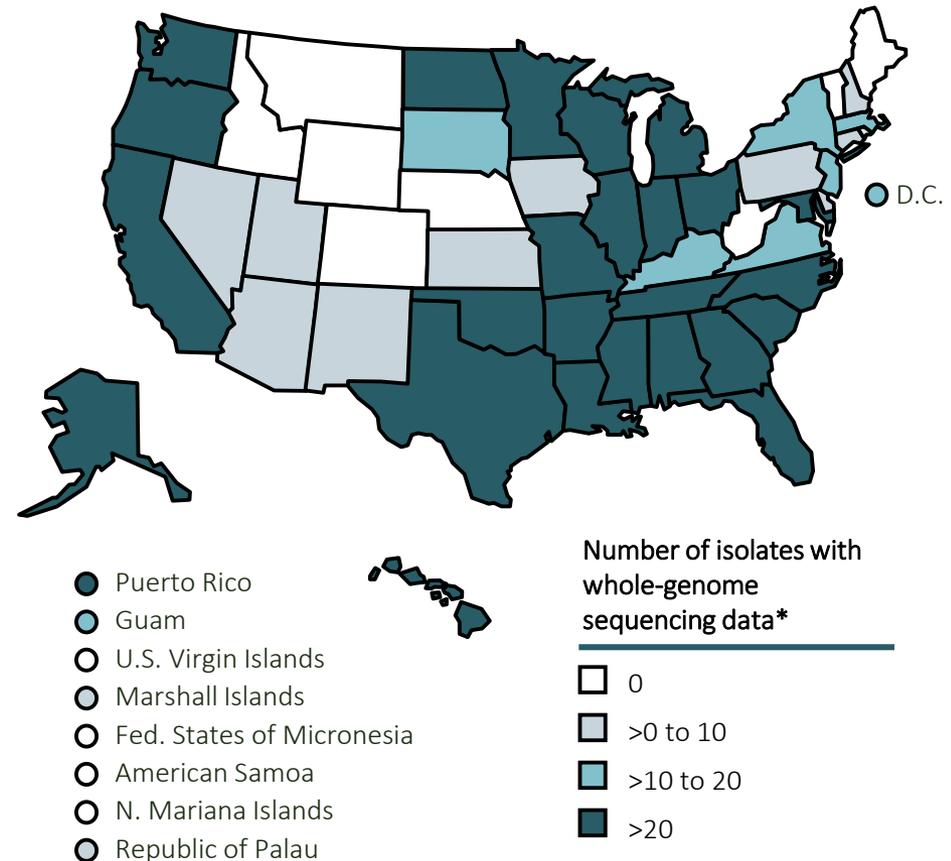
Using Recent Transmission Estimates

- Monitor trends in recent transmission within a jurisdiction
- Plan and prioritize TB control activities
- Enhance service delivery by applying sufficient resources
- Identify geographic, demographic, and social disparities in proportion of cases attributed to recent transmission
- Develop specific prevention strategies and interventions to interrupt transmission
- Facilitate inter-jurisdictional connections to share TB control strategies

National WGS service

WGS for genotype clusters

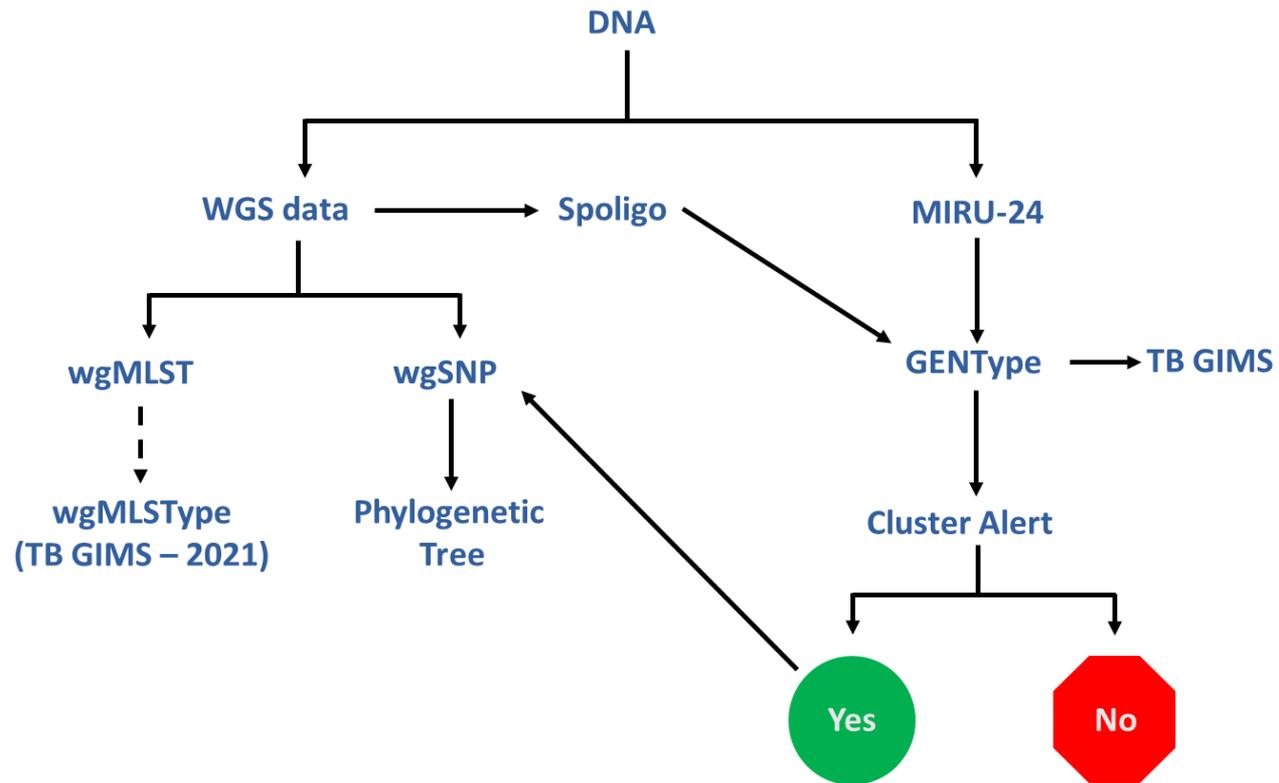
- WGS and phylogenetic analysis of hundreds of clusters nationally
 - 2012: first WGS of a GENType cluster
 - 2014: WGS performed for all GENType clusters that alerted for large outbreak surveillance
 - 2016: WGS expanded to include other select GENType clusters that could inform public health
 - 2018: Universal WGS



