

# From Researcher to Patient: The Role of the Laboratory in Diagnostics and Treatment

Max Salfinger, MD

Director, Mycobacteriology & Pharmacokinetics Laboratories <u>salfingerm@njhealth.org</u>

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 $\Box$  Tool Box 1 & 2 **Growth Detection** Identification of NTM **Antimicrobial Susceptibility Testing (AST) Survey 2010 & 2017** 





#### **Financial Disclosure**

# **NONE to report**



**P-NTM Species** 

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# Four integrated health care delivery systems\*, 1991-2007

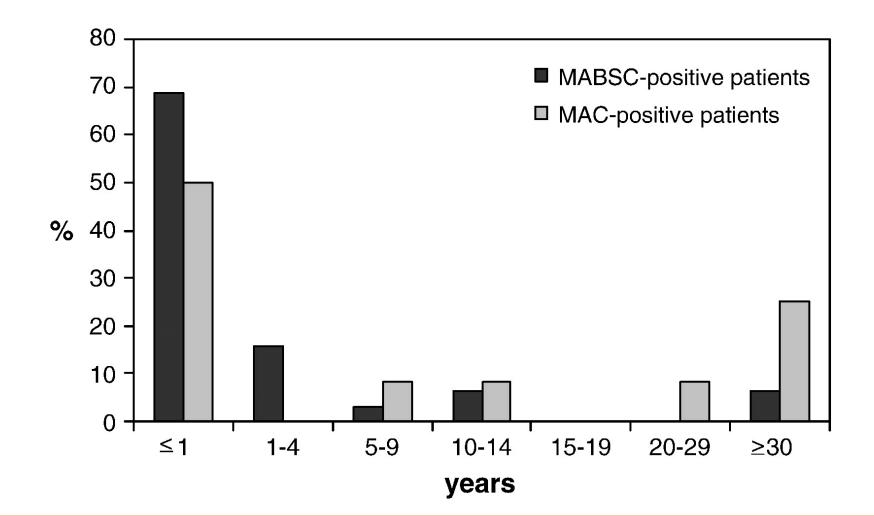
• *M. avium* complex 1,495 (80.1%) M. chelonae/abscessus (12.1%)225 • M. fortuitum 106 (5.6%) M. kansasii 102 (5.5%)(2.8%)• M. simiae 53 M. xenopi (1.7%)33

\*KP Southern California, KP Southern Colorado, Group Health, Geisinger



NTM in CF – Age Related

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Catherinot et al. J Cyst Fibros. 2013 Jan;12(1):74-80 <sup>5</sup>





**Tool Box 1 & 2 Growth Detection** Identification of NTM **Operation Operation Opera Testing (AST) Survey 2010 & 2017** 



**Toolbox-1** 

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#### Specimen – sputum, bronchoscopy, formalin-fixed tissue

- NALC-NaOH versus Oxalic acid (CF w/history of Pseudmonas aeruginosa)
- AFB microscopy
- Solid (LJ, Middlebrook bi-plate, NTM plate) & broth-based media
- NAAT-D (TB complex, NTM -mostly MAC)
- NAAT-R (RIF, INH and more)
- Direct AST

Ideally, molecular testing 7 days a week





# AFB positive culture (broth-, solid-based media)

- NAAT-D (TB complex)
- NAAT-R (RIF, INH and more; NTM- macrolide & aminoglycoside)
- Identification (Sequencing-*rpoB* or 16S; MALDI-TOF; Nucleic acid probe kits; Line Probes)
- High Performance Liquid Chromatography (HPLC); PCR Restriction Analysis (PRA); Biochemicals
- Minimal Inhibitory Concentration (MIC) (rapidly and slowly growing NTM)
- Combination MIC



# $\Box$ Tool Box 1 & 2 **Growth Detection** Identification of NTM **Operation Operation Opera Testing (AST) Survey 2010 & 2017**

Topics



## **Processing Sputum**

- Procedures kill all but 10-20% of the mycobacteria
- Contamination

2-5% of sputum specimens on Loewenstein-Jensen medium (LJ)





# M. abscessus (Rough)





## **RGM Medium-1**

- Selective Medium (7H9 base + OADC + 4 antimicrobials)
- Sputum samples (N=212) from CF patients (N=172)
- Comparison BCSA vs RGM vs MGIT & LJ
- Direct inoculation onto the plates
- Double decontamination for standard AFB work up (MGIT & LJ)
- Incubation 28d (plates) and 56d (MGIT & LJ)



