# Schedule at a Glance:
**APHL 11th National Conference on Laboratory Aspects of Tuberculosis**

## MONDAY April 22

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>4:00 pm – 7:00 pm</td>
<td>APHL Registration</td>
<td>Atrium Foyer</td>
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<tr>
<td>3:00 pm – 6:00 pm</td>
<td>Exhibitor and Poster Set Up</td>
<td>Atrium A</td>
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## TUESDAY April 23

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<tr>
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<td>APHL Registration</td>
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<tr>
<td>7:00 am – 7:00 pm</td>
<td>APHL/NTCA Exhibit Hall and Poster Viewing</td>
<td>Atrium A</td>
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<tr>
<td>8:30 am – 10:00 am</td>
<td>Opening Session and Keynote</td>
<td>Room A703/704</td>
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<tr>
<td>10:00 am – 10:30 am</td>
<td>Morning Break</td>
<td>Atrium A</td>
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<tr>
<td>10:30 am – 12:00 pm</td>
<td>The Role of Next Generation Sequencing</td>
<td>Room A703/704</td>
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<tr>
<td>12:00 am – 1:00 pm</td>
<td>Lunch (on your own)</td>
<td>Room A703/704</td>
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<tr>
<td>1:00 pm – 1:30 pm</td>
<td>TB Case Studies: Lessons from the Field</td>
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<td>Afternoon Break</td>
<td>Atrium A</td>
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<tr>
<td>3:30 pm – 4:30 pm</td>
<td>Collecting Wisdom and Sharing Knowledge</td>
<td>Room A703/704</td>
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<tr>
<td>4:30 pm – 5:00 pm</td>
<td>Poster Flash Talks</td>
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<tr>
<td>5:30 pm – 7:00 pm</td>
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## WEDNESDAY April 24

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<tr>
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<td>APHL/NTCA Exhibit Hall and Poster Viewing</td>
<td>Atrium A</td>
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<tr>
<td>7:00 am – 7:50 am</td>
<td>Working Together for TB Elimination</td>
<td>Room A702</td>
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<tr>
<td>8:00 am – 10:00 am</td>
<td>Combined APHL and NTCA Opening Session</td>
<td>Atrium B</td>
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<tr>
<td>10:00 am – 10:30 am</td>
<td>Morning Break</td>
<td>Atrium A</td>
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<tr>
<td>10:30 am – 12:00 pm</td>
<td>Drug Susceptibility Testing</td>
<td>Room A703/704</td>
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<tr>
<td>12:00 pm – 1:00 pm</td>
<td>Lunch (on your own)</td>
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<tr>
<td>1:00 pm – 2:30 pm</td>
<td>Data Driven Science in the TB Laboratory</td>
<td>Room A703/704</td>
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<td>2:30 pm – 3:00 pm</td>
<td>Afternoon Break</td>
<td>Atrium A</td>
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<tr>
<td>3:00 pm – 4:30 pm</td>
<td>The Evolution of TB Research</td>
<td>Room A703/704</td>
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<tr>
<td>4:30 pm – 5:15 pm</td>
<td>TB Case Studies: Lessons from the Field</td>
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<tr>
<td>5:15 pm – 5:30 pm</td>
<td>Awards and Closing Remarks</td>
<td>Room A703/704</td>
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*Events highlighted in red are combined sessions with NTCA.*
## Schedule at a Glance:
### NTCA National TB Conference
**Innovate, Implement, Impact**

#### MONDAY April 22
- **4:00 pm – 7:00 pm** | NTCA Registration | Atrium Foyer
- **3:00 pm – 6:00 pm** | Exhibitor and Poster Set Up | Atrium A

#### TUESDAY April 23
- **7:00 am – 5:30 pm** | NTCA Registration | Atrium Foyer
- **7:00 am – 7:00 pm** | NCTA/APHL Exhibit Hall and Poster Viewing | Atrium A
- **8:00 am – 5:30 pm** | NTCA Pre-meetings | (see NTCA program)
- **5:30 pm – 7:00 pm** | Combined APHL and NTCA Poster Session | Atrium A

#### WEDNESDAY April 24
- **7:00 am – 5:30 pm** | NTCA Registration | Atrium Foyer
- **7:00 am – 5:30 pm** | NTCA/APHL Exhibit Hall and Poster Viewing | Atrium A
- **8:00 am – 10:00 am**
  - **10:00 am – 10:30 am** | Session I: NTCA Opening Session | Atrium B
  - **10:30 am – 12:30 pm** | Session III: Moving Toward TB Elimination | Atrium B
  - **12:30 pm – 1:30 pm** | Lunch (on your own) | Atrium B
- **1:30 pm – 4:00 pm**
  - **3:30 pm – 4:00 pm** | Breakout Sessions: A1 and A2 | Pulse Loft
  - **4:00 pm – 5:30 pm** | New Member Reception | Atrium A
- **6:30 pm – 9:00 pm** | 2019 NTCA Social | Atrium A

#### THURSDAY April 25
- **7:00 am – 5:30 pm** | NTCA Registration | Atrium Foyer
- **10:00 am – 3:30 pm** | Breakout Sessions: B1: The Essential Role of NAAT B2: DR–TB: Diagnostic and Clinical Implications of a Changing Landscape | A703/704 or Atrium B 706/707
- **8:00 am – 10:00 am**
  - **10:00 am – 10:30 am** | Morning Break | Atrium A
  - **10:30 am – 12:15 pm** | Session IV: WGS for TB | Atrium B
  - **12:15 pm – 1:30 pm** | Lunch (on your own) | Atrium B
- **1:30 pm – 3:00 pm**
  - **3:00 pm – 3:30 pm** | NTCA Award Presentations | Atrium B
  - **3:30 pm – 5:00 pm** | Centers of Excellence Breakout Sessions | (see NTCA program)

#### FRIDAY April 26
- **7:00 am – 12:00 pm** | NTCA Registration | Atrium Foyer
- **8:00 am – 10:00 am**
  - **10:00 am – 10:30 am** | Morning Break | Atrium A
  - **10:30 am – 12:00 pm** | Session VI: The Changing Landscape of TB Screening and LTBI Treatment | Atrium B
- **12:00 pm – 2:30 pm** | DTBE Remarks and Closing Remarks | Atrium B
Welcome to the 11th National Conference on the Laboratory Aspects of Tuberculosis, co-located with the 2019 National TB Conference!

It’s a thrilling time for public health laboratories as we continue to grow and adapt to changing technology. We constantly work to find opportunities to collaborate and network with our fellow TB clinicians and TB control programs.

To create a collaborative atmosphere, we will co-host a poster session on Tuesday, April 23 at 5:30 pm and a joint opening session on Wednesday, April 24 at 8:00 am as well as coordinated breaks and lunch schedules for networking.