*N = 3,700 isolates, data current as of Aug. 2018

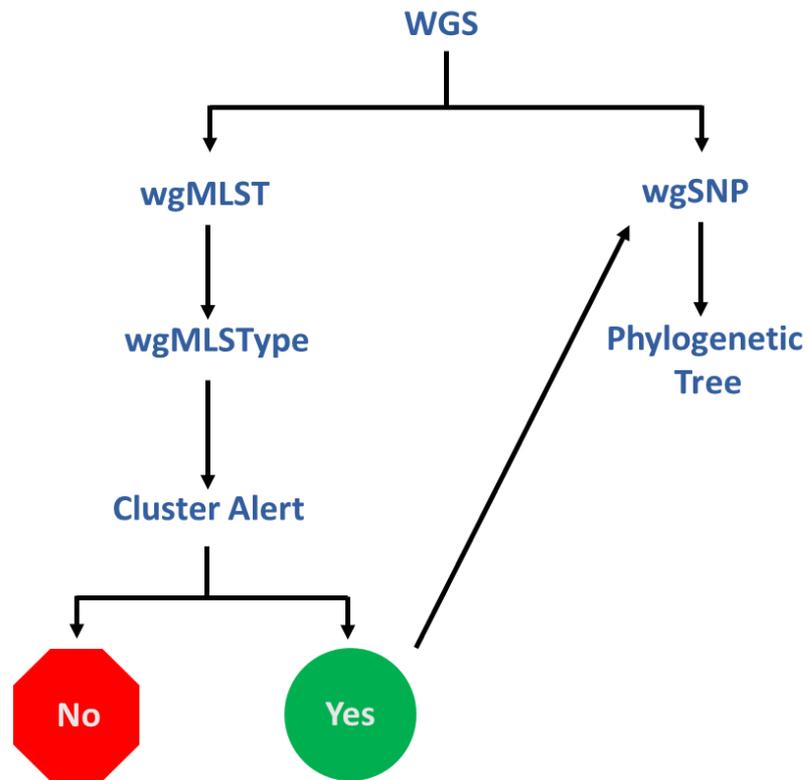
Universal prospective WGS began in 2018

TB Genotyping Methods and Data Flow (2018 – 2020)



wgMLSType will replace GENType for cluster alerting in 2021

TB Genotyping Methods and Data Flow (2021)



WGS training



- Home Guide to the Application of Genotyping to Tuberculosis Prevention and Control
- Acknowledgments
- Introduction to Tuberculosis Genotyping +
- Tuberculosis Genotyping Case Studies +
- CDC Tuberculosis Genotyping Laboratory Procedures +
- Combining Genotyping and Epidemiologic Data to Improve Our Understanding of TB Transmission +
- Developing a Tuberculosis Genotyping Program +

TB Genotyping

TB genotyping is a laboratory-based approach used to analyze the genetic material (e.g., DNA) of *Mycobacterium tuberculosis*, the bacterium that cause TB disease. The total genetic content is referred to as the genome. Specific sections of the *M. tuberculosis* genome form distinct genetic patterns that help distinguish different strains of *M. tuberculosis*.

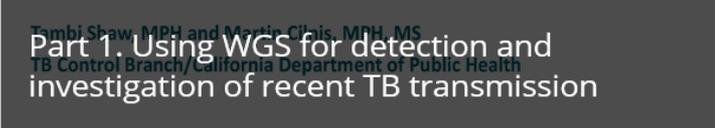
Why use TB genotyping?

TB genotyping results, when combined with epidemiologic data, help identify persons with TB disease involved in the same chain of recent transmission. In the same way, TB genotyping helps distinguish between persons whose TB disease is the result of TB infection that was acquired in the past, as compared to recently or newly acquired infection with development of TB disease. TB genotyping is a tool that can add value to conventional contact investigation.



