Mycobacterium tuberculosis Complex

Drug Susceptibility Testing Program

AUGUST 2025

U.S. CENTERS FOR DISEASE CONTROL AND PREVENTION

Model Performance Evaluation Program

Report of Results, August 2025

Mycobacterium tuberculosis Complex Drug Susceptibility Testing Report for August 2025 Panel

Purpose

To present results of the U.S. Centers for Disease Control and Prevention (CDC) Model Performance Evaluation Program (MPEP) for *Mycobacterium tuberculosis* complex (MTBC) drug susceptibility testing panel sent to participants in August 2025.

Report Content

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Note on Accessibility: Find descriptions and explanations of figures in Appendix 1: Accessible Explanation of Figures on page 34.

Contents

Technical Notes

The following information pertains to all tables and figures for the 2025 MTBC isolates F, G, H, I, and J included in this report.

- The source of data in all tables and figures is the August 2025 MPEP MTBC DST panel.
- First-line and second-line drugs have been separated into individual tables for each isolate. Streptomycin is classified as a second-line drug for this report.
- Separate tables for molecular testing are included.
- Mutations of the *rpoB* gene are noted with the *M. tuberculosis* numbering system.
- Laboratories that use more than one DST method are encouraged to test isolates with each of the available methods and equivalent critical concentrations. Some laboratories have provided results for multiple DST methods. Consequently, the number of results for some drugs may be greater than the number of participating laboratories. This report contains all results reported by participating laboratories.
- The Sensititre® system allows determination of a MIC for each drug in the panel. Laboratories using this method may establish breakpoints individually, for some drugs, to provide a categorical interpretation of S or R.
- For participant result tables that have drug-method totals equal to 0, results were not received.
- Although data were collected for delamanid, no laboratories reported growth-based testing for this drug. Therefore, this drug was not included in growth-based tables of participants' results.
- Due to a 2024 manufacturer recall, BD MGIT™ PZA susceptibility test kits were not widely available during the August 2025 MPEP panel testing timeframe. The number of reported results for this method and drug was lower than typically observed, reflecting laboratories' inability to perform testing.

Abbreviations and Acronyms

Acronym	Definition
AMK	amikacin
AP	agar proportion — performed on Middlebrook 7H10 or 7H11
BDQ	bedaquiline
CAP	capreomycin
CDC	U.S. Centers for Disease Control and Prevention
CFZ	clofazimine
CIP	ciprofloxacin
CLSI	Clinical and Laboratory Standards Institute
CYS	cycloserine
DLM	delamanid
DNA	deoxyribonucleic acid
DST	drug susceptibility testing
EMB	ethambutol
ETA	ethionamide
FQ	fluoroquinolone
INH	isoniazid
KAN	kanamycin
LVX	levofloxacin
LZD	linezolid
MDR	multidrug-resistant
MGIT™	BACTEC™ MGIT™ – Mycobacteria Growth Indicator Tube
MIC	minimum inhibitory concentration
MOX	moxifloxacin
MPEP	Model Performance Evaluation Program
MTBC	*Mycobacterium tuberculosis* complex
PAS	*p*-aminosalicylic acid
PTM	pretomanid
PZA	pyrazinamide
OFL	ofloxacin
R	resistant
RBT	rifabutin
RIF	rifampin
RPT	rifapentine
RNA	ribonucleic acid
S	susceptible
Sensititre®	Thermo Scientific Sensititre® MYCOTB AST or customized plate
STR	streptomycin
TB	tuberculosis
VersaTREK™	Thermo Scientific VersaTREK™ Myco susceptibility
XDR	extensively drug-resistant

Introduction: Overview of MPEP Final Report

The Model Performance Evaluation Program (MPEP) is an educational, self-assessment tool in which five isolates of *M. tuberculosis* complex (MTBC) are sent to participating laboratories biannually for staff to monitor their ability to determine drug resistance among the isolates. It is not a formal, graded proficiency testing program. The associated report includes results for a subset of laboratories performing drug susceptibility testing (DST) for MTBC in the United States. MPEP is a voluntary program, and this report reflects data received from participating laboratories. This aggregate report is prepared in a format that will allow comparison of DST results with those obtained by other participants using the same methods and drugs, for each isolate. We encourage circulation of this report to personnel who are either involved with DST or reporting and interpreting results for MTBC.

CDC is neither recommending nor endorsing testing practices reported by participants. For standards, participants should refer to consensus documents published by the Clinical and Laboratory Standards Institute (CLSI), "M24: Susceptibility Testing of Mycobacteria, *Nocardia* spp., and Other Aerobic Actinomycetes" and "M24S: Performance Standards for Susceptibility Testing of Mycobacteria, *Nocardia* spp., and Other Aerobic Actinomycetes" [1, 2]. Additionally, the World Health Organization (WHO) published two technical reports investigating critical concentrations, by method, for anti-tuberculosis drugs [3, 4].

Expected Drug Susceptibility Testing Results

Anticipated growth-based and molecular results for the panel of MTBC isolates sent to participants in August 2025 are shown in the tables below. Although CDC recommends broth-based methods for routine first-line DST of MTBC isolates, the results obtained by the reference agar proportion method (except for pyrazinamide, for which MGIT™ was performed, when possible) are shown in Table 1. Molecular results obtained by whole genome sequencing are listed in Table 2.