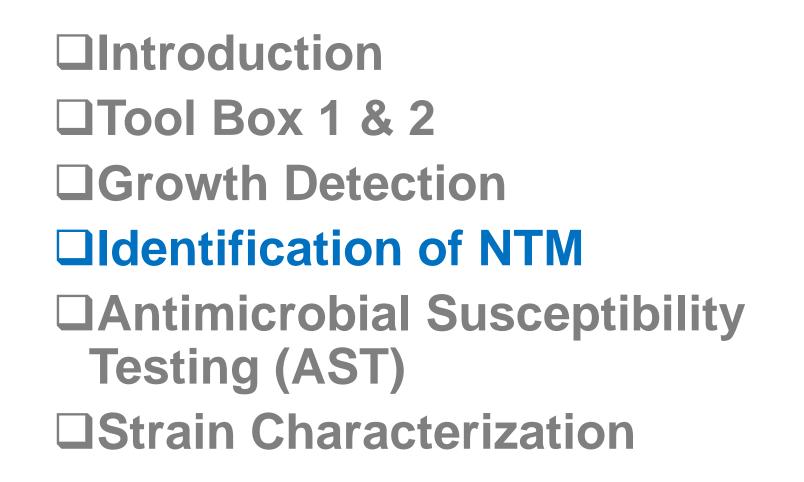
**RGM Medium-2** 

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|   |                         | Total | BCSA | AFB | RGM |
|---|-------------------------|-------|------|-----|-----|
| • | <i>M. abscessus</i> ssp | 29    | 7    | 18  | 28  |
| • | M. chelonae             | 5     | 3    | 0   | 5   |
| • | M. immunogenum          | 3     | 1    | 0   | 2   |
| • | MAC                     | 7     | 0    | 6   | 5   |
| • | M. mucogenicum          | 4     | 0    | 6   | 5   |
| • | M. gordonae             | 3     | 0    | 0   | 3   |
|   |                         |       |      |     |     |
| • | Total                   | 51    | 11   | 24  | 47  |

Plongla et al J Clin Microbiol May 2017<sup>13</sup>





Topics

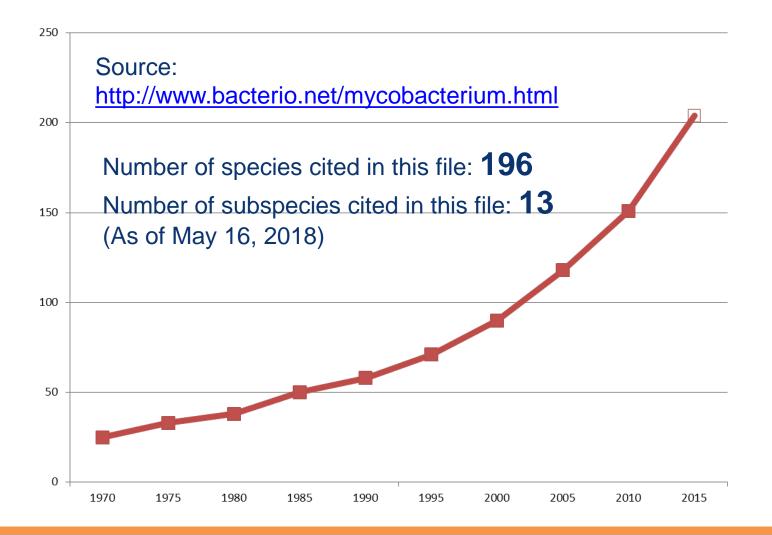


#### M. abscessus [rough + smooth] & M. avium [translucent]





Mycobacterium sp.





#### MALDI-TOF MS (Matrix-Assisted Laser Desorption ionization - time of flight mass spectrometry)

MALDI-TOF MS offers a rapid, protein-profiling based technique for identification of mycobacterial isolates from liquid or solid culture media, with high analytical capabilities at a less expensive cost compared to *rpoB* gene sequence analyses.