Whole-genome sequencing for investigation of recent TB transmission in the United States: Current uses and future plans

Sarah Talarico, PhD and Benjamin Silk, PhD
Surveillance, Epidemiology, and Outbreak Investigations Branch



Whole-genome sequencing for investigation of recent TB transmission in the United States: Current uses and future plans

Small Text: Sarah Talarico, PhD, FID; Benjamin Silk, PhD, FID; Tommi Shaw, MPH and Martin O'Leary, MPH, MS; Surveillance, Epidemiology, and Outbreak Investigations Branch; Division of Tuberculosis Elimination; National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention; U.S. Department of Health and Human Services

Part 2: Case Studies: Using WGS to investigate TB cluster alerts in California

Part 3: Plans for transition to universal, prospective WGS

<https://www.cdc.gov/tb/programs/genotyping/default.htm>

TB GIMS updates

TB GIMS updates in 2018

- Cluster alert tracking for alerted clusters
- Prompt and open data reporting for surveillance of large TB outbreaks in the United States (LOTUS)
- Transition to universal prospective whole-genome sequencing (WGS)
- Recent Transmission estimate pre-release
- TB GIMS online help
- TB GIMS directory

**December TB GIMS updates:
TB GIMS Directory**

TB GIMS Directory

TB GIMS Home
Search
Genotype Results
Patient Results
Blank State Case Numbers
Blank Surveillance
Records
Submitted Isolates
New Isolates
Edit Isolates
Submit Isolates
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Import Data
Reports and Tools
Watch List
Cluster Snapshot
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Additional Testing
WGS Request
Directory
» View Users
Contact Us



TB GIMS Directory

- Shows county jurisdiction
- Excludes inactive users
- Export to Excel

	Role	First Name ▼	Last Name	Email	Jurisdiction
	State TB Program Standard User	Tawanda	Washington	tawanda.washington@flhealth.gov	DUVAL
	State TB Program Standard User	Sherrie	Arnwine	sherrie.arnwine@flhealth.gov	
	State TB Program Standard User	Sharlene	Edwards	sharlene.edwards@flhealth.gov	PINELLAS
	State TB Program Standard User	Rick	Stevens	Rick_Stevens@doh.state.fl.us	
	State TB Program Standard User	Rachel	Steele	Rachel.Steele@flhealth.gov	PINELLAS
	State TB Program Standard User	Patrice	Boon	patrice.boon@flhealth.gov	
	State TB Program Standard User	Oswaldo	Curbelo	oswaldocurbelo@flhealth.gov	MIAMI-DADE
🚩	State TB Program Super User	Mia	Rosario	mia.rosario@flhealth.gov	
	State TB Program Standard User	Manuel	Lorenzo Hurtado	Manuel_LorenzoHurtado@doh.state.fl.us	PALM BEACH
🚩	State TB Lab-Program Super User	Lori	Johnston	lori_johnston@doh.state.fl.us	
🚩	State TB Lab-Program Super User	LaTweika	Salmon	Latweika.Salmon@flhealth.gov	
	State TB Program Standard User	Kristen	Pate	Kristen.Pate@flhealth.gov	PINELLAS
	State TB Program Standard User	Jylmarie	Lewis	jylmarie.lewis@flhealth.gov	
🚩	State TB Program Super User	Jose	Zabala	Jose_Zabala@doh.state.fl.us	
	State TB Program Standard User	Johnny	Lloyd	johnny.lloyd@flhealth.gov	

Export

**August TB GIMS updates:
Recent Transmission estimates, online help**

Recent Transmission estimates

 Centers for Disease Control and Prevention
Your Online Source for Credible Health Information

User: Self, Julie L. Tuberculosis Genotyping Information Management System

TB GIMS Home

- Search
 - Genotype Results
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 - Blank State Case Numbers
 - Blank Surveillance
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 - Cluster Tracking List
 - Recent Transmission**
- Additional Testing**
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 - View Users
 - Contact Us

Tuberculosis Genotyping Information Management System

The last TB GIMS Surveillance Upload includes data transmitted
Searches and reports will only include data reported to CDC by the state.

Announcements:
No New Announcements.

Recent GENType Cluster Alert Changes

No Alerts in the past 3 months.

Timeliness of Genotyping - by Isolate

Time From → To

- Specimen collection → Isolate shipped to genotyping lab ⓘ
- Receipt at genotyping lab → Genotype create date ⓘ
- Genotype create date → State Case No. entered ⓘ
- Genotype create date → Isolate Linked ⓘ
- Specimen collection → Isolate Linked ⓘ

*Year to date. NA-Not Available.

Isolate Linking ⓘ

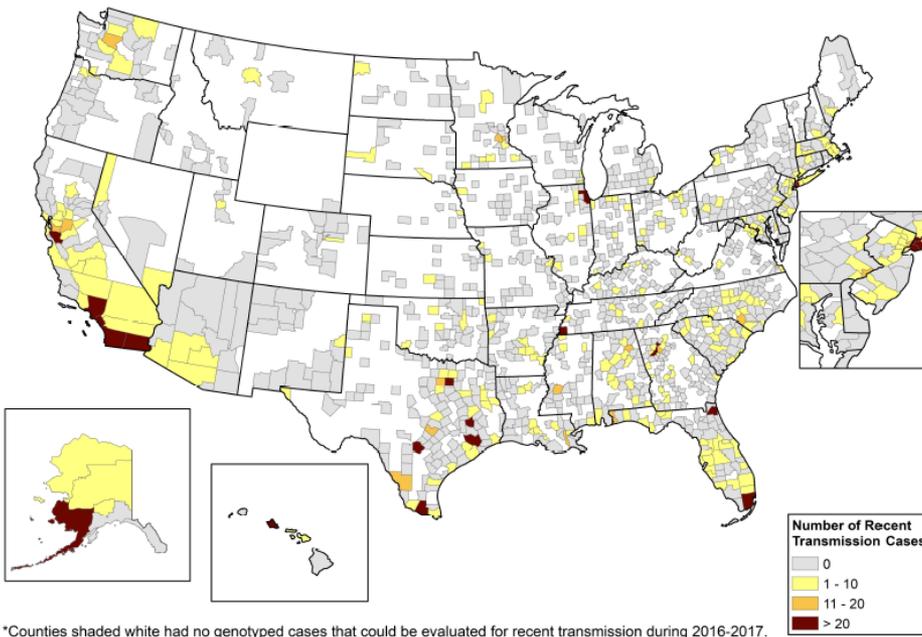
Number of Isolates	2017	2018*
Total isolates	0	0