Table 1. Expected Growth-based Results for August 2025 Panel

Isolate	RIF	INH	EMB	PZA	FQ	Second-line Drug Resistances:
2025F	S	R (high-level*)	S	S	S	
2025G	R[†]	S	S	S	S	
2025H	S	S	S	S	S	
2025I	R	S	S	S	S	RBT
2025J	S	R (high-level*)	R[§]	No Result[¶]	S	STR

Note: RIF=rifampin, INH=isoniazid, EMB=ethambutol, PZA=pyrazinamide, FQ=fluoroquinolones, RBT=rifabutin, STR=streptomycin, S=susceptible, R=resistant. Growth-based DST results were obtained by indirect agar proportion method, except for pyrazinamide, for which MGIT™ was performed.

* Resistant at 0.2 µg/ml and 1.0 µg/ml by agar proportion. See Equivalent Critical Concentration table on page 8 for more information.

[†] 80% consensus for a single categorical result of susceptible or resistant across all methods reported for this drug was not achieved for this isolate among participating laboratories.

[§]93% of participant results were EMB susceptible despite expected resistance by growth-based testing and the mutation's association with resistance [5]. The reason for the unexpected susceptible result is unknown; laboratories may consider excluding this isolate from quality assurance assessments for growth-based methods.

[¶]No result available. See Expected Molecular Result table below.

Table 2. Expected Molecular Results (Mutations Detected in Loci Associated with Resistance) for August 2025 Panel

Isolate	*rpoB**	*katG*	*embB*	*rpsL*
2025F		Ser315Thr		
2025G	His445Leu			
2025H				
2025I	Ser450Leu			
2025J[†]		Ser315Thr	Tyr319Cys	Lys43Arg

Note: Empty cell=No mutation detected. Molecular results were obtained by whole genome sequencing. High confidence mutations were not detected in these loci: *inhA, fabG1, pncA, gyrA, gyrB, ethA, rrs, eis, and tlyA.*

* *M. tuberculosis* numbering system used [6, 7].

[†] No mutation detected in *pncA*; consistent with likely PZA susceptible.

Equivalent Critical Concentrations

(Concentrations listed as µg/ml)

Agar Proportion

First-line Drugs	7H10 agar	7H11 agar
Isoniazid	0.2 and 1.0*	0.2 and 1.0*
Rifampin	0.5†	1.0
Ethambutol	5.0	7.5
Pyrazinamide	Not recommended	Not recommended

NOTE: Critical concentrations as indicated in CLSI M24 document, unless otherwise stated [1].

*The higher concentration of INH should be tested as second-line drug after resistance at the critical concentration is detected [1].

†WHO recommended critical concentration of 0.5 µg/ml differs from CLSI critical concentration of 1.0 µg/ml for RIF [1, 4].

Second-line Drugs	7H10 agar	7H11 agar
Streptomycin	2.0	2.0
Levofloxacin	1.0	Not determined
Moxifloxacin	0.5	0.5
Amikacin	4.0*	Not determined
Capreomycin	10.0*	10.0†
Kanamycin	5.0*	6.0†
Ethionamide	5.0	10.0
Rifabutin	0.5	0.5
***p*-Aminosalicylic acid**	2.0†	8.0†
Rifapentine	Not determined¶	Not determined¶
Bedaquiline	Not determined¶	0.25§
Linezolid	1.0§	1.0§
Clofazimine	Not determined¶	Not determined¶
Delamanid	Not determined¶	0.016§
Pretomanid	Not determined¶	Not determined¶

NOTE: Critical concentrations as indicated in CLSI M24 document [1].

*CLSI critical concentrations differ from revised WHO recommendations published in 2018 [1, 3].

- For AMK, the WHO recommended critical concentration for 7H10 agar is 2.0 µg/ml.
- For CAP, the WHO recommended critical concentration for 7H10 agar is 4.0 µg/ml and 'Not determined' for 7H11 agar.
- For KAN, the WHO recommended critical concentration for 7H10 agar is 4.0 µg/ml.

†WHO has withdrawn the recommended critical concentrations for CAP and KAN for 7H11 agar and PAS for 7H10 and 7H11 [3].

§Critical concentrations as indicated in WHO 2018 Technical Report on critical concentrations [3].

¶Critical concentrations for establishing susceptibility have not been determined.

Broth-Based Media

First-line Drugs	MGIT™	VersaTREK™
Isoniazid	0.1 (and 0.4*)	0.1 (and 0.4*)
Rifampin	0.5†	1.0
Ethambutol	5.0	5.0 (and 8.0*)
Pyrazinamide	100.0	300.0

NOTE: Critical concentrations as indicated in applicable manufacturer package inserts, unless otherwise stated.
*The higher concentration of INH and EMB should be tested after resistance at the critical concentration is detected [1].
†WHO recommended critical concentration of 0.5 µg/ml differs from CLSI critical concentration of 1.0 µg/ml for RIF [4].

Second-line Drug	MGIT™
Streptomycin	1.0 (and 4.0*)
Levofloxacin	1.0†
Moxifloxacin	0.25
Amikacin	1.0
Capreomycin	2.5
Kanamycin	2.5
Ethionamide	5.0
Cycloserine	16.0§
***p*-Aminosalicylic acid**	Not recommended†
Rifapentine	Not determined
Bedaquiline	1.0
Linezolid	1.0
Clofazimine	1.0
Delamanid	0.06
Pretomanid	0.5 and 2.0¶

NOTE: Critical concentrations as indicated in WHO 2018 Technical Report on critical concentrations unless noted otherwise [3]. Data for second-line critical concentrations not available for VersaTREK™.
*Critical concentration as indicated in applicable manufacturer package insert. The higher concentration of STR should be tested after resistance at the critical concentration is detected.
†WHO critical concentrations differ from CLSI M24S recommendations published in 2023 [2, 3].