This year we will continue to meet and bring inspired people together to ensure the testing and services provided by laboratories remains at the cutting edge. This conference will address the role of next generation sequencing, drug susceptibility challenges including generating and utilizing MIC data, brushing up on the latest recommendations and guidelines, lessons from implementation of MALDI-TOF by our Canadian neighbors and exciting research happening within CDC’s Division of TB Elimination. We will also be showcasing the work of many of our public health laboratories through poster flash talks and a session on data driven science as well as several case studies that are always such a fun time. No laboratory conference would be complete without a discussion about reporting and we have invited colleagues from NTCA to join a lively panel discussion to provide multiple perspectives on what makes a useful report.

In addition to the tremendous sessions you’ve come to expect, we are proud to bring you a new session and roundtable called Collecting Wisdom and Sharing Knowledge. This new session will address enhancing multigenerational workforces for the elimination of TB and developing a knowledge retention tool. This conference will dive into the heart of all matters relating to Tuberculosis.

On behalf of the planning committee for the 11th National Conference, it is my great pleasure to present you with a motivating and interactive agenda. Countless hours of thought and effort have led us to this day and I truly appreciate all the hard work the members of the program planning committee have given.

Angie Schooley, MT (ASCP)
Chair, program planning committee, 11th National Conference on the Laboratory Aspects of Tuberculosis
About APHL

The Association of Public Health Laboratories (APHL) is a non-profit 501(c)(3) organization representing public health laboratory interests. The members are the states, represented by the state public health laboratory director as well as county and city laboratory directors, individual members with interest in public health and laboratory issues and organizations that share common goals with APHL. The association links local, state, national and global leaders in order to promote the highest quality laboratory practices worldwide. The APHL mission is: “To promote the role of public health laboratories in support of national and global health objectives and to promote policies and programs which assure continuous improvement in the quality of laboratory practice.”

APHL’s Mission

Shape national and global health outcomes by promoting the value and contributions of public health laboratories and continuously improving the public health laboratory system and practice.

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Tamara Theisen, MT(ASCP), local institutional member representative
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Wadsworth Center, New York State Department of Health

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California Department of Public Health

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Alaska State Public Health Laboratory

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Wisconsin State Laboratory of Hygiene

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National Institutes of Health

Continuing Education Credits Available

APHL is an approved provider of continuing education programs in the clinical laboratory sciences through the American Society of Clinical Laboratory Science (ASCLS) P.A.C.E® program. Attendees have the opportunity to earn up to 13.5 contact hours by attending the entire conference. Attendance rosters must be signed in each attended session that credit is requested for and the P.A.C.E® certificate must be signed and certified by APHL staff at the registration desk at the end of your time at the conference.

Continuing Education Credits Available

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Conference Schedule

MONDAY, APRIL 22
APHL/NTCA Registration: 4:00 pm – 7:00 pm
Exhibitor and Poster Setup: 3:00 pm – 6:00 pm

TUESDAY, APRIL 23
Registration: 7:00 am – 5:30 pm • Atrium Foyer
APHL Sessions: 8:30 am – 7:00 pm • Room A703/704
Poster Viewing: 7:00 am – 7:00 pm • Atrium A
(Combined Poster Session with NTCA 5:30 pm – 7:00 pm)

DAY 1
588-844-19, 6.5 contact hours for the day
At the conclusion of this day, the participant will be able to:
• Discuss the different approaches for utilizing next generation sequencing technology for TB diagnosis and surveillance
• Summarize best practices in reporting TB laboratory results
• Describe methods that public health laboratories can retain knowledge and utilize the voices of all generations in the laboratory

8:30 am – 10:00 am
Opening Session and Keynote
Welcome! The keynote address will be delivered by Dr. Derrick Crook, Professor at the University of Oxford and the Director of Microbiology at Public Health England

Welcome to the 11th National Conference on Laboratory Aspects of Tuberculosis
Angie Schooley, Michigan Department of Health and Human Services

Keynote Address
Derrick Crook, PhD, Public Health England

10:00 am – 10:30 am
Morning Break (Atrium A)
10:30 am – 12:00 pm

**A Time and A Place: The Role of Next Generation Sequencing**

In a time when so many new technologies are emerging, it can be hard to know what is right or necessary for your laboratory. Balancing the need to keep up with performing appropriate testing, this session will focus on providing practical information related to the use of sequencing methods in the TB laboratory. Each speaker will address the processes for decision making and/or implementing the given method to help other laboratories think through their own decision-making and ensure it is appropriate to meet their own needs.

Moderator: Angela Starks, PhD, Centers for Disease Control and Prevention

**National Overview of Next Generation Sequencing Approaches for Tuberculosis**

Kelly Wroblewski, MPH, Association of Public Health Laboratories

**One Stop Shop: New York State’s Approach to TB Diagnosis**

Joseph Shea, MS, New York State Department of Health, Wadsworth Center

**Targeted NGS for TB Drug Resistance Detection**

Linlin Li, PhD, California Department of Public Health, Microbial Diseases Laboratory

**“Where Do We Go From Here?” Panel and Group Discussion**

James E. Posey, PhD, Centers for Disease Control and Prevention

Edward P. Desmond, PhD, California Department of Public Health, Microbial Diseases Laboratory

Vincent E. Escuyer, PhD, New York State Department of Health, Wadsworth Center

12:00 – 1:00 pm

**Lunch (on your own)**

1:00 pm – 1:30 pm

**TB Case Studies: Lessons from the Field**

During this session, attendees will hear two fascinating case study presentations from their colleagues from a ‘boots on the ground’ perspective.

Moderator: Monica Youngblood, MPH, Centers for Disease Control and Prevention

**The Missing IS6110 Gene**

Drew Francis, ASCP(M), Arizona State Public Health Laboratory

**Communication Works!**

Robin Connelly, MMSc., M(ASCP), Georgia Public Health Laboratory
1:30 pm – 3:00 pm

**Back to the Basics — Guidelines, Algorithms, Reports, Oh My!**

*Mycobacteriology laboratory methods and testing algorithms continuously evolve and the necessity of clearly and effectively reporting test results is a constant challenge. In this session, highlights of the recently published practice guidelines for the clinical mycobacteriology laboratory will be presented, as well as developments in the use of MALDI-TOF mass spectrometry for the identification of mycobacteria. A presentation on reporting mycobacteriology test results will help laboratorians create understandable reports for the diverse audience that receives them.**

Moderator: David Warshauer, PhD, Wisconsin State Laboratory of Hygiene

**Cliff Notes of Recently Published Recommendations and Guidelines**  
Max Salfinger, MD, University of South Florida, College of Public Health