County-level recent transmission estimates pre-released to each jurisdiction before publication of annual report

	A	B	C	D	E	F	G
1	Estimates of Recent Transmission						
2		State: STATE A		Timeframe: 2016 - 2017			
3		County: ALL					
4			Total No. of Genotyped Cases*	Cases Attributed to Recent Transmission**		Cases Attributed to Extensive Recent Transmission***	
5	State	County		no.	%	no.	%
6	National	-	13650	1787	13.1	625	4.6
7	STATE A	ALL	400	70	17.5	25	6.3
8	STATE A	County A	1	0	0	0	0
9	STATE A	County B	5	0	0	0	0
10	STATE A	County C	3	0	0	0	0
11	STATE A	County D	1	0	0	0	0
12	STATE A	County E	8	1	12.5	0	0
13	STATE A	County F	1	0	0	0	0
14	STATE A	County G	1	0	0	0	0
15	STATE A	County H	62	11	17.7	1	1.6
16	STATE A	County I	1	0	0	0	0
17	STATE A	County J	2	0	0	0	0
18	STATE A	County K	17	1	5.9	0	0
19	STATE A	County L	31	2	6.5	0	0
20	STATE A	County M	10	1	10	0	0
21	STATE A	County N	1	0	0	0	0
22	STATE A	County O	4	0	0	0	0
23	STATE A	County P	1	0	0	0	0

National map and state recent transmission estimates released with annual report

Figure 1. Estimated Cases Attributed to Recent Transmission of Tuberculosis, United States, 2016–2017*



*Counties shaded white had no genotyped cases that could be evaluated for recent transmission during 2016-2017.

Estimates of Recent Transmission

State: ALL

Timeframe: 2016 - 2017

County: ALL

State	Total No. of Genotyped Cases*	Cases Attributed to Recent Transmission**		Cases Attributed to Extensive Recent Transmission**	
		no.	%	no.	%
National	13650	1787	13.1	625	4.6
ALABAMA	179	56	31.3	23	12.8
ALASKA	90	38	42.2	22	24.4
ARIZONA	295	18	6.1	0	0
ARKANSAS	105	11	10.5	4	3.8
CALIFORNIA	3198	431	13.5	169	5.3
COLORADO	94	1	1.1	0	0
CONNECTICUT	85	3	3.5	0	0
DELAWARE	22	0	0	0	0
FLORIDA	931	131	14.1	42	4.5
GEORGIA	407	70	17.2	25	6.1
HAWAII	182	27	14.8	6	3.3
IDAHO	19	0	0	0	0
ILLINOIS	463	62	13.4	16	3.5
INDIANA	143	12	8.4	0	0
IOWA	69	1	1.4	0	0
KANSAS	60	1	1.7	0	0
KENTUCKY	114	9	7.9	0	0
LOUISIANA	151	27	17.9	0	0
MAINE	33	2	6.1	0	0
MARYLAND	312	27	8.7	10	3.2
MASSACHUSETTS	282	14	5	3	1.1
MICHIGAN	155	4	2.6	4	2.6
MINNESOTA	278	35	12.6	10	3.6
MISSISSIPPI	90	19	21.1	10	11.1
MISSOURI	120	12	10	1	0.8
MONTANA	5	1	20	0	0
NEBRASKA	32	1	3.1	0	0
NEVADA	102	9	8.8	2	2
NEW HAMPSHIRE	26	2	7.7	0	0
NEW JERSEY	443	38	8.6	10	2.3
NEW MEXICO	63	1	1.6	0	0
NEW YORK	278	13	4.7	1	0.4
NEW YORK CITY	895	157	17.5	58	6.5
NORTH CAROLINA	353	50	14.2	24	6.8
NORTH DAKOTA	25	2	8	0	0
OHIO	208	19	9.1	6	2.9
OKLAHOMA	92	14	15.2	1	1.1
OREGON	96	5	5.2	0	0
PENNSYLVANIA	258	25	9.7	3	1.2
RHODE ISLAND	16	0	0	0	0

* Total number of M. tuberculosis genotyped cases who are eligible to be evaluated for recent transmission (i.e., complete data for the plausible-source case method's algorithm).

** Number of cases attributed to recent transmission includes any given case with a plausible source case regardless of cluster size.

Online Help



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User: Self, Julie L.
Tuberculosis Genotyping Information Management System Version 2.0.13
Role: Super User

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- [Patient Results](#)
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- [Blank Surveillance](#)

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Tuberculosis Genotyping Information Management System

The last TB GIMS Surveillance Upload includes data transmitted to CDC through: 01/08/2019
Searches and reports will only include data reported to CDC by the state and included in the latest TB GIMS surveillance upload.

Announcements:

No New Announcements.

State:

Genotyping Surveillance Coverage

Year	2016	2017	2018	2019*
National (%)	97.4	97.3	82.9	0.0

*Year to date. NA-Not Available. Source: NTIP

Timeliness of Genotyping - by Isolate

Time From → To	Median number of days		Goal (days)
	National		
	2018	2019*	
Genotype create date → State Case No. entered	1	68	56
Genotype create date → Isolate Linked	6	54	90
Specimen collection → Isolate Linked	89	131	NA
Specimen collection → Isolate shipped to genotyping lab	51	57	NA
Receipt at genotyping lab → Genotype create date	14	20	14

*Year to date. NA-Not Available.