- For LVX, the CLSI recommended critical concentration for MGIT™ is 1.5 µg/ml.
- For PAS, the CLSI recommended critical concentration for MGIT™ is 4.0 µg/ml.

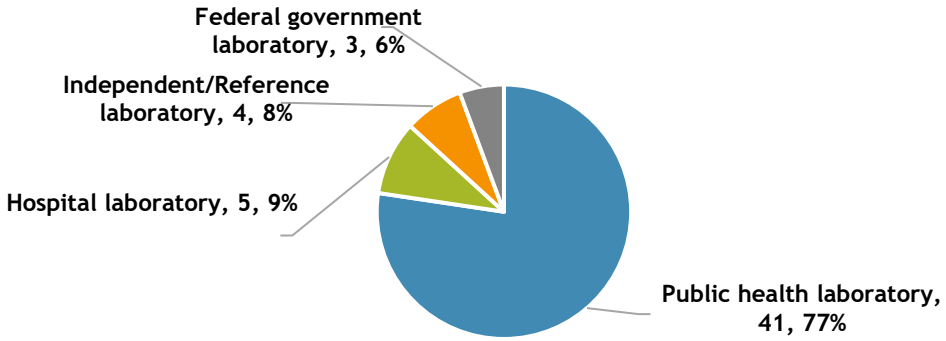
§Critical concentration as indicated in WHO 2024 Module 3: Diagnosis—Rapid diagnostics for tuberculosis detection (Third Edition) [8].
¶Per WHO 2024 Module 3: Diagnosis—Rapid diagnostics for tuberculosis detection (Third Edition), no growth at 0.5 µg/ml is susceptible; growth at 0.5 µg/ml and no growth at 2.0 µg/ml is susceptible, but with a comment on uncertainty; growth at 2.0 µg/ml is resistant [8].

Descriptive Information about Participant Laboratories

Primary Classification

This report contains DST results submitted to CDC by panel participants at 53 laboratories in 29 states, all of whom have participated in previous MPEP panels.
Participants were asked to indicate the primary classification of their laboratory (Figure 1).

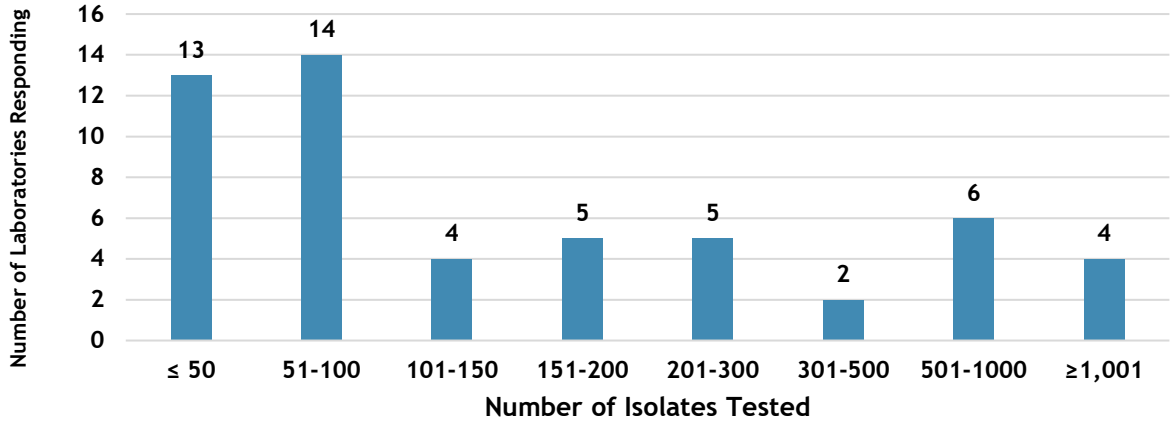
Figure 1. Primary Classification of Participating Laboratories, August 2025



Annual Number of MTBC Drug Susceptibility Tests Performed

The number of MTBC isolates tested for drug susceptibility by the 53 participants in 2024 (excluding isolates used for quality control) is shown in Figure 2. In 2024, the counts ranged from 0 to 2,190 tests. Participants at 13 (25%) laboratories reported testing 50 or fewer isolates per year. Laboratories with low MTBC DST volumes are encouraged to consider referral of testing because of concerns about maintaining testing proficiency [9].

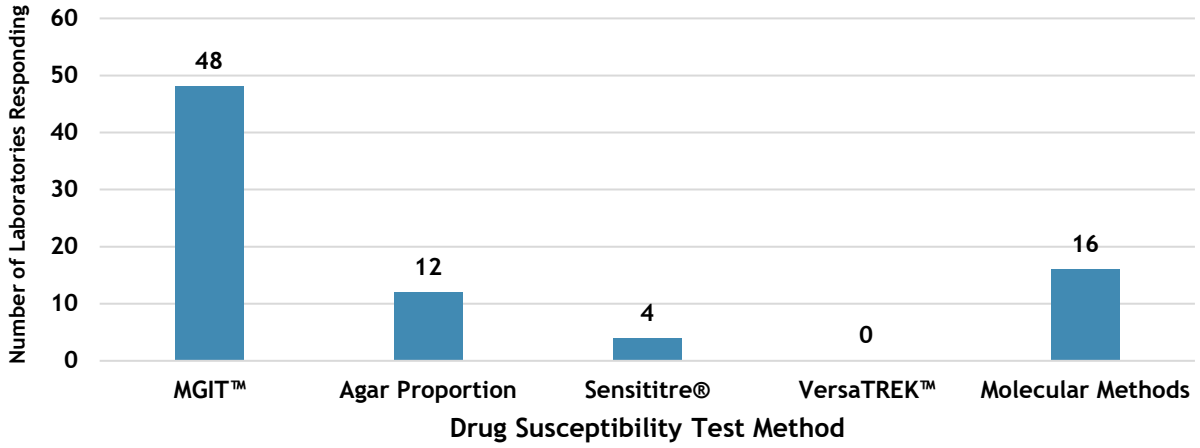
Figure 2. Distribution of the Annual Volume of MTBC Isolates Tested for Drug Susceptibility by Participants in Previous Calendar Year, 2024 (n=53)