**MALDI-‘Tough’: Implementation and Lessons Learned from a High Volume Mycobacteriology Laboratory**  
Frances Jamieson, MD, FRCPC, Public Health Ontario

**TB Laboratory Reports Panel Discussion: Is It All Greek to You?**  
Barbara Seaworth, MD, Texas Center for Infectious Disease

Kimberly Townsend MPA, BSN, RN, Montgomery County Department of Health and Human Services

Paula M. Snippes Vagnone, MT(ASCP), Minnesota Department of Health

3:00 pm – 3:30 pm

**Afternoon Break**

3:30 pm – 4:30 pm

**Collecting Wisdom and Sharing Knowledge: Enhancing Multi-Generational Workforces**

*TB laboratory staff are critical to the diagnosis, treatment, and prevention of TB. This session will discuss tools available to aid in the process of knowledge succession and how improved communication within an organization will help capitalize on people’s strengths.*

Co-Moderator: Yvette Vergnetti, Alaska State Public Health Laboratory

Co-Moderator: Angie Schooley, Michigan Department of Health and Human Services
Addressing the Multigenerational TB Workforce
Catherine Stakenas, MA, American Society for Clinical Pathology (ASCP)

APHL Knowledge Retention Toolkit
Lorelei Kurimski, MS, Association of Public Health Laboratories
Jaye Boman, MT (AMT), State Hygienic Laboratory at the University of Iowa

4:30 pm – 5:00 pm
**Poster Flash Talks**

*This session will highlight the outstanding submitted poster abstracts in 1-2 minute flash presentations.*

Moderator: Anne M Gaynor, PhD, Association of Public Health Laboratories

5:30 pm – 7:00 pm
**Combined APHL and NTCA Poster Session (Atrium A)**

*This session will be in the exhibit hall with all of the accepted posters to allow ample time for viewing of all posters and networking with our colleagues attending the National TB Conference sponsored by the National TB Controller’s Association (NTCA).*

Co-Moderator: John Bernardo, MD, Boston University School of Medicine
Co-Moderator: Kelly Wroblewski, MPH, Association of Public Health Laboratories

Thank you to our exhibitors for their support of the conference!

Please visit them in Atrium A during breaks.
WEDNESDAY, APRIL 24

**Registration:** 7:00 am – 5:30 pm • Atrium Foyer

**APHL Sessions:** 7:00 am – 5:30 pm • Room A 702, A703/704

**NTCA Sessions:** 7:00 am – 5:30 pm • See NTCA Schedule

**Exhibit Hall/Poster Viewing:** 7:00 am – 5:30 pm • Atrium A

**DAY 2**

588-845-19, 7.0 contact hours for the entire day

At the conclusion of this day, the participant will be able to:

- Identify different approaches to drug susceptibility testing that may lead to changes in laboratory practice
- Discuss how public health laboratories can use their own data to change practice in their laboratory
- Describe new developments in TB diagnostics and approaches to TB treatment

**7:00 am – 7:50 am**

**Generations — Working Together for TB Elimination (A702)**

There are currently multiple generations of workers in our TB public health laboratories nationwide, each with its unique strengths and characteristics. How can laboratorians leverage these differences in a way that encourages the TB laboratory to grow and evolve to meet the needs of the public health workforce? In this roundtable discussion led by Catherine Stakenas, Consultant, Organizational Development/Leadership Strategist at the American Society for Clinical Pathology (ASCP), attendees will work on exercises focused on identifying generational differences and harnessing their strengths.

Co-Moderator: Yvette Vergnetti, Alaska State Public Health Laboratory

Co-Moderator: Anne M Gaynor, PhD, Association of Public Health Laboratories

**8:00 am – 10:00 am**

**Combined APHL/NTCA Opening Session (Atrium B)**

In the spirit of TB public health programmatic and laboratory collaboration, the attendees of the 11th National Conference on Laboratory Aspects of Tuberculosis will join our NTCA colleagues for their opening session. The opening session will set the tone for the conference, highlighting the progress of TB elimination activities in the United States, the nexus between domestic and global TB efforts, the importance of strong collaborations between laboratories and public health programs, the impact of innovation in TB diagnostics, treatment, care and prevention, and our deep commitment to those we serve: our patients, their families, and our communities.
Moderator: Julie Higashi, MD, PhD, Los Angeles County Department of Public Health

**Welcome and Opening Remarks**
Diana Fortune, New Mexico Department of Health

Marie-Claire Rowlinson, PhD, D(ABMM), Florida Department of Health, Bureau of Public Health Laboratories

**Tuberculosis Prevention, Control and Elimination in the US in 2019: Perspective from the Director of the National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention**
Jonathan Mermin, MD, MPH, Centers for Disease Control and Prevention

**The Genomics of Mycobacterium tuberculosis: Changing the Focus of Public Health**
Barry Kreiswirth, PhD, New Jersey Medical School, Public Health Research Institute Center

10:00 am – 10:30 am

**Morning Break (Atrium A)**

10:30 am – 12:00pm

**Drug Susceptibility Testing — MICs, Challenges, and Results Interpretations (A703/704)**

*Drug susceptibility testing for MTBC can be challenging for a laboratory. This session examines different approaches and aspects of providing reliable DST results, and highlights emerging concepts in improved service delivery.*

Moderator: Vincent E. Escuyer, PhD, New York State Department of Health, Wadsworth Center

**Discordant Results**
Beverly Metchock, DrPH, D(ABMM), Centers for Disease Control and Prevention

**Are We Ready to Report MIC Results?**
Daniela Cirillo, PhD, San Raffaele Scientific Institute, Milan, Italy

**MIC Clinical Perspective**
Megan Ninneman, PA, Jackson Memorial Hospital, Miami, Florida
12:00 pm – 1:00 pm
Lunch

1:00 pm – 2:30 pm
Data Driven Science in the TB Laboratory
Numerous types of TB laboratory data are recorded and reported each day, month, quarter, and year. This session describes approaches in which that data can be used to monitor and improve laboratory best practices, efficiency, and quality assurance.