Online Help



[Introduction to TB GIMS](#)

[TB GIMS Homepage](#)

[TB GIMS User Roles](#)

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Reports and Tools Overview

The Reports and Tools functions will enable you to create reports and maps based on genotype results (Generate Reports), download templates for importing data (Templates), export TB GIMS Genotyping and Surveillance data (Export), view profiles of county clusters (County Cluster Snapshot), and create saved searches that you wish to be notified on when a new isolate or patient record is added (Watch List).

Click on each link below to see specific functions

[Watch List](#)

The Watch List feature may be used to monitor for recent activity of specific GENTypes or PCRTypes, allowing a TB program to monitor the known clusters or outbreaks or new cases that may be attributed to recent transmission.

[Cluster Snapshot](#)

The Cluster Snapshot feature may be used to generate a report that summarizes the genotyping and surveillance data for a genotype cluster as defined by the input criteria on the selection screen. The snapshot can be used with the cluster investigation worksheet to assist with reviewing and prioritizing genotype clusters for additional investigation or intervention.

[Generate Reports](#)

The Generate Reports feature may be used to access various reports within the TB GIMS system that will merge and analyze genotyping and surveillance data within the database. The frequency of each report is dynamic and will be based on the data that is in the TB GIMS database at the time the user initiates the selected report.

[Templates](#)

The Templates feature may be used to create records for multiple isolates at one time (i.e., batch mode).

[Export Data](#)

The Export Data feature may be used to export all TB GIMS genotyping and surveillance data .

[Cluster Tracking List](#)

The Cluster Tracking feature is a system-automated process to handle Cluster Alerts. These alerts coordinate with the weekly cluster alert reporting process within TB GIMS. This process captures point-in-time cluster characteristics consistent with the Cluster Snapshot feature.

[Recent Transmission](#)

The Recent Transmission feature may be used to generate reports report displaying the number of genotyped cases, the number of cases attributed to recent transmission, the number of cases attributed to extensive recent transmission, and the proportion of genotyped cases that are attributed to extensive recent transmission by jurisdiction during the selected 2-year period.

**June TB GIMS updates:
Cluster alerts, LOTUS, and WGS**

Cluster alerts

- Email notifications enabled nationally for LLR alerts
- Searchable tracking list of LLR and LOTUS alerts
- Alert details page
 - Line list of patients included in the cluster alert
 - Summary epi information about alerted cluster
 - CDC's priority assessment and notes about cluster
 - Attachments related to the cluster

Cluster alerts



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Tuberculosis Genotyping Information Management System Version 2.0.13
Role: Super User 

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Genotype Results

Patient Results

Blank State Case Numbers

Blank Surveillance

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Tuberculosis Genotyping Information Management System

The last TB GIMS Surveillance Upload includes data transmitted to CDC through: 02/05/2019
Searches and reports will only include data reported to CDC by the state and included in the latest TB GIMS surveillance upload.

Announcements:  No New Announcements.

State: ALL Submit

Genotyping Surveillance Coverage 

Year	2016	2017	2018	2019*
National (%)	97.4	97.3	87.9	5.4

*Year to date. NA-Not Available. Source: NTIP

Timeliness of Genotyping - by Isolate

Time From → To	Median number of days		Goal (days)
	National		
	2018	2019*	
Specimen collection → Isolate shipped to genotyping lab 	51	55	NA
Receipt at genotyping lab → Genotype create date 	14	13	14
Genotype create date → State Case No. entered 	1	8	56
Genotype create date → Isolate Linked 	5	14	90
Specimen collection → Isolate Linked 	89	97	NA

*Year to date. NA-Not Available.

Isolate Linking 

Number of Isolates	2018	2019*
Total isolates	8,814	976
Linkable isolates ¹	8,558	969

Pending Isolates

Number of Isolates	2018	2019*
Pending genotype results	76	469
Pending additional results (MIRU2 or RFLP)	1	0

Cluster alert tracking list

Cluster Tracking List Items **(11 Total Records)** Page of [Go](#)

				Alert Date	State ID	County	GENType	PCRTYPE	Alert Level	CDC Action	Source	Type	Method	Overall LOTUS Classification
				06/06/2018	STATE A	COUNTY B	G00010	PCR00002	High	CDC Engagement	LLR	GENType		
				07/19/2017	STATE A	COUNTY A	G35781	PCR26534	Medium	CDC Engagement	LLR	GENType		
				03/29/2017	STATE A	COUNTY D	G00617	PCR00001	High		LOTUS	GENType	County	Pending
				05/24/2016	STATE A	COUNTY A	G03953	PCR00039	High	CDC Engagement	LLR	GENType		
				03/31/2016	STATE A	COUNTY B	G00013	PCR00016	High		LOTUS	GENType	County	Previous alert in same jurisdiction
				10/08/2015	STATE A	COUNTY C	G21931	PCR02280	Medium	CDC Monitoring	LLR	GENType		
				06/30/2014	STATE A	COUNTY B	G00013	PCR00016			LOTUS	GENType	State	Counted (>=10 cases)
				11/13/2013	STATE A	COUNTY D	G00617	PCR00001	High	CDC Engagement	LLR	GENType		
				12/07/2012	STATE A	COUNTY A		PCR01540	Medium	CDC Monitoring	LLR	PCRTYPE		
				04/20/2011	STATE A	COUNTY D	G00617	PCR02397	Medium	CDC Engagement	LLR	GENType		
				06/28/2011	STATE A	COUNTY F	G00010	PCR00002	Medium	CDC Monitoring	LLR	GENType		

[View](#) [Export](#)