MTBC Drug Susceptibility Test Methods Performed by Participants

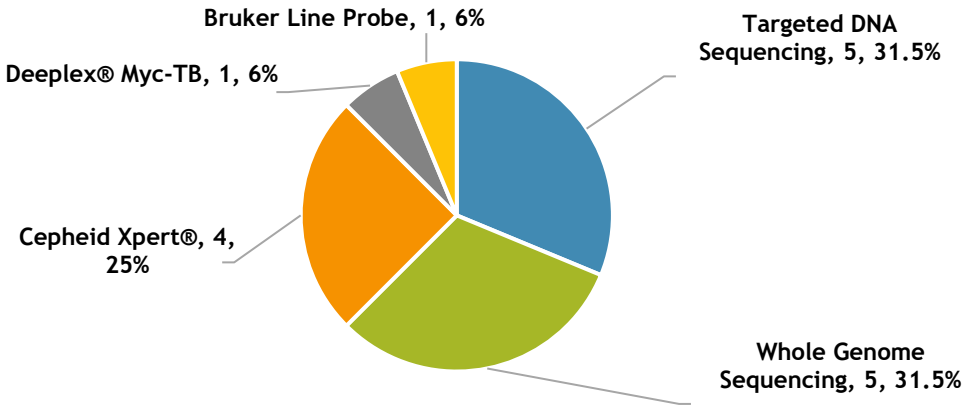
The DST methods that were performed by participating laboratories for this panel of MTBC isolates are displayed in Figure 3. Of participating laboratories, 31 (58%) reported results for only one method, 18 (34%) reported two methods, 3 (6%) reported three susceptibility methods, and 1 (2%) reported four susceptibility methods. Forty-eight (91%) participating laboratories indicated use of MGIT™.

Figure 3. MTBC Drug Susceptibility Test Methods Performed (n=80 responses)



Molecular methods reported by participants are shown in Figure 4. The methods performed most frequently were targeted DNA sequencing (31.5%) and whole genome sequencing (31.5%).

Figure 4. Molecular Method Reported (n=16 responses)

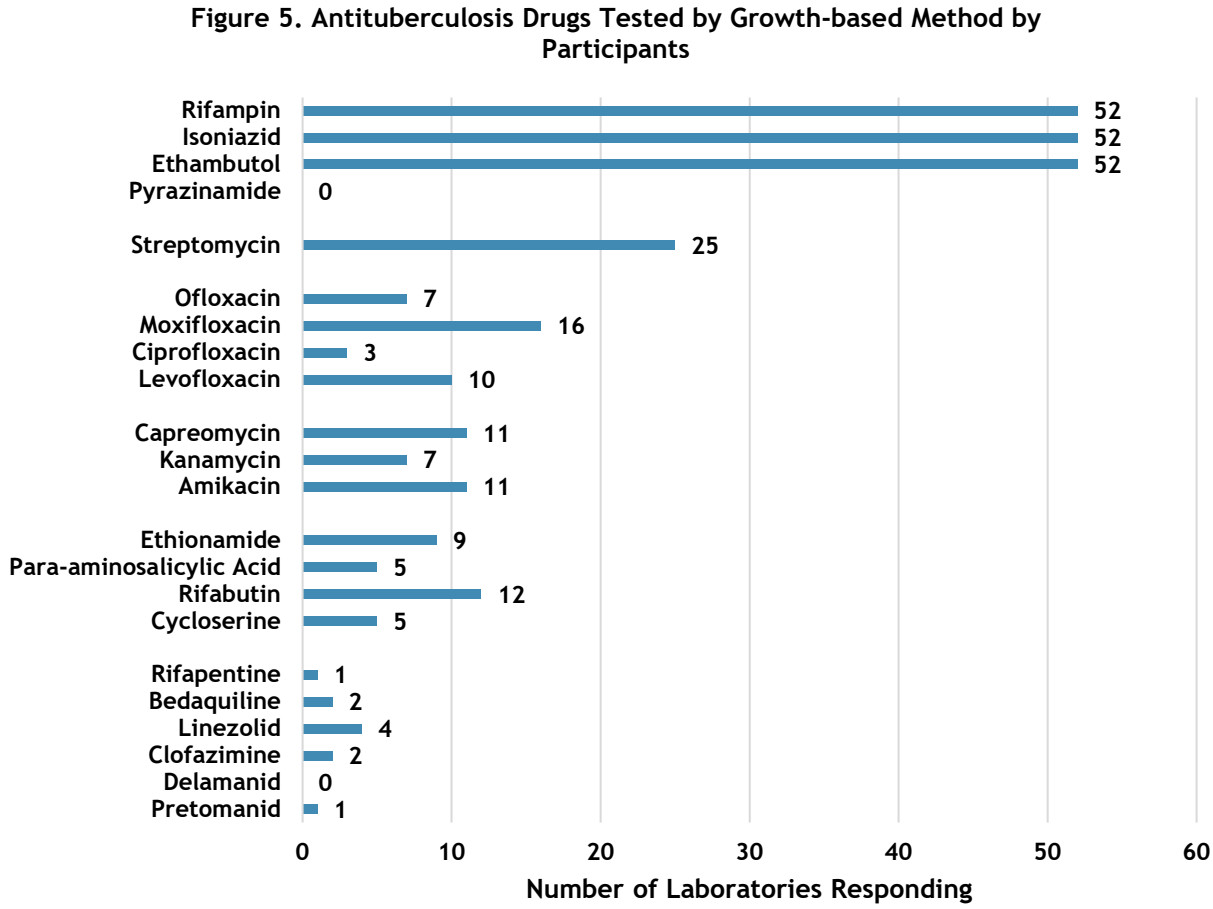


Antituberculosis Drugs Tested by Participants

The number of participating laboratories that reported testing each antituberculosis drug in the August 2025 panel is presented in Figure 5. Although 53 laboratories participated in the August 2025 MPEP panel, only 52 laboratories provided growth-based testing results; one laboratory only reported results for molecular testing.