Moderator: Stephanie Johnston, MS, Centers for Disease Control and Prevention

False Positive Investigation Toolkit
Robert Domaoal, PhD, Centers for Disease Control and Prevention

Monica Youngblood, MPH, MT (ASCP), Centers for Disease Control and Prevention

Assessing Laboratory Specific Data
Cortney Stafford, MPH, Centers for Disease Control and Prevention

Panel Discussion
Jane Voyles, BS, Arkansas Public Health Laboratory
Jasmine Guillet, MPH, BS, Massachusetts State Public Health Laboratory
Tunisia King, BS, New Jersey Public Health and Environmental Laboratories
Dorothy Baynham, BS, Tennessee Department of Health, Laboratory Services
Denise Dunbar, BA, Texas Department of State Health Services

2:30 pm – 3:00 pm
Afternoon Break
3:00 pm – 4:30 pm

**The Evolution of TB Research**

*During this session, we will hear about the latest research and findings related to novel host-directed therapy approaches, TB diagnostics, and the public health laboratory role in clinical trials.*

Moderator: Tracy Dalton, PhD, Centers for Disease Control and Prevention

- **Host-Directed Approaches to TB Therapy**
  Suraj Sable, PhD, DVM, Centers for Disease Control and Prevention

- **Novel TB Diagnostics**
  Patricia Hall, PhD, MS, Centers for Disease Control and Prevention

- **An Overview of the TB Trials Consortium**
  Anne E. Purfield, PhD, Centers for Disease Control and Prevention

4:30 pm – 5:15 pm

**TB Case Studies: Lessons from the Field**

*During this session, attendees will hear two fascinating case study presentations from their colleagues from a ‘boots on the ground’ perspective.*

Moderator: Cortney Stafford, MPH, MT (ASCP), Centers for Disease Control and Prevention

- **Cross-Contamination — Beyond Laboratory Testing**
  Jasmine Guillet, MPH, BS, Massachusetts Department of Public Health

- **Saturday Night Fever**
  Shaka Brown, Capital Congress

5:15 pm – 5:30 pm

**Awards and Closing Remarks**

Angie Schooley, BS, Michigan Department of Health and Human Services
Exhibitors

- Alpha-Tec Systems, Inc.
- Cepheid
- Coastal Telehealth Specialists
- Conduent
- eMocha
- IMMY
- Janssen (sponsor, not exhibiting)
- National Jewish Health Advanced Diagnostics Laboratories
- Sanofi (sponsor, not exhibiting)
- SureAdhere Mobile Technologies, Inc.
- Oxford Immunotec USA, Inc.
- QIAGEN
- WestPrime Systems, Inc.
Poster Abstracts

Poster 1

An evaluation of testing activities undertaken by the National Public Health Laboratory Drug Susceptibility Testing (DST) Reference Center, 2016-2018

N Ancona,¹ S Yu,² G Lin,² E Desmond,² T Dalton,³ S Johnston,³ A Starks,³ K Wroblewski,¹ A Gaynor¹

1. Association of Public Health Laboratories, 2. Microbial Disease Laboratory, California Department of Public Health, 3. Centers for Disease Control and Prevention, Division of Tuberculosis Elimination, Laboratory Branch.

Objective: The National Public Health Laboratory (PHL) Drug Susceptibility Testing Reference Center for *Mycobacterium tuberculosis* (TB DST Reference Center) provides timely and quality assured DST services for eligible US PHLs with fewer than 50 TB isolates per year. Services offered include growth-based DST using Mycobacteria Growth Indicator Tube (MGIT) and molecular detection of drug resistance using pyrosequencing (PSQ). The first-line DST (FL-DST) panel includes rifampin (RIF), isoniazid (INH), pyrazinamide (PZA) and ethambutol (ETB), and the second-Line DST (SL-DST) panel includes ethionomide (ETO), capreomycin (CAP), amikacin (AMK), moxifloxacin (MOX), kanamycin (KAN) and rifabutin (RFB).

Study Design: California Microbial Diseases Laboratory (MDL) serves as the TB DST Reference Center. MDL submits monthly line-listed data to APHL and CDC. Data on samples submitted for testing between July 1, 2016 – June 30, 2018 were examined. Turnaround time (TAT) was measured from date of isolate/sediment receipt at MDL to final report date, includes holidays and weekends and excludes reflex testing for SLDST.

Results: During this time, the reference center tested 518 samples (462 isolates, 56 sediments) from 17 eligible submitting laboratories (Table 1). PSQ was performed on 38.6% (200/518) of samples with median TAT of 3 days. Of note, the median PSQ TAT includes samples where PSQ was ordered late or reflexed and therefore the mode was also included (Table 1). The most frequent test performed was FL-DST with 88.9% (460/518) of samples tested with a median TAT of 14.5 days. SL-DST was performed on 15.4% (80/518) of total samples with a median TAT of 14.5 days. From the 518 samples, drug resistant isolates were identified as follows: 30 INH, 16 PZA (31% of these were M. bovis), 3 ETO, 5 dual resistant (1 INH and PZA resistant, 6 INH and ETO resistant, 1 PZA and ETO resistant, and 1 PZA and MOX resistant) and 4 multidrug resistant isolates.

Conclusions: The TB DST Reference center has demonstrated the feasibility and success of a consolidated service model for reference DST. It provides high quality DST services for PHLs with low TB incidence in an effort to improve testing across the country.
Evaluation of Direct versus Concentrated NAAT on Respiratory Specimens for Rapid Diagnosis of Pulmonary Tuberculosis in a Local Jurisdiction

MH Zhowandai\textsuperscript{1}, M Ghajar\textsuperscript{1}, S Prabhu\textsuperscript{1}, J Low,\textsuperscript{1} C Bittencourt\textsuperscript{2}, D Constable\textsuperscript{2}, M Crumpler\textsuperscript{1}, L Thrupp\textsuperscript{2}

1. Orange County Health Care Agency, Santa Ana, CA 2. University of California Irvine Health, Orange, California

Background: The Cepheid Xpert® MTB/RIF Assay is a rapid Nucleic Acid Amplification Test (NAAT) for the identification of *Mycobacterium tuberculosis* (MTB) and detection of Rifampin (Rif) resistance (indicative of MDR-TB). Rapid tuberculosis (TB) diagnosis can facilitate initiation of TB therapy, minimize unnecessary use of other antibiotics, assess need for Airborne Isolation (AI), and prioritize contact investigations. Routinely, respiratory specimens are digested/decontaminated and NAAT is performed the following day on the concentrate.

Objective: The objective of this study was to analyze the performance of the NAAT on direct vs routine concentrated respiratory specimens, using conventional culture as the gold standard.

Methods: This was a joint prospective observational study between a local public health laboratory and a university hospital in southern California. Both sites followed the same protocol. Standard of care sputum specimens were tested from suspect TB patients over age 18 and not on TB treatment for 3 days or more prior to collection. An aliquot from each adequate specimen was used for direct NAAT and AFB smear. The remaining specimen was processed and NAAT, smear, culture, and susceptibility testing was performed per routine procedures. Lab turn-around time (TAT) was noted for both methods, and time to culture detection (TTD) was recorded.