Cluster tracking list filter and search criteria

▼ Basic Options

• State
STATE A ▼

County
Select a County
COUNTY A
COUNTY B
COUNTY C
COUNTY D
COUNTY E
COUNTY F

Genotype:
GENType: ⓘ
PCRTYPE:

Source
Select
LLR
LOTUS

Alert Level
Select
Medium
High

Type
Select
GENType
PCRTYPE

CDC Action
Select
CDC Engagement
CDC Monitoring
Not Assigned

Overall LOTUS Classification
Select
Pending
Counted (>=10 cases)
Uncounted (5-9 cases)
Refuted by WGS (<5 cases)

Date Type
Alert Date ▼

Start Date
01/01/2011 📅

End Date
06/05/2018 📅

Find Clear

Cluster Details for LLR: G35781, COUNTY A, STATE A

Cluster Information

Alert Date: 07/19/2017

State ID: STATE A

County: COUNTY A

GENType: G35781

PCRTYPE: PCR26534

LLR: 5.834901

Alert Level: Medium ⓘ

Source: LLR

of cases: 4

cases in rest of state: 0

cases in adjacent states: 2

Adjacent states with cases: State B

Isolates with no linked surveillance record: 1

of recent cases: 2 ⓘ

Demographics n (%)

Characteristic	COUNTY A
Race/Ethnicity	
American Indian/Alaska Native	0 (0.0%)
Asian	0 (0.0%)
Black	1 (25.0%)
Hispanic	2 (50.0%)
Multiple Race	0 (0.0%)
Native Hawaiian/Pacific Islander	0 (0.0%)
White	1 (25.0%)
Gender	
Female	1 (25.0%)
Male	3 (75.0%)
Birth	
U.S.-born	3 (75.0%)
Non-U.S.-born	1 (25.0%)

High risk characteristics for transmission or poor outcome n (%)

Characteristic	n (%)
Case with smear positive and cavitary pulmonary disease	1 (25.0%)
Homeless	0 (0.0%)
Corrections	0 (0.0%)
Long term care facility	0 (0.0%)
Any substance abuse	3 (75.0%)
Alcohol abuse	3 (75.0%)
Non-IDU	1 (25.0%)
IDU	0 (0.0%)
MDR	0 (0.0%)
INH-resistance only	0 (0.0%)
Child (<5 years)	1 (25.0%)
Child (5-14 years)	0 (0.0%)
HIV	0 (0.0%)
Dead at diagnosis or died while on therapy	0 (0.0%)

Line List (4 Total Records) ⓘ

StateCaseNo	Rpt.Date	Cnt.Date	County	Age3	Sex	RaceHisp	CountryLN	YrsInUS2	Smear	Cavity	DrugRes	HIV
2017AA00004	06/15/2017	06/15/2017	COUNTY A	65+	F	BLACK	UNITED STATES		NEG	N	None	NEG
2017AA00003	03/01/2017	03/01/2017	COUNTY A	00-04	M	HISP	UNITED STATES		NEG	N	None	NEG
2016AA00002	02/01/2016	02/01/2016	COUNTY A	25-44	M	WHITE	UNITED STATES		NEG	N	None	NEG
2015AA00001	05/31/2015	06/01/2015	COUNTY A	25-44	M	HISP	MEXICO	8	POS	Y	None	NEG

Note: The patient line list is a static list of patients that were included in the alert at the time of detection.

Status

CDC Action ⓘ

CDC Engagement

Current CDC Notes ⓘ

This field will be used to communicate any pertinent information or data nuances that CDC staff encounter during routine review of the clusters.

Attachments

File Name	Attachment Type	State View	County View	Uploaded by	Uploaded Date
📎 WGS results.pdf	WGS	Y	Y	CDC user	06/05/2018 09:30 AM
📎 Other attachment.ppt	Other	Y	N	CDC user	06/05/2018 09:00 AM

Close

Generate PDF

Large outbreak (LOTUS) detection in TB GIMS

- County and state LOTUS detection methods implemented in TB GIMS
 - Run in TB GIMS on a quarterly basis
 - E-mail notifications for state- and county-based methods
- LOTUS clusters detected by SaTScan, jurisdiction report, or CDC review manually entered into TB GIMS

Cluster tracking for LOTUS alerts

Cluster Tracking List Items (11 Total Records)

Page 1 of 1 Go

			Alert Date	State ID	County	GENType	PCRType	Alert Level	CDC Action	Source	Type	Method	Overall LOTUS Classification
			06/06/2018	STATE A	COUNTY B	G00010	PCR00002	High	CDC Engagement	LLR	GENType		
			07/19/2017	STATE A	COUNTY A	G35781	PCR26534	Medium	CDC Engagement	LLR	GENType		
			03/29/2017	STATE A	COUNTY D	G00617	PCR00001	High		LOTUS	GENType	County	Pending
			05/24/2016	STATE A	COUNTY A	G03953	PCR00039	High	CDC Engagement	LLR	GENType		
			03/31/2016	STATE A	COUNTY B	G00013	PCR00016	High		LOTUS	GENType	County	Previous alert in same jurisdiction
			10/08/2015	STATE A	COUNTY C	G21931	PCR02280	Medium	CDC Monitoring	LLR	GENType		
			06/30/2014	STATE A	COUNTY B	G00013	PCR00016			LOTUS	GENType	State	Counted (>=10 cases)
			11/13/2013	STATE A	COUNTY D	G00617	PCR00001	High	CDC Engagement	LLR	GENType		
			12/07/2012	STATE A	COUNTY A		PCR01540	Medium	CDC Monitoring	LLR	PCRType		
			04/20/2011	STATE A	COUNTY D	G00617	PCR02397	Medium	CDC Engagement	LLR	GENType		
			06/28/2011	STATE A	COUNTY F	G00010	PCR00002	Medium	CDC Monitoring	LLR	GENType		