#### MALDI-TOF MS can reliably and rapidly identify

- approximately 88% of *Mycobacterium* species, 90% of *Nocardia* species, and 51% of other aerobic actinomycetes encountered in routine clinical practice at a tertiary medical center/reference laboratory.
  - Using a custom, enhanced library and a streamlined extraction procedure
- Described the ability of the manufacturer's library to identify these groups of organisms and described the effects of lowering the accepted cutoff score from 2.0 to 1.7
  - ✓ As the manufacturer continues to expand its database, many laboratories will have the ability to identify many of the isolates they routinely encounter using MALDI-TOF MS.
  - An expanded custom library may ultimately be the most useful tool for identification of the uncommon species encountered most often in a reference laboratory setting.



erm(41) gene variant

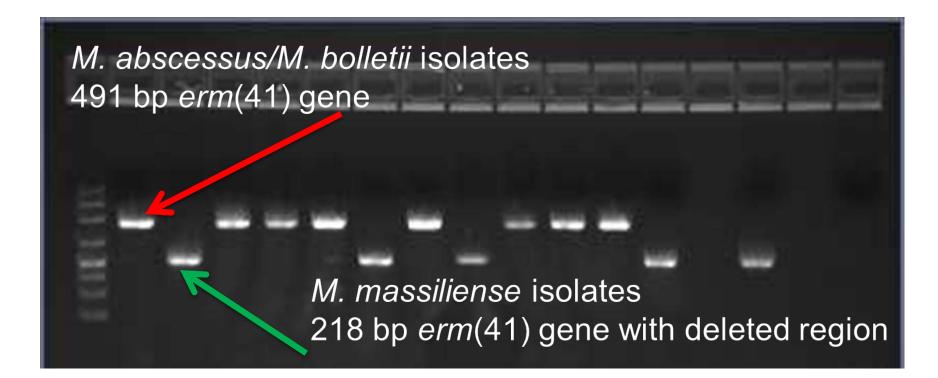
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# Erythromycin Methylase Gene(41)

- Macrolide antibiotics activate the *erm(*41) gene
- Results in inducible (delayed) resistance to clarithromycin and/or azithromycin
- Mutations or deletions inactivate this gene resulting in macrolide susceptibility
- Presence of wildtype or a mutated sequence differs within the 3 subspecies



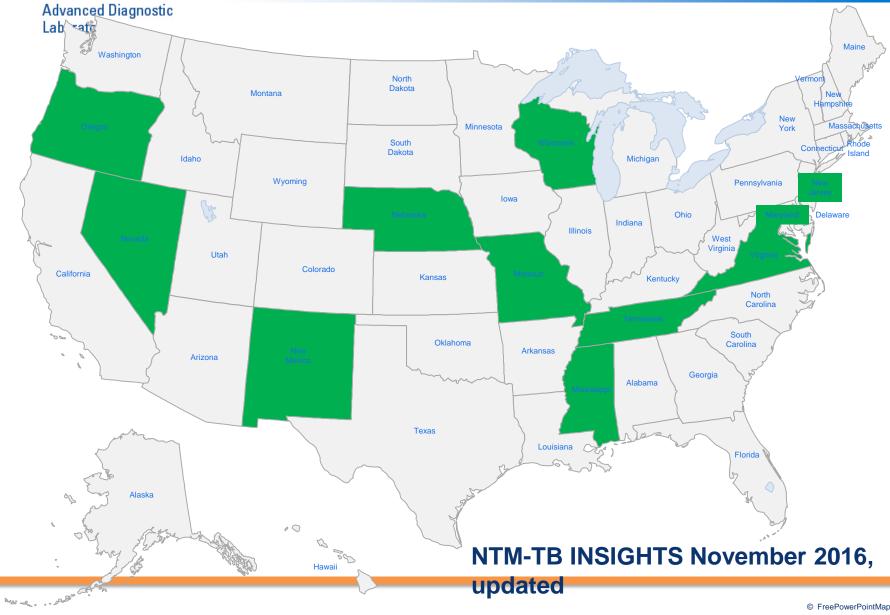




*M. massiliense* is positive for the *erm*(41) gene but contains a 273- bp deletion within the gene rendering the gene nonfunctional.