CLSI recommends testing a full panel of first-line drugs (rifampin, isoniazid, pyrazinamide, and ethambutol) [1] because it represents a combination of tests that provides the clinician with comprehensive information related to the 6- or 9-month, four-drug RIPE TB treatment regimen used for many patients. Laboratories should consider the addition of fluoroquinolones to their testing panel as CDC recommends susceptibility testing for fluoroquinolones (e.g., moxifloxacin) with use of the alternate 4-month rifapentine-moxifloxacin treatment regimen; rifampin may be used as a proxy for rifapentine [10].

Figure 5. Antituberculosis Drugs Tested by Growth-based Method by Participating Laboratories



Isolate 2025F

Expected Results:

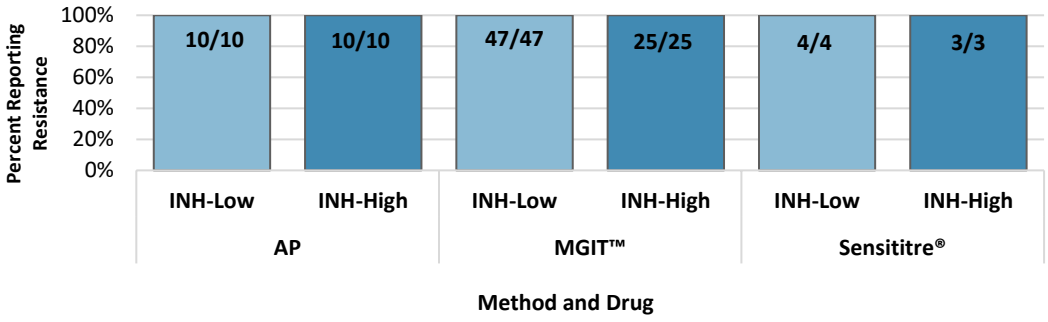
Drug	Growth-based*	Molecular*
RIF	S	*rpoB* wild-type
INH	R (high-level†)	*katG* Ser315Thr; *inhA* & *fabG1* wild-type
EMB	S	*embB* wild-type
PZA	S	*pncA* wild-type
FQ	S	*gyrA* & *gyrB* wild-type

Note: RIF=rifampin, INH=isoniazid, EMB=ethambutol, PZA=pyrazinamide, FQ=fluoroquinolones, S=susceptible, R=resistant.
*Growth-based expected results determined by agar proportion. Molecular expected results determined by whole genome sequencing.
† Resistant at 0.2 µg/ml and 1.0 µg/ml by agar proportion. See Equivalent Critical Concentration table on page 8 for more information.

Isoniazid

DNA sequence analysis of *inhA, katG,* and *fabG1* of Isolate 2025F revealed a G>C point mutation in the *katG* locus resulting in wild-type serine being replaced by threonine at codon 315 (Ser315Thr); *inhA* and *fabG1* were wild-type (i.e., no mutations were detected). The *katG* Ser315Thr mutation is known to cause high-level isoniazid resistance [5, 11, 12].

Figure 6. Isolate 2025F: Percent of Laboratories Reporting INH-low and INH-high Resistance, by Growth-based Method



Note: INH-Low=isoniazid-low concentration, INH-High=isoniazid-high concentration, AP=agar proportion. Laboratories performing Sensititre® reported INH MIC values as 2 µg/ml (n=2), >3.2 µg/ml (n=1), and 4 µg/ml (n=1).

For internal comparison purposes, isolate 2025F was previously sent as MPEP 2024I. Similar INH results were reported across all methods for MPEP 2025F and MPEP 2024I.

Complete first-line DST, second-line DST, and molecular results submitted by all participants for Isolate 2025F are listed in Tables 3–9.

Table 3. Isolate 2025F—Participant Results for First-Line DST by AP

Drug	Susceptible	Resistant	Total
Rifampin	10	0	10
Isoniazid—Low	0	10	10
Isoniazid—High	0	10	10
Ethambutol	10	0	10

Table 4. Isolate 2025F—Participant Results for First-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Rifampin	46	1	47
Isoniazid—Low	0	47	47
Isoniazid—High	0	25	25
Ethambutol	46	0	46*
Pyrazinamide	0	0	0

*One additional laboratory reported 'No Interpretation' for EMB by MGIT™.