[View](#) [Export](#)

LOTUS alerts

Submitted Isolates

New Isolates

Edit Isolates

Submit Isolates

Find Duplicates

Import Data

Reports and Tools

Watch List

Cluster Snapshot

Generate Reports

Templates

Export Data

> Cluster Tracking List

Recent Transmission

Additional Testing

Submit Requests

View Pending Results

Directory

View Users

Contact Us

Information Required

Basic Options

State

Select a State

- ALL
- ALABAMA
- ALASKA
- AMERICAN SAMOA
- ARIZONA
- ARKANSAS
- CALIFORNIA

County

Select a County

Source

Select

- LLR
- SATSCAN
- LOTUS**

Alert Level

Select

- Medium
- High

Overall LOTUS Classification

Select

- Pending
- Counted (≥ 10 cases)
- Uncounted (5-9 cases)
- Refuted by WGS (< 5 cases)

Start Date

01/01/2011

End Date

09/12/2018

Genotype:

GENType:

PCRTYPE:

Type

Select

- GENType
- PCRTYPE

Status

Select

- Not started
- Initial review
- Team review
- Program outreach

Assigned To

Select

- Sandy P Althomsons (soa4@cdc.gov)
- Jonathan Wortham (vij5@cdc.gov)
- Kristine M Schmit (yxn0@cdc.gov)
- Rebekah Stewart (yxp5@cdc.gov)

Date Type

Alert Date

Find **Clear**

Cluster Details for LOTUS: G00013, COUNTY B, STATE A

▼ Cluster Information

Alert Date: 06/30/2014

State ID: STATE A

County: COUNTY B

GENType: G00013

PCRType: PCR00016

LOTUS Detection Window Period: 07/01/2011 - 06/30/2014 ⓘ

Source: LOTUS

of cases at detection: 10

Date of First Case: 08/01/2011

Method: State

Lag: 0 months ⓘ

Cumulative Cases to Date: 15 ⓘ

Trend: -0.75 ⓘ

Total Cases past 12 months: 1

Demographics n (%)

Characteristic	COUNTY B
Race/Ethnicity	
American Indian/Alaska Native	0 (0.0%)
Asian	0 (0.0%)
Black	5 (50.0%)
Hispanic	4 (40.0%)
Multiple Race	0 (0.0%)
Native Hawaiian/Pacific Islander	0 (0.0%)
White	1 (10.0%)
Gender	
Female	2 (20.0%)
Male	8 (80.0%)
Birth	
U.S.-born	8 (80.0%)
Non-U.S.-born	2 (20.0%)

High risk characteristics for transmission or poor outcome n (%)

Characteristic	n (%)
Case with smear positive and cavitary pulmonary disease	6 (60.0%)
Homeless	0 (0.0%)
Corrections	0 (0.0%)
Long term care facility	0 (0.0%)
Any substance abuse	7 (70.0%)
Alcohol abuse	6 (60.0%)
Non-IDU	3 (30.0%)
IDU	0 (0.0%)
MDR	0 (0.0%)
INH-resistance only	0 (0.0%)
Child (< 5 years)	1 (10.0%)
Child (5-14 years)	1 (10.0%)
HIV	1 (10.0%)
Dead at diagnosis or died while on therapy	2 (20.0%)

Line List (10 Total Records) 📄

StateCaseNo	Rpt.Date	Cnt.Date	County	Age3	Sex	RaceHisp	CountryLN	YrsInUS2	Smear	Cavity	DrugRes	HIV
2014AA00001	06/01/2014	06/01/2014	COUNTY B	65+	F	BLACK	UNITED STATES		NEG	N	None	NEG
2013AA00002	08/01/2013	08/01/2013	COUNTY B	45-64	M	HISP	UNITED STATES		POS	N	None	NEG
2013AA00001	02/01/2013	02/01/2013	COUNTY A	25-44	M	BLACK	UNITED STATES		NEG	N	None	NEG
2012AA00003	05/01/2012	05/01/2012	COUNTY B	25-44	M	HISP	MEXICO	8	POS	N	None	NEG
2012AA00002	03/01/2012	03/01/2012	COUNTY B	15-24	M	BLACK	UNITED STATES		POS	Y	None	POS
2012AA00001	01/01/2012	01/01/2012	COUNTY D	00-04	F	HISP	UNITED STATES		NEG	N	None	NEG
2011AA00004	11/01/2011	11/01/2011	COUNTY B	15-24	M	WHITE	UNITED STATES		POS	Y	None	NEG
2011AA00003	09/01/2011	09/01/2011	COUNTY A	05-14	M	BLACK	UNITED STATES		NEG	N	None	NEG
2011AA00002	09/01/2011	09/01/2011	COUNTY B	25-44	M	BLACK	UNITED STATES		POS	N	None	NEG
2011AA00001	08/01/2011	08/01/2011	COUNTY B	45-64	M	HISP	MEXICO	2	POS	Y	None	NEG

Note: The patient line list is a static list of patients that were included in the alert at the time of detection.

▼ Status

Overall LOTUS Classification ⓘ

Counted (>=10 cases)

LOTUS Classification

Finalized with State Program ⓘ

Yes

Date LOTUS Classification

Finalized with State Program ⓘ

06/01/2018

Current CDC Notes ⓘ

This field will be used to communicate any pertinent information or data nuances that CDC staff encounter during routine review of the clusters.