Results: Specimens from 275 patients were tested, with 266 valid NAAT and culture results. Thirty-two cultures were positive for MTB (12.0%) and none were Rif-resistant. For Direct vs. Concentrated NAAT: SENSITIVITY was 71.9 vs. 75.0%, SPECIFICITY and PPV were 100% for both, and NPV was 96.3 vs. 96.7%. As expected, AFB smears on direct specimens had lower sensitivity (41%) than from concentrates (59%). TAT for NAAT on direct specimens was approx. one day vs. two days for routine concentrates. Of the 25% concentrated (28% direct) specimens with negative NAAT that still grew MTB, all had TTD >9 days (mean: 29-31 days), indicating the organism load is low and thus expected rates of potential transmission are low.

Conclusions: NAAT on direct specimens had only marginally lower sensitivity (72%) compared to routine concentrates (75%). One negative direct NAAT result can facilitate safely discontinuing AI for hospitalized patients at least one day sooner in most patients, saving an estimated 200 AI days per year.
Poster 3

Fast and Easy Extraction for both TB Genotyping and WGS


Objective: The Michigan Department of Health and Human Services (MDHHS) performs Mycobacterial Interspersed Repetitive Units – Variable Number Tandem Repeats (MIRU-VNTR) and Whole Genome Sequencing (WGS) on approximately 9000 tuberculosis isolates per year. To accomplish this high throughput testing, the goal was to implement one extraction method that could be used for both genotyping methods and satisfy the volume, concentration, and purity requirements.

Study Design: MDHHS began this investigation by analyzing several popular DNA extraction methods currently used for Mycobacterium tuberculosis. These methods included the Zymo ZR Fungal/Bacterial DNA Microprep Kit, the BioRad Instagene Matrix, and MDHHS’s current FastPrep method. Methods were evaluated based on recommended sample growth, tolerance for heat inactivation, extraction bead size, elution volume, elution concentration, and employee time.

Several batches of isolates were extracted with each of the methods, prepped for sequencing, and loaded onto the Illumina MiSeq platform for WGS. Acceptability of results was determined by CDC.

Results: The ZR Fungal/Bacterial DNA extraction did not meet the volume requirement and was very time consuming and expensive. The Instagene Matrix DNA and FastPrep extraction both fulfilled the volume requirement, but the extractions did not yield significant surplus volume and yielded low concentration, respectively. To counter the low concentration from the FastPrep extraction, the input volume of the elution reagent was reduced, resulting in a stronger elution concentration. MDHHS was able to modify the existing Fast Prep protocol to satisfy the needs of both MIRU and WGS, with an average input DNA concentration of 5.5 ng/μL.

Conclusions: The modified FastPrep extraction provides our laboratory with a minimum savings of $4000 or more per year in reagents, as well as improved time efficiency in the genotype testing process. DNA quality and quantity are sufficient to provide high throughput services for all aspects of Mycobacterium tuberculosis, genotyping.
**Poster 4**

**Rapid Mycobacterial Identification using Real Time PCR and MALDI-TOF Testing**

H Seymour, J Vanneste, S Church, A Schooley, M. Soehnlen. Michigan Department of Health and Human Services, Bureau of Laboratories, Lansing, MI

**Objective:** The primary goal for a Mycobacteriology laboratory in the public health setting is to rule in/out the presence of *Mycobacterium tuberculosis* complex (MTBC) in clinical specimens and cultures positive for acid-fast bacilli. The Michigan Department of Health and Human Services (MDHHS) goal was to create an algorithm using real time PCR and MALDI-TOF testing platforms that would maintain the turnaround time of the Hologic *Mycobacterium* Direct (MTD) amplification and HPLC tests.

**Study Design:** MDHHS began this task by validating a real time PCR test for clinical specimens, both respiratory and non-respiratory sources, and broth cultures. Within 24 hours of receipt in the laboratory, a physician will have a result of MTBC DNA Detected or Not Detected. Broth cultures are the majority of culture types received at MDHHS for identification, but they have a poor success rate when directly tested with MALDI-TOF. Our algorithm validated testing of these broth cultures with the real time PCR assay to rule in/out MTBC and then utilize the MALDI-TOF platform for final identification. The MALDI-TOF validation for *Mycobacterium* sp. cultures included cultures grown on solid media and 7H9 broth subcultures of the original culture. The subcultures are tested using MALDI-TOF when they reach an approximate turbidity of a 3.0 McFarland standard, usually 1-4 days after incubation. Acid-fast bacilli positive cultures on solid medium are tested directly with MALDI-TOF. All clinical specimens and culture aliquots are heat killed before real time PCR or MALDI-TOF testing is performed. MALDI-TOF testing is performed as per the manufacturer instructions for *Mycobacterium* sp. from Bruker Daltonics. The real time PCR test is a laboratory developed test, originally designed by the Wadsworth Center, involving a simple extraction procedure followed by DNA detection.

**Results:** MDHHS has been able to transition from using MTD and HPLC testing without compromising turnaround time or cost.

**Conclusions:** The current MDHHS algorithm provides the laboratory with cost effective testing, while providing the physician with the most rapid identification possible to aid in patient treatment.
Setting up first-line drug susceptibility testing (DST) directly from a positive Mycobacteria Growth Indicator Tube (MGIT): the catalyst for a structured workflow in the Virginia Division of Consolidated Laboratory Services (DCLS) Tuberculosis (TB) Laboratory

K Milloy, S McReynolds, R Mehr, T Bateman, B Gardner, S Kelley, R Oglesby. Division of Consolidated Laboratory Services, Richmond, VA

Objective: To reduce the turnaround time (TAT) and meet CDC TB Elimination Healthy People 2020 goals for identification and drug susceptibility testing of Mycobacterium tuberculosis complex (MTBC) through progressive workflow improvements and scheduled testing.

Study Design: DCLS sought to improve timeliness in DST by evaluating the laboratory practice of initiating first-line DST from a Middlebrook 7H9 culture. The lab designed an alternate laboratory workflow, for which DST was initiated from positive MGITs within 5 days of positivity on the MGIT 960. In addition, AccuProbe MTBC identifications and DSTs were performed twice a week to identify new MTBC cases and promptly initiate susceptibility testing. Lab personnel created a job aid to exhibit the new testing schedule and quickly identify MGITs that required re-seeding to meet the required 5 day set-up time. A visual board was created to track new MTBC cases and the testing performed in real-time. The board also provided a feedback mechanism to display the monthly DST TAT and track the improvements over time.

Results: Since implementation of the new workflow in February 2018, the lab reduced the average TAT for identification of MTBC by 6.1 days (23.6 days in 2017, 17.5 days in 2018) and the average TAT for DST by 10.2 days (25.6 days in 2017, 15.4 days in 2018). The lab has increased the percentage of cases identified as MTBC within 21 days of received date by 16% (65.5% in 2017, 81.6% in 2018), exceeding the CDC target goal of 75%. The lab has also increased the percentage of cases with DST reported within 17 days of identification by 51% (29.0% in 2017, 80.4% in 2018), exceeding the CDC target goal of 69%.