# Notifiable NTM by State

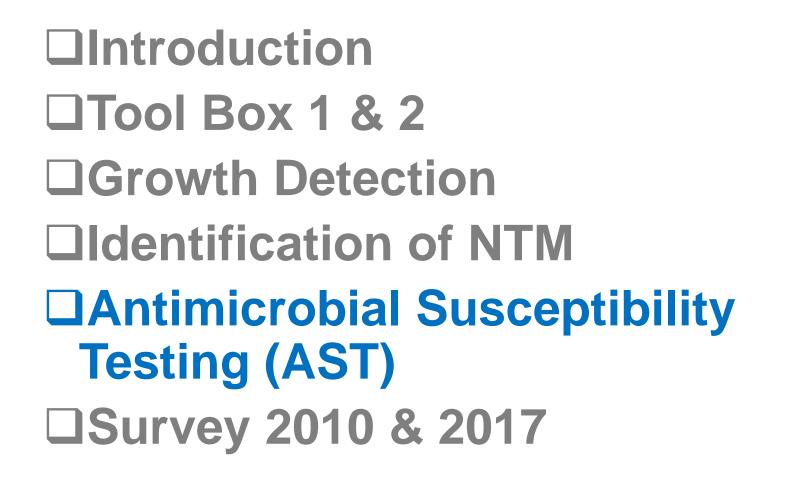




#### **NTM Reporting Requirements**

| State<br>Maryland          | <b>Reporting Time for NTM</b> within one working day       | What is Required to be Reported (websites accessed on 12-11-2016)<br>Mycobacterium spp., other than Mycobacterium tuberculosis complex or<br>Mycobacterium leprae   |
|----------------------------|--|---|
| Mississippi                | one week   | Nontuberculous mycobacterial disease  |
| Missouri                   | within 3 days  | Nontuberculosis mycobacteria (NTM)  |
| Nebraska                   | within 7 days  | <i>Mycobacteria</i> spp. (including <i>M. tuberculosis</i> complex organisms [for genotyping] and all "atypical" species, to include culture, nucleic acid tests, or positive histological evidence indicative of tuberculosis infection or disease)  |
| Nevada                     | not specified  | Submission of isolates of Mycobacterium spp.  |
| New Jersey                 | within 72 hours  | Mycobacterium, atypical   |
| New Mexico                 | within 24 hours  | Tuberculosis or other nontuberculous mycobacterial infections (including <i>Mycobacterium avium</i> complex or leprosy)   |
| Ohio<br>Oregon<br>Virginia | close of the next biz. day<br>one working day<br>immediate | <ul> <li>Mycobacterial disease other than tuberculosis (MOTT)</li> <li>Nontuberculous mycobacterial infection (nonrespiratory)</li> <li>Results of cultures positive for any member of the <i>Mycobacterium tuberculosis</i></li> <li>complex (i.e., <i>M. tuberculosis, M. bovis, M. africanum</i>) or any other mycobacteria.</li> <li>Results of rapid methodologies, including acid hybridization or nucleic acid</li> <li>amplification, which are indicative of <i>M. tuberculosis</i> complex or any other</li> <li>mycobacteria.</li> </ul> |
| Wisconsin                  | within 72 hours  | Mycobacterial disease (nontuberculous)  |









> *Mycobacterium tuberculosis* complex *Mycobacterium avium* complex *Mycobacterium kansasii Mycobacterium marinum* Miscellaneous slowly growing NTM Rapidly growing mycobacteria (RGM)

CLSI M24-A2 (2011) Susceptibility testing of mycobacteria, nocardia, and other aerobic actinomycetes – Approved standard, second edition (in revision)





# **First-line drugs:** Macrolide (Clarithromycin) Amikacin

Second-line drugs: Moxifloxacin Linezolid Clofazimine (only MIC, no interpretation)





## **First-line drugs:**

Amikacin, cefoxitin, ciprofloxacin,, clarithromycin, doxycycline, imipenem, linezolid, moxifloxacin, trimethoprimsulfamethoxazole, tobramycin **Second-line drugs:** 

Tigecycline (only MIC, no interpretation) Clofazimine (only MIC, no interpretation)



# Rapidly growing NTM NTM4: 15-Drug MIC, including Clofazimine/Amikacin Combo NTM6: 20-Drug MIC, including Clofazimine/Amikacin Combo

#### **Slowly growing NTM**

 NTM10: 10-Drug MIC, incl. RIF-EMB Combo
 NTM9: RIF-EMB Combo, including RIF and EMB single drug MIC