▼ Attachments

File Name	Attachment Type	State View	County View	Uploaded by	Uploaded Date
📄 WGS results.pdf	WGS	Y	N	CDC user	06/01/2018 02:30 PM

Close

Generate PDF

LOTUS reports

New Isolates
Edit Isolates
Submit Isolates
Find Duplicates
Import Data
Reports and Tools
Watch List
Cluster Snapshot
>> Generate Reports
Templates
Export Data
Cluster Tracking List
Recent Transmission
Additional Testing
Submit Requests
View Pending Results
Directory
View Users
Contact Us

Basic Options

• Required

• **Report:** LOTUS

Type: GENType:

• **State:** Select a State

• **Method:** ALL

• **Date Type:** Alert Date

• **Date Range:** 03/31/2014 (Begin) 09/12/2018 (End)

The last TB GIMS Surveillance Upload includes data transmitted to CDC through: **09/11/2018**
Reports and maps only include data from this year and the 10 previous calendar years.

• **Report Type:** PDF

Run Clear

WGS result delivery through TB GIMS

- DTBE uploads wgSNP analysis to cluster tracking in TB GIMS
- E-mail notification when DTBE uploads attachment in TB GIMS



Wed 6/6/2018 9:00 AM

TBGIMS (CDC)

TB GIMS – CDC Attachment – COUNTY B, State A, G00010

To ■ CDCUser@cdc.gov

This message is to notify you that CDC has uploaded whole-genome sequencing results for your review in TB GIMS. The attachment was uploaded to cluster tracking for G00010 in COUNTY B, State A. Please log into the TB GIMS application to access the attachment.

If you have any questions regarding the attachment, please contact the CDC staff included on this email.

Please note that this e-mail is generated by **TBGIMS** application. For technical issues, please send e-mail to DTBESupport@cdc.gov.

Cluster Details for LLR: G00010, COUNTY B, STATE A

Cluster Information

Alert Date: 06/06/2018	State ID: STATE A	County: COUNTY B	Alert Level: High ⓘ
GENType: G00010	PCRTYPE: PCR00002	LLR: 10.834901	
Source: LLR	# of cases: 4	# cases in rest of state: 0	
# cases in adjacent states: 2	Adjacent states with cases: State B	# of recent cases: 2 ⓘ	
# Isolates with no linked surveillance record: 1			

Demographics n (%)

Characteristic	COUNTY A
Race/Ethnicity	
American Indian/Alaska Native	0 (0.0%)
Asian	0 (0.0%)
Black	1 (25.0%)
Hispanic	2 (50.0%)
Multiple Race	0 (0.0%)
Native Hawaiian/Pacific Islander	0 (0.0%)
White	1 (25.0%)
Gender	
Female	1 (25.0%)
Male	3 (75.0%)
Birth	
U.S.-born	3 (75.0%)
Non-U.S.-born	1 (25.0%)

High risk characteristics for transmission or poor outcome n (%)

Characteristic	n (%)
Case with smear positive and cavitary pulmonary disease	1 (25.0%)
Homeless	0 (0.0%)
Corrections	0 (0.0%)
Long term care facility	0 (0.0%)
Any substance abuse	3 (75.0%)
Alcohol abuse	3 (75.0%)
Non-IDU	1 (25.0%)
IDU	0 (0.0%)
MDR	0 (0.0%)
INH-resistance only	0 (0.0%)
Child (<5 years)	1 (25.0%)
Child (5-14 years)	0 (0.0%)
HIV	0 (0.0%)
Dead at diagnosis or died while on therapy	0 (0.0%)

Line List (4 Total Records) 📄

StateCaseNo	Rpt.Date	Cnt.Date	County	Age3	Sex	RaceHisp	CountryLN	YrsInUS2	Smear	Cavity	DrugRes	HIV
2018AA00004	06/01/2018	06/01/2018	COUNTY B	65+	F	BLACK	UNITED STATES		NEG	N	None	NEG
2018AA00003	03/01/2018	03/01/2018	COUNTY B	00-04	M	HISP	UNITED STATES		NEG	N	None	NEG
2017AA00002	02/01/2017	02/01/2017	COUNTY B	25-44	M	WHITE	UNITED STATES		NEG	N	None	NEG
2016AA00001	05/31/2016	06/01/2016	COUNTY B	25-44	M	HISP	MEXICO	8	POS	Y	None	NEG

Note: The patient line list is a static list of patients that were included in the alert at the time of detection.

Status

CDC Action ⓘ

CDC Engagement

Current CDC Notes ⓘ

This field will be used to communicate any pertinent information or data nuances that CDC staff encounter during routine review of the clusters.

Attachments

File Name	Attachment Type	State View	County View	Uploaded by	Uploaded Date
📄 WGS results.pdf	WGS	Y	Y	CDC user	06/06/2018 09:30 AM
📄 Other attachment.ppt	Other	Y	N	CDC user	06/06/2018 09:00 AM

Close

Generate PDF

Other small changes

- Include case count in Cluster Tracking List
- Change isolates to “Not linkable”
- Specify timeframe for Change in Cluster Alert Level report

Acknowledgments

- **TB GIMS Development team**
 - Jeff Chrismon
 - Shonna Luten
 - Destini Hutcherson
- **DTBE Laboratory Branch**
- **DTBE Surveillance, Epidemiology, and Outbreak Investigations Branch**
- **National TB Molecular Surveillance Center**
- **TB program partners**



Genotyping Questions: tbgenotyping@cdc.gov

TB GIMS Questions: dtbesupport@cdc.gov

For more information, contact CDC
1-800-CDC-INFO (232-4636)
TTY: 1-888-232-6348 www.cdc.gov

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