Conclusions: Data generated by the DCLS TB Laboratory demonstrates the positive impact of a defined schedule and modified workflow on timeliness for diagnostic reporting of MTBC and DST results. Workflow organization and a feedback mechanism added value to the study and encouraged laboratory scientists to adhere to the new structured workflow.
Poster 6

Drug susceptibility testing of *Mycobacterium tuberculosis* complex isolates at the Florida State Public Health Laboratory: A six-year study

C Chiribau, C Tanner, and M-C Rowlinson, Florida – Bureau of Public Health Laboratories (FBPHL), Jacksonville, FL, USA

**Objective:** This study examined drug resistance profiles of *Mycobacterium tuberculosis* complex (MTBC) isolates from 2,761 unique patients by analysis of drug susceptibility testing (DST) data for 15 TB drugs.

**Study Design:** MTBC DST was performed by the Sensititre MIC method. Data was collected from 12/2012 to 8/2018 and included Florida patients only, one isolate per patient. Drug resistance percentages were calculated, average and most prevalent MIC values were determined, and yearly trends as well as drug resistance profiles of multi-drug resistant (MDR) strains were analyzed.

**Results:** DST data for first-line drugs: the resistance percentage (R%) for rifampin was 1.52% (42/2761), 5/42 rifampin resistant isolates were mono-resistant. The R% for isoniazid was 8.62%, and for ethambutol was 14.99%. For other TB drugs, the non-susceptible percentage (NS%) to ofloxacin was 11.03%, and to levofloxacin was 11.30%. The NS% for amikacin (0.14%) and capreomycin (0.24%) were both very low, while R% of kanamycin was 3.02%. DST for linezolid, with an MIC range of 0.12-2 µg/ml, indicated an average MIC of 0.62 µg/ml, MIC50=0.5 µg/ml and MIC90= 1 µg/ml. Only 3/446 isolates (0.67%) were linezolid non-susceptible. This study included n=37 MDR-TB, with n=11 detected in 2014.

**Conclusions:** By analyzing a significant number of isolates, the study revealed important information about drug resistance in Florida TB patients. According to our data, non-susceptibility to fluoroquinolones and resistance to isoniazid are on declining trends, while resistance to rifampin appears to be rising in 2017 compared to the previous two years. NS% of injectable drugs and R% to linezolid is remarkably low.
Poster 7

Comparison of Magnetic beads bridging flocculation technique with Gene Xpert MTB/RIF assay for diagnosis of tuberculous meningitis (TBM) in high endemic low resource settings

K Sharma, M Modi, A Sharma, S Singh, P Ray. Post Graduate Institute of Medical Education and Research, Chandigarh, India.

Objectives: Rapid and specific diagnosis of tuberculous meningitis (TBM) is of paramount importance to decrease associated morbidity and mortality. Therefore, the present study was undertaken to compare Gene Xpert MTB/RIF (GX) assay and Magnetic beads bridging flocculation technique for diagnosis of TBM

Study Design: Magnetic beads bridging flocculation technique and GX were performed on 150 cerebrospinal fluid samples (CSF). These included samples from 100 patients with culture positive for MTB, samples from 25 non-TB infectious meningitis cases and 25 non-infectious neurological disorder samples. These 50 non-TB CSF samples were included in control group. Phenotypic drug susceptibility testing of 100 isolates for rifampicin (Rif) and isoniazid (INH) was carried out by 1% proportion method. katG gene and rpoB gene sequencing was also performed. We have taken culture as gold standard.

Results: GX and Magnetic beads bridging flocculation technique were positive in 68/100(68%) and 94/100 (94%) patients. Both tests were negative in all 50 controls samples. Rif resistance was detected in 11 of 68 (16.17%) by GX, and in 10 of 94 (10.6%) Magnetic beads bridging flocculation technique positive samples with rpoB gene sequencing. Out of the 100 culture isolates subjected to phenotypic drug susceptibility testing, 90 were sensitive to Rif and INH and 10 were found to be resistant to both Rif and INH. Thus, there was one case of false Rif resistance detected by GX, which was Rif sensitive on rpoB gene sequencing and phenotypic DST. False Rif resistance was observed with probe B of Gene Xpert. Cost of doing Magnetic beads bridging flocculation technique is less than 1 dollar where as GX is 10 dollars.

Conclusion: Magnetic beads bridging flocculation technique had a higher sensitivity than GX for diagnosing TBM. It is a robust and cost effective method for diagnosis of TBM in low resource and high endemic settings.
Poster 8

Pyrazinamide susceptibility by BACTEC MGIT 960: Are the discrepancies always due to the test method?

D Kohlerschmidt, S Wolfe, M Isabelle, J Shea, TA Halse, K Musser, VE Escuyer. Wadsworth Center, New York State Department of Health

Objective: Pyrazinamide (PZA) is an important first-line drug used in combination with other tuberculosis (TB) drugs for the treatment of drug-susceptible TB and multidrug-resistant TB (MDR-TB). PZA has a critical role in shortening TB therapy. Culture-based drug susceptibility testing (DST) using the BACTEC MGIT 960 system and a PZA breakpoint of 100 µg/mL has been the gold standard for years to test for PZA resistance. This assay has been thought to give poor reproducibility, often ascribed to inoculum density. Further, this method has been reported to show false resistance when DST results don’t correlate with pncA sequencing results. Our objective is to show that some Mycobacterium tuberculosis (MTB) strain lineage(s) may contribute to these disparities and that what was once considered false resistance may indeed be low level PZA resistance inherent to these strains.

Study Design: A collection of M. tuberculosis isolates with no pncA mutations and showing discrepant culture-based PZA susceptibility results when repeated were analyzed by whole-genome sequencing and culture-based DST. Culture-based PZA susceptibility testing was performed in triplicate using the BACTEC MGIT 960 system with reduced inoculum density and PZA breakpoints of both 75 µg/mL and 100 µg/mL.

Results: The study showed that a high percentage (60%) of strains showing initial PZA discrepant results belonged to the Indo-Oceanic lineage (lineage 1). Statistical analysis showed that the proportion of discrepant strains within lineage 1 is significantly higher than within the 3 other major lineages, indicating that some genetic factor might be involved. A significantly higher percentage of discrepant lineage 1 strains showed resistance to PZA when tested at 75 µg/mL, compared to the other lineages.