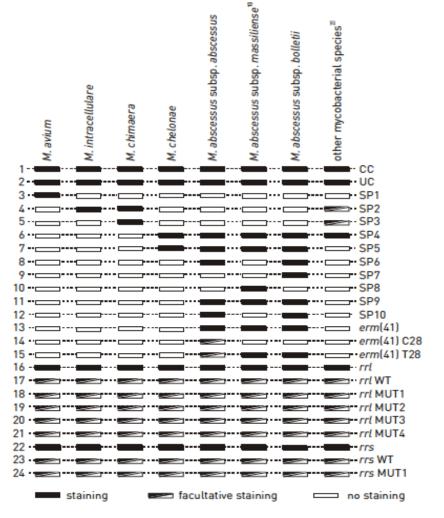
**National Jewish Health 2018** 



## **NTM-DR Line Probe Assay**

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|      | Conjugate Control (CC)<br>Universal Control (UC)<br>SP1<br>SP2<br>SP3<br>SP4<br>SP5<br>SP6<br>SP7<br>SP8<br>SP9<br>SP10  |
|------|--|
| <br> | erm[41] Locus Control (erm[41)]<br>erm[41] C28<br>erm[41] T28  |
|      | <i>rrl</i> Locus Control ( <i>rrl</i> )<br><i>rrl</i> wild type probe ( <i>rrl</i> WT)<br><i>rrl</i> mutation probe 1 ( <i>rrl</i> MUT1)<br><i>rrl</i> mutation probe 2 ( <i>rrl</i> MUT2)<br><i>rrl</i> mutation probe 3 ( <i>rrl</i> MUT3)<br><i>rrl</i> mutation probe 4 ( <i>rrl</i> MUT4) |
|      | rrs Locus Control (rrs)<br>rrs wild type probe (rrs WT)<br>rrs mutation probe 1 (rrs MUT1)<br>colored marker   |



Band No. 1 (CC): Conjugate Control Band No. 2 (UC): Universal Control



## **Identification**

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|  | L       | LPA v WGS |      |  |
|--|---------|-----------|------|--|
| NTM species ID                             | n (163) | sens †    | spec |  |
| M. abscessus subsp. abscessus              | 122     | 100       | 100  |  |
| M. abscessus subsp. massiliense            | 36      | 100       | 100  |  |
| <i>M. abscessus</i> subsp. <i>bolletii</i> | 5       | 100       | 100  |  |

Table 1: Hain Genotype NTM-DR Ver. 1.0 results compared to whole genome sequencing (WGS) phylogenomic results. sens, % sensitivity; spec, % specificity; n, number of samples in each category. Number of samples for each species (n), Line Probe Assay (LPA). <sup>†</sup> Sensitivity and specificity are reported in percentages.



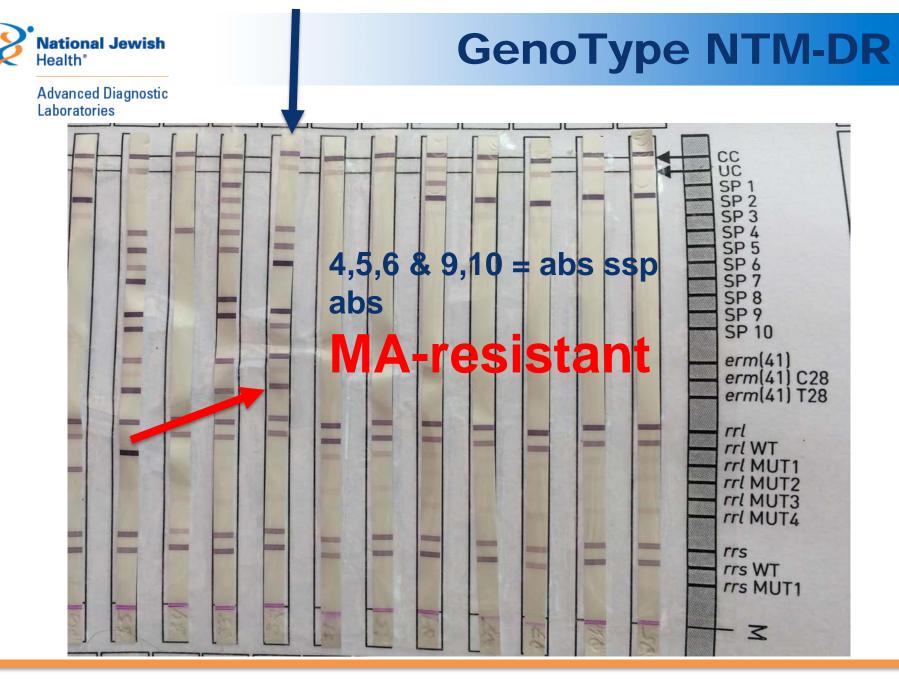
# **Drug Resistance Markers**

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|                            |      | LPA v WGS |      |                                      |
|----------------------------|------|-----------|------|--------------------------------------|
| locus                      | n    | sens      | spec | n, resistant                         |
| 16S rDNA ( <i>rrs</i> ) AG | 151  | 100       | 100  | 14 (9%)                              |
| 23S rDNA ( <i>rrl</i> ) MA | 156  | 100       | 100  | 3 (2%)                               |
| <i>erm</i> (41) MA         | 127* | 100       | 100  | 109 <sup>†</sup> (86% <sup>‡</sup> ) |

Table 2: Hain Genotype NTM-DR Ver. 1.0 results compared to site-specific extractions of whole genome sequence results for three loci interrogated by the line probe assay, 16S rRNA, 23S rRNA, and erm(41) \**M. abscessus* subspp. *abscessus* and *bolletii* only, <sup>†</sup>T at position 28 of full length *erm*(41) indicates inducible macrolide resistance, <sup>‡</sup>In spite of their full length *erm*(41) gene, 14% of samples possessed C at position 28, indicating macrolide susceptibility for these strains

**Epperson et al NJH: Unpublished Data** 





# $\Box$ Tool Box 1 & 2 **Growth Detection** Identification of NTM **Operation Operation Opera Testing (AST) Survey 2010 & 2018**



# **APHL Survey 2010**

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- Distributed to **1,444** laboratories enrolled in mycobacteriology proficiency testing program
- **656 (45%)** responded, 580 performed some level of mycobacteriology service in-house
- N=580 laboratories
  - 80% hospital-based
  - 9% state public health
  - 4% commercial
  - 4% local public health
  - 3% other

#### Source:

https://www.aphl.org/programs/infectious\_disease/Documents/NationalTBReport\_June 2012.pdf



**APHL Survey 2010** 

| Culture positivity (N=212) |                |            |                       |  |
|----------------------------|----------------|------------|-----------------------|--|
| # of labs                  | NTM-positivity | # of labs  | <b>TBC-positivity</b> |  |
| 8                          | <1%            | 72         | <1%                   |  |
| <u>164</u>                 | 1-10%          | <u>118</u> | 1-10%                 |  |
| <u>40</u>                  | >10%           | <u>22</u>  | >10%                  |  |



**APHL Survey 2010** 

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# Identification (N=189)

| Service             | Hospital | State PH | Com. | %    |
|---------------------|----------|----------|------|------|
| AFB only            | 1        | 0        | 0    | 0.5  |
| TBC vs NTM          | 8        | 1        | 4    | 6.9  |
| <b>TBC/some NTM</b> | 76       | 14       | 8    | 51.9 |
| <b>TBC/most NTM</b> | 25       | 22       | 5    | 27.5 |
| <b>TBC/all NTM</b>  | 10       | 13       | 2    | 13.2 |
| Total               | 120      | 50       | 19   | 100  |

Data not shown for Local PH and other



- Distributed to 50 state public health laboratories (10 days ago)
- 50 (100%) responded
- U.S. population 2016: **323,127,513** (D.C. not included)



% States

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# NAAT Testing (N=50)

- No response 1
- No TB NAAT 1
- TB NAAT only
   37
   74

   TB + NTM NAAT
   11
   22
   17.7

#

**%**Pop.



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# NTM work-up (N=50)

# %States No ID 2 In-house all 54 27 In-house some 20 40 Sent to Ref Lab 2 1



| NTM ID (N=45, multiple responses) |    |         |  |
|-----------------------------------|----|---------|--|
|                                   | #  | %States |  |
| Probes                            | 19 | 42.2    |  |
| HPLC                              | 11 | 24.4    |  |
| <b>MALDI-TOF*</b>                 | 17 | 37.8    |  |
| Sequencing                        | 19 | 42.2    |  |
| WGS                               | 1  | 2.2     |  |
| Other – Line Probes               | 2  | 4.4     |  |



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# M. abscessus subspecies ID (N=47) # %States %Pop Yes 6 12.8 28.8 No 41 87.2



#### **NTM-TB INSIGHTS**

- Bi-monthly newsletter
- Please feel free to sign up it is free ©
- <u>https://www.nationaljewish.org/for-</u> professionals/newsletters/ntm-tb-insights-newsletter/ntmtb-insights-sign-up
- Or GOOGLE



# Thank you!

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Maroon Bells, CO