Table 5. Isolate 2025F—Participant Results for First-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Rifampin	4	0	4
Isoniazid—Low	0	4	4
Isoniazid—High	0	3	3
Ethambutol	4	0	4

Table 6. Isolate 2025F—Participant Results for Second-Line DST by AP

Drug	Susceptible	Resistant	Total
Streptomycin	8	0	8
Ofloxacin	4	0	4
Ciprofloxacin	2	0	2
Moxifloxacin	4	0	4
Levofloxacin	4	0	4
Amikacin	6	0	6
Kanamycin	4	1	5
Capreomycin	6	0	6
Ethionamide	5	0	5
Rifabutin	5	0	5
Cycloserine	3	0	3
p-Aminosalicylic acid	3	0	3
Rifapentine	0	0	0
Bedaquiline	0	0	0
Linezolid	0	0	0
Clofazimine	0	0	0
Pretomanid	0	0	0

Table 7. Isolate 2025F—Participant Results for Second-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Streptomycin	16	0	16
Ofloxacin	2	0	2
Ciprofloxacin	1	0	1
Moxifloxacin	11	0	11*
Levofloxacin	5	0	5
Amikacin	2	0	2
Kanamycin	1	0	1
Capreomycin	2	0	2
Ethionamide	2	0	2
Rifabutin	3	0	3
Cycloserine	0	0	0
p-Aminosalicylic acid	0	0	0
Rifapentine	0	0	0
Bedaquiline	1	0	1
Linezolid	2	0	2
Clofazimine	1	0	1
Pretomanid	0	0	0

*One additional laboratory reported 'Contaminated/No Growth' for MOX by MGIT™.

Table 8. Isolate 2025F—Participant Results for Second-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Streptomycin	2	0	2
Ofloxacin	1	0	1
Ciprofloxacin	0	0	0
Moxifloxacin	1	0	1*†
Levofloxacin	1	0	1
Amikacin	2	0	2
Kanamycin	1	0	1
Capreomycin	1	0	1*
Ethionamide	1	0	1
Rifabutin	2	0	2*
Cycloserine	0	0	0*†
p-Aminosalicylic acid	2	0	2
Rifapentine	0	0	0*
Bedaquiline	0	0	0*
Linezolid	1	0	1*
Clofazimine	0	0	0*
Pretomanid	0	0	0*

*One additional laboratory reported 'No Interpretation' for MOX, CAP, RBT, CYS, RPT, BDQ, LZD, CFZ, and PTM by Sensititre®.

†One additional laboratory reported 'No Interpretation' for MOX and CYS by Sensititre®.

Table 9. Isolate 2025F—Participant Results for Molecular Testing

Drug	Mutation Not Detected	Mutation Detected	Total
Rifamycins (Rifampin, Rifabutin, Rifapentine)	14	0	14
Isoniazid	0	10*	10
Ethambutol	9	0	9
Pyrazinamide	9	0	9
Streptomycin	6	0	6
Fluoroquinolones (Ofloxacin, Ciprofloxacin, Moxifloxacin, Levofloxacin)	8	0	8
Amikacin	8	0	8
Kanamycin	8	0	8
Capreomycin	7	0	7
Ethionamide	6	0	6
Cycloserine	1	0	1
p-Aminosalicylic acid	1	0	1
Bedaquiline	6	0	6
Linezolid	7	0	7
Clofazimine	6	0	6
Delamanid	2	0	2
Pretomanid	2	0	2

*Nine of 10 laboratories specifically noted the detection of *katG* Ser315Thr mutation.

Isolate 2025G

Expected Results:

Drug	Growth-based*	Molecular*
RIF	R†	*rpoB* His445Leu
INH	S	*katG, inhA, & fabG1* wild-type
EMB	S	*embB* wild-type
PZA	S	*pncA* wild-type
FQ	S	*gyrA* & *gyrB* wild-type

Note: RIF=rifampin, INH=isoniazid, EMB=ethambutol, PZA=pyrazinamide, FQ=fluoroquinolones, S=susceptible, R=resistant.

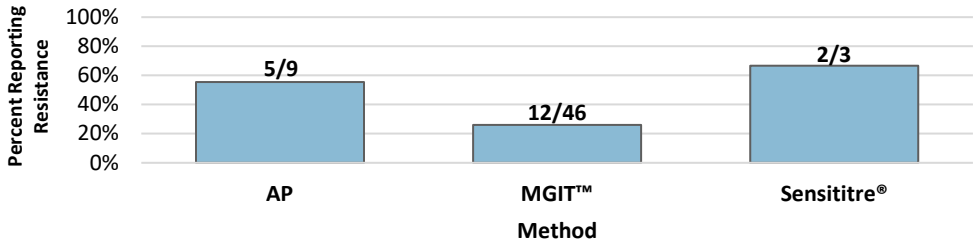
*Growth-based expected results determined by agar proportion, except for PZA which was determined by MGIT™. Molecular expected results determined by whole genome sequencing.

†80% consensus for a single categorical result of susceptible or resistant across all methods reported for this drug was not achieved for this isolate among participating laboratories.

Rifampin

DNA sequence analysis of *rpoB* in Isolate 2025G revealed an A>T point mutation in codon 445 resulting in wild-type histidine being replaced by leucine (His445Leu). Isolates with His445Leu mutations are associated with low-level rifampin resistance and can test as susceptible in growth-based assays [5, 13, 14]. Although this mutation is associated with low-level rifampin resistance, a lower proportion of participating laboratories performing MGIT™ growth-based DST detected resistance relative to laboratories performing other methods; this is likely due to the RIF critical concentration used for testing. Consideration may be given to evaluating a lower critical concentration for RIF [5, 15, 16].

Figure 7. Isolate 2025G: Percent of Laboratories Reporting RIF resistance, by Growth-based Method



Note: RIF=rifampin, AP=agar proportion. Laboratories performing Sensititre® reported RIF MIC values as 0.25 µg/ml (n=1), 2 µg/ml (n=1), and >8 µg/ml (n=1).

For internal comparison purposes, isolate 2025G was previously sent as MPEP 2022B. Similar RIF results were reported for Sensititre®, but a decrease in the proportion of laboratories reporting RIF resistance was noted for laboratories performing agar proportion and MGIT™ for MPEP 2025G compared to MPEP 2022B.

Complete first-line DST, second-line DST, and molecular results submitted by all participants for Isolate 2025G are listed in Tables 10–16.

Table 10. Isolate 2025G—Participant Results for First-Line DST by AP

Drug	Susceptible	Resistant	Total
Rifampin	4	5	9
Isoniazid—Low	9	0	9
Isoniazid—High	9	0	9
Ethambutol	9	0	9

Table 11. Isolate 2025G—Participant Results for First-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Rifampin	34	12	46*
Isoniazid—Low	47	0	47
Isoniazid—High	15	0	15
Ethambutol	47	0	47
Pyrazinamide	0	0	0

*One additional laboratory reported 'Intermediate' for RIF by MGIT™.

Table 12. Isolate 2025G—Participant Results for First-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total*
Rifampin	1	2	3
Isoniazid—Low	3	0	3
Isoniazid—High	2	0	2
Ethambutol	3	0	3

*One additional laboratory reported 'Contaminated/No Growth' for RIF, INH, and EMB by Sensititre®

Table 13. Isolate 2025G—Participant Results for Second-Line DST by AP

Drug	Susceptible	Resistant	Total
Streptomycin	6	0	6*
Ofloxacin	4	0	4
Ciprofloxacin	2	0	2
Moxifloxacin	4	0	4
Levofloxacin	4	0	4
Amikacin	6	0	6
Kanamycin	5	0	5
Capreomycin	6	0	6
Ethionamide	5	0	5
Rifabutin	5	0	5
Cycloserine	3	0	3
p-Aminosalicylic acid	3	0	3
Rifapentine	0	0	0
Bedaquiline	0	0	0
Linezolid	0	0	0
Clofazimine	0	0	0
Pretomanid	0	0	0

*One additional laboratory reported 'Intermediate' for STR by AP.

Table 14. Isolate 2025G—Participant Results for Second-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Streptomycin	15	0	15
Ofloxacin	2	0	2
Ciprofloxacin	1	0	1
Moxifloxacin	11	0	11
Levofloxacin	5	0	5
Amikacin	2	0	2
Kanamycin	1	0	1
Capreomycin	2	0	2
Ethionamide	2	0	2
Rifabutin	3	0	3
Cycloserine	0	0	0
p-Aminosalicylic acid	0	0	0
Rifapentine	0	0	0
Bedaquiline	1	0	1
Linezolid	2	0	2
Clofazimine	1	0	1
Pretomanid	0	0	0

Table 15. Isolate 2025G—Participant Results for Second-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Streptomycin	1	0	1*
Ofloxacin	0	0	0*
Ciprofloxacin	0	0	0
Moxifloxacin	1	0	1*†
Levofloxacin	1	0	1
Amikacin	1	0	1*
Kanamycin	1	0	1*
Capreomycin	1	0	1†
Ethionamide	0	0	0*
Rifabutin	1	0	1*†
Cycloserine	0	0	0†§
p-Aminosalicylic acid	1	0	1*
Rifapentine	0	0	0†
Bedaquiline	0	0	0†
Linezolid	1	0	1†
Clofazimine	0	0	0†
Pretomanid	0	0	0†

*One additional laboratory reported 'Contaminated/No Growth' for STR, OFL, MOX, AMK, KAN, ETA, RBT, and PAS by Sensititre®.

†One additional laboratory reported 'No Interpretation' for MOX, CAP, RBT, CYS, RPT, BDQ, LZD, CFZ, and PTM by Sensititre®.

§One additional laboratory reported 'No Interpretation' for CYS by Sensititre®.

Table 16. Isolate 2025G—Participant Results for Molecular Testing

Drug	Mutation Not Detected	Mutation Detected	Total
Rifamycins (Rifampin, Rifabutin, Rifapentine)	0	14*	14
Isoniazid	10	0	10
Ethambutol	9	0	9
Pyrazinamide	9	0	9
Streptomycin	6	0	6
Fluoroquinolones (Ofloxacin, Ciprofloxacin, Moxifloxacin, Levofloxacin)	8	0	8
Amikacin	7	0	7[†]
Kanamycin	8	0	8
Capreomycin	7	0	7
Ethionamide	6	0	6
Cycloserine	1	0	1
p-Aminosalicylic acid	1	0	1
Bedaquiline	5	1[§]	6
Linezolid	7	0	7
Clofazimine	5	1[§]	6
Delamanid	2	0	2
Pretomanid	2	0	2

*Nine of 14 laboratories noted the detection of *rpoB* His445Leu mutation and two laboratories performing Xpert® MTB/RIF assay noted Probe D.

[†]One additional laboratory reported 'No Result'.

[§]One laboratory noted the detection of *mmpL5* Ala147Thr mutation with unknown significance.

Isolate 2025H

Expected Results:

Drug	Growth-based*	Molecular*
RIF	S	*rpoB* wild-type
INH	S	*katG, inhA,* & *fabG1* wild-type
EMB	S	*embB* wild-type
PZA	S	*pncA* wild-type
FQ	S	*gyrA* & *gyrB* wild-type

Note: RIF=rifampin, INH=isoniazid, EMB=ethambutol, PZA=pyrazinamide, FQ=fluoroquinolones, S=susceptible, R=resistant.
*Growth-based expected results determined by agar proportion. Molecular expected results determined by whole genome sequencing.

Pan-susceptible

Isolate 2025H was expected to be susceptible to all first- and second-line drugs.

For internal comparison purposes, isolate 2025H was previously sent as MPEP 2018J. Similar results were reported across all methods for MPEP 2025H and MPEP 2018J.

Complete first-line DST, second-line DST, and molecular results submitted by all participants for Isolate 2025H are listed in Tables 17–23.

Table 17. Isolate 2025H—Participant Results for First-Line DST by AP

Drug	Susceptible	Resistant	Total
Rifampin	**9**	**0**	**9**
Isoniazid—Low	**9**	**0**	**9**
Isoniazid—High	**9**	**0**	**9**
Ethambutol	**9**	**0**	**9**

Table 18. Isolate 2025H—Participant Results for First-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Rifampin	**47**	**0**	**47**
Isoniazid—Low	**47**	**0**	**47**
Isoniazid—High	**15**	**0**	**15**
Ethambutol	**47**	**0**	**47**
Pyrazinamide	**0**	**0**	**0**

Table 19. Isolate 2025H—Participant Results for First-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Rifampin	**4**	**0**	**4**
Isoniazid—Low	**3**	**0**	**3**
Isoniazid—High	**2**	**0**	**2**
Ethambutol	**4**	**0**	**4**

Table 20. Isolate 2025H—Participant Results for Second-Line DST by AP

Drug	Susceptible	Resistant	Total
Streptomycin	4	3	7
Ofloxacin	4	0	4
Ciprofloxacin	2	0	2
Moxifloxacin	4	0	4
Levofloxacin	4	0	4
Amikacin	5	1	6
Kanamycin	3	2	5
Capreomycin	2	4	6
Ethionamide	5	0	5
Rifabutin	5	0	5
Cycloserine	3	0	3
p-Aminosalicylic acid	3	0	3
Rifapentine	0	0	0
Bedaquiline	0	0	0
Linezolid	0	0	0
Clofazimine	0	0	0
Pretomanid	0	0	0

Table 21. Isolate 2025H—Participant Results for Second-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Streptomycin	15	0	15
Ofloxacin	2	0	2
Ciprofloxacin	1	0	1
Moxifloxacin	11	0	11
Levofloxacin	5	0	5
Amikacin	2	0	2
Kanamycin	1	0	1
Capreomycin	2	0	2
Ethionamide	2	0	2
Rifabutin	3	0	3
Cycloserine	0	0	0
p-Aminosalicylic acid	0	0	0
Rifapentine	0	0	0
Bedaquiline	1	0	1
Linezolid	2	0	2
Clofazimine	1	0	1
Pretomanid	0	0	0

Table 22. Isolate 2025H—Participant Results for Second-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Streptomycin	2	0	2
Ofloxacin	1	0	1
Ciprofloxacin	0	0	0
Moxifloxacin	1	0	1*†
Levofloxacin	1	0	1
Amikacin	2	0	2
Kanamycin	1	0	1
Capreomycin	1	0	1*
Ethionamide	1	0	1
Rifabutin	2	0	2*
Cycloserine	0	0	0*†
p-Aminosalicylic acid	2	0	2
Rifapentine	0	0	0*
Bedaquiline	0	0	0*
Linezolid	1	0	1*
Clofazimine	0	0	0*
Pretomanid	0	0	0

*One additional laboratory reported 'No Interpretation' for MOX, CAP, RBT, CYS, RPT, BDQ, LZD, and CFZ by Sensititre®.

†One additional laboratory reported 'No Interpretation' for MOX and CYS by Sensititre®.

Table 23. Isolate 2025H—Participant Results for Molecular Testing

Drug	Mutation Not Detected	Mutation Detected	Total
Rifamycins (Rifampin, Rifabutin, Rifapentine)	14	0	14
Isoniazid	10	0	10
Ethambutol	9	0	9
Pyrazinamide	9	0	9
Streptomycin	6	0	6
Fluoroquinolones (Ofloxacin, Ciprofloxacin, Moxifloxacin, Levofloxacin)	8	0	8
Amikacin	8	0	8
Kanamycin	8	0	8
Capreomycin	7	0	7
Ethionamide	6	0	6
Cycloserine	1	0	1
p-Aminosalicylic acid	1	0	1
Bedaquiline	6	0	6
Linezolid	7	0	7
Clofazimine	6	0	6
Delamanid	2	0	2
Pretomanid	2	0	2

Isolate 2025I

Expected Results:

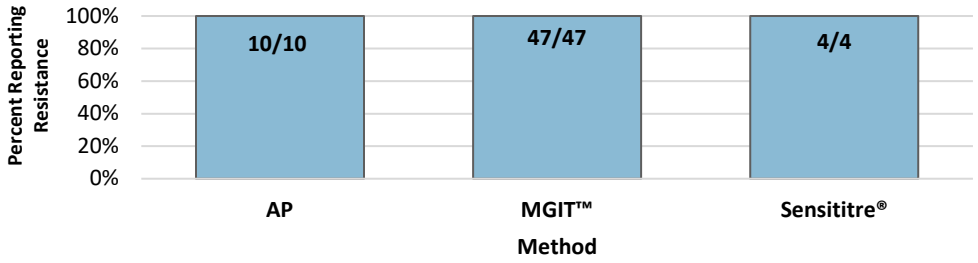
Drug	Growth-based*	Molecular*
RIF	R	*rpoB* Ser450Leu
INH	S	*katG*, *inhA, & fabG1* wild-type
EMB	S	*embB* wild-type
PZA	S	*pncA* wild-type
FQ	S	*gyrA & gyrB* wild-type

Note: RIF=rifampin, INH=isoniazid, EMB=ethambutol, PZA=pyrazinamide, FQ=fluoroquinolones, S=susceptible, R=resistant, U=unknown.