Conclusions: While the PZA susceptibility assay is not perfect, some of the discrepant results observed during testing might be attributed to the genetic background of certain strains. We argue that when a discrepant result upon repeat testing is observed, genotype information should be obtained before concluding that this discrepancy is due to the limitations of the PZA susceptibility assay. Furthermore, our data suggests that the critical concentration of 100µg/mL currently in use should probably be revised to a higher concentration.
**Poster 9**

**Evaluation of Vitek MS v3.0 MALDI-TOF for identification of *Mycobacterium tuberculosis* and common Non tuberculous mycobacteria (NTM) isolates from clinical specimens**

K Sharma, R Panwar, S Sethi, M Modi, S Singh, A Sharma, P Ray. Post Graduate Institute of Medical Education and Research, Chandigarh, India.

**Objectives:** India constitutes nearly 25% of the world’s tuberculosis burden. Non-tuberculous mycobacteria (NTM) are also gaining importance as opportunistic pathogens; responsible for a variety of clinical diseases. There is need for rapid, accurate and cost effective identification of *Mycobacterial* species to aid in diagnosis and for initiating appropriate therapy. The aim of the present study was to evaluate Vitek MS v3.0 matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry system compared to DNA sequencing for the identification and differentiation of mycobacterial species from various clinical isolates.

**Study Design:** A total of 120 mycobacterial culture isolates were evaluated by Vitek MS v3.0 MALDI-TOF system. The identification of all isolates was confirmed by *hsp65/16s RNA* sequencing which was taken as gold standard.

**Results:** All of the tuberculous mycobacteria (20/20; 100%) and most of the NTM (90/100; 90%) were correctly identified at least to the group or complex level. The 90 NTM isolates identified by MALDI-TOF were *M. fortuitum* (n=20), *M. abscessus* (n=20), *M. immunogenum* (n=10), *M. avium* (n=9), *M. phlei* (n=9), *M. gordonae* (n=5), *M. smegmatis* (n=5), *M. kansasii* (n=4), *M. intracellulare* (n=3), *M. flavescence* (n=4), *M. scrofulaceum* (n=2) and *M. chelonea* (n=1). However, not all species or subspecies within the *M. tuberculosis*, *M. abscessus*, and *M. avium* complexes and within the *M. fortuitum* group could be differentiated.

**Conclusions:** MALDI-TOF MS is a robust and promising tool for the identification of MTB and NTM and has utility for the routine identification of mycobacteria in clinical practice.
Reduction of phenotypic susceptibility testing through implementation of universal whole-genome sequencing of *Mycobacterium tuberculosis* complex isolates in New York State

J Shea, TA Halse, D Kohlerschmidt, P Lapierre, VE Escuyer, KA Musser. Wadsworth Center, New York State Department of Health

Objectives:

1. To assess the performance characteristics of a whole-genome sequencing (WGS) assay on isolates of *M. tuberculosis* complex for the prediction of drug resistance and susceptibility compared to gold-standard phenotypic methods.

2. If determined to be viable, to implement this assay as the first-tier drug susceptibility test for isolates of *M. tuberculosis* complex in New York State, supplanting culture-based phenotypic testing for WGS predicted fully susceptible strains.

Study Design: WGS was implemented universally for all culture positive cases of *M. tuberculosis* complex in New York State in March 2016. Comprehensive drug resistance profiles were generated using an in-house developed pipeline that detects high-confidence mutations and were compared to phenotypic DST (BACTEC MGIT 960 and agar proportion) for a period of 2.5 years. Sensitivity, specificity, resistance and susceptibility-predictive values for nine drugs/ drug classes were assessed, with analytical updates being made to the bioinformatic pipeline annually. In October 2018, our laboratory adopted a new testing algorithm featuring WGS as the primary resistance profiling method in which isolates predicted to be susceptible to all drugs do not have any culture-based phenotypic testing performed while isolates predicted to be resistant or harbor mutations of unknown significance have confirmatory phenotypic DST done.

Results: This WGS assay was found to be highly predictive of susceptibility to first-line drugs (rifampin, 100%, isoniazid, 99%, pyrazinamide 98%, ethambutol, 99%). WGS results were reported an average of 8 days sooner than first-line MGIT susceptibility results, in a clinically relevant timeframe to impact treatment decisions. Since implementing a new testing algorithm, the number of phenotypic susceptibility tests performed in our laboratory has been reduced by 80%.

Conclusions: Due to the reliability of WGS at predicting susceptibility to first-line TB drugs, it is possible to perform routine susceptibility profiling by WGS instead of culture-based phenotypic methods. A reduced susceptibility testing algorithm streamlined laboratory testing, saving time and money, while comprehensive drug resistance profiles were reported at a reduced turnaround time.
Poster 11

Evaluation of \textit{rpoB} mutations in \textit{Mycobacterium tuberculosis} and their association with rifampin resistance during 2.5 years of prospective side-by-side whole-genome sequencing and phenotypic testing

J Shea,\textsuperscript{1} TA Halse,\textsuperscript{1} D Kohlerschmidt,\textsuperscript{1} M Isabelle,\textsuperscript{1} S Wolfe,\textsuperscript{2} A Fiero,\textsuperscript{2} JL Rakeman,\textsuperscript{2} J Lemon,\textsuperscript{2} P Lapierre, VE Escuyer, KA Musser

\textsuperscript{1}Wadsworth Center, New York State Department of Health 2. NYC Department of Health and Mental Hygiene

\textbf{Objective:} To assess the prevalence, diversity, and type of \textit{rpoB} mutations detected in isolates of \textit{M. tuberculosis} complex (MTBC) collected during a 21/2-year period with concurrent whole-genome sequencing (WGS) and phenotypic susceptibility testing.

\textbf{Study Design:} One isolate from every culture-positive tuberculosis patient was submitted to the Wadsworth Center for WGS on the Illumina MiSeq from March 2016 through September 2018. Phenotypic susceptibility testing (BACTEC MGIT 960 and agar proportion) was performed at either the New York City Public Health Labs or the Wadsworth Center. A subset of these isolates had minimum inhibitory concentration (MIC) testing performed using the Sensititre MYCOTB MIC plate. Mutations within the full \textit{rpoB} gene were detected using an in-house developed bioinformatic pipeline and classified based on association with phenotypic resistance and/or elevation in MIC as well as support in literature.

\textbf{Results:} Of 1778 strains sequenced prospectively, 136 (7.6\%) were found to have one or more nonsynonymous mutation(s) in \textit{rpoB}. A total of 51 mutations in 49 strains (2 strains were double mutants) were identified to be associated with rifampin (RIF) resistance. 40 of these strains exhibiting RIF resistance at 1.0 \textmu g/mL, while the remaining 9 were susceptible at 1.0 \textmu g/mL but had an elevated RIF MIC. These low-level resistance mutations, referred to as disputed mutations, comprised 18.4\% (9/49) of strains with \textit{rpoB} mutations associated with RIF resistance.

\textbf{Conclusions:} The molecular detection of \textit{rpoB} mutations for predicting RIF resistance offers a reduced turnaround time and improved breadth of information compared to phenotypic assays. Improving upon the knowledge base by linking rare \textit{rpoB} mutants with phenotypic results, particularly MIC results, is critical to the future of sequencing-based methods. The prevalence of disputed \textit{rpoB} mutations among TB isolates in New York State is higher than other regional reports have suggested. These mutations, which may have gone previously undetected, might contribute to treatment failures and/or aid in the selection of further resistance.
Poster 12

TB Puerto Rico Response to Hurricane Maria

B Jones,1 K Milloy,2 MR Connelly,3 AM Gaynor,4 B Metchock,5 K Klein,5 S Johnston,5 M Youngblood,5 C Stafford,5 M Yakrus,5 C Chiribau,1 M-C Rowlinson1


Introduction: On September 20, 2017, Hurricane Maria made landfall in Puerto Rico (PR) as a category 4 storm, with sustained 155 mph winds. Maria is considered the deadliest hurricane on record to affect PR, causing 2,975 (in) direct deaths and damages upwards of 90 billion USD. Despite intense preparations, infrastructure and services, including healthcare, were severely affected. An initial assessment of the PR public health laboratory determined that it was inoperable and would be unable to provide many services including testing for tuberculosis (TB). Through CDC and APHL, an initiative to temporarily externalize PR’s TB testing was put in place. By October 3, 2017, three state public health laboratories (Florida, Georgia and Virginia) had agreed to provide this testing.

Methods: Clinical specimens for TB testing were received and triaged by CDC, and shipped to a state laboratory depending on capacity, specimen type, and previous receipt of specimens from the same patient. Laboratories performed their routine testing algorithms for identification and drug susceptibility testing. Isolates of M. tuberculosis (MTB) were archived and submitted for genotyping. Critical values were communicated by phone, and all results (preliminary/final) were communicated by e-mail, fax, or secure data transfer.

Results: Between October 2017 and July 2018, a total of 633 clinical specimens (17 samples/week, on average) were received. Acid fast bacilli smear was performed for 632 specimens and 13.6% (86) were smear-positive. Nucleic acid amplification testing was performed on 136 specimens, with a positivity rate of 19.85% (27/136). Regarding culture, 128 specimens were culture positive with 68 of these positive for MTB. Twenty-seven cultures were contaminated. Drug susceptibility testing was performed for 23 MTB isolates (one isolate/first-time TB patient); no drug resistant strains were detected.

Conclusions: The public health laboratory response is an example of successful cooperation between federal agencies and state laboratories that demonstrates the value and the flexibility of the U.S. public health system when confronted with a large-scale natural disaster. This highlights the importance of preparedness, continuity of operations planning, and the ability to perform surge and emergency testing.
Public-private partnership collaboration for rapid molecular tuberculosis testing in Guam

AC Whelen,1 T Koyamatsu,1 AM Santos,2 MJ Jacar,3 C Henson3

1. Diagnostic Laboratory Services, Inc. (DLS), Aiea, HI, 2. Department of Public Health and Social Services (GDPHSS), Mangilao, GU, 3. DLS Guam, Tamuning, GU.

Objective: Neither the private (DLS) nor the public (GDPHSS) laboratory systems had sufficient resources to serve their patients, so a public-private partnership was proposed, implemented, and assessed in which the public component (GDPHSS) provides analytical infrastructure and the private component (DLS) provides consumables, pre-analytic, post-analytic components. Additionally, DLS provides consumables to GDPHSS as compensation for their contribution.

Study Design: Guam medical providers and public health disease controllers both have the need for rapid molecular tuberculosis testing in Guam. A mutually beneficial Memorandum of Understanding (MOU) was proposed, coordinated, and executed that leveraged public health laboratory infrastructure with private resources for collection, transport, consumables, and results delivery. Measurements to indicate improvement to services were designed for both parties. The DLS monitor was reduction in turn-around-time and the GDPHSS monitor was increase in test capacity.

Results: Turn-around-time for DLS-Guam clients was significantly reduced because specimens no longer needed to be flown to Hawaii for testing. Testing capacity for GDPHSS laboratory to serve public health clients significantly increased because of the additional consumables provided by DLS as compensation for the use of their instrumentation and testing expertise.

Conclusions: In Guam, both partners were better able to serve their clients by leveraging each other’s strengths and resources.
Poster 14

Multi targeted Loop-Mediated Isothermal Amplification (LAMP) for rapid diagnosis of gastrointestinal tuberculosis in 60 minutes

S Singh, K Sharma, M Modi, A Sharma, P Ray Post Graduate Institute of Medical Education and Research, Chandigarh, India

Objectives: Prompt and accurate diagnosis of gastrointestinal tuberculosis (GITB) is highly challenging. Conventional techniques are time consuming and lack sensitivity. Multi-targeted Loom amplification mediated polymerase chain reaction (LAMP) using two targets (IS6110 and MPB64) is a promising technique for rapid diagnosis of TB. The aim of the study was to evaluate multi-targeted LAMP for detection of \textit{M. tuberculosis} complex on ileocecal biopsy samples in patients suspected of GITB.

Study Design: LAMP test using primers for IS6110 and MPB64 was performed on ileocecal biopsy samples from 35 patients with clinically suspected gastrointestinal tuberculosis and 30 ileocecal biopsy samples of non tuberculosis control subjects. The results were compared with ziehl-neelsen (ZN) staining, mycobacterial culture, IS6110 PCR and histopathologic examination.

Results: Multi-targeted LAMP test (positive for any of the two targets) had a sensitivity and specificity of 100% and 100%, respectively, for five culture-confirmed GITB cases and 85.71% and 100%, respectively for 30 culture-negative clinically suspected GITB cases. All non-tuberculosis control samples were negative for LAMP (using both targets). Amongst culture- confirmed GITB cases (n=5) the sensitivity of IS6110 LAMP, MPB64 LAMP and IS6110 PCR was 80%, 100% and 60% respectively. The sensitivity of IS6110 LAMP, MPB64 LAMP and IS6110 PCR for clinically suspected GITB cases (n=30) was 73.33%, 80% and 70%, respectively. Amongst all 35 GITB patients, the sensitivity of microscopy, culture, IS6110 PCR, IS6110 LAMP, MPB64 LAMP and the multi-targeted LAMP assay was 5.71%, 14.28%, 68.57%, 74.28%, 82.85% and 85.71%, respectively. Specificity of all the tests was 100%. There were 3 cases (2 clinically suspected and one culture confirmed GITB) which were missed by IS6110 LAMP and 2 cases (both clinically suspected GITB) by MPB64 LAMP.

Conclusions: Multi-targeted LAMP is a promising technique for rapid diagnosis of GITB in resource limited endemic settings still battling with this deadly disease.
# Attendee List (as of April 8)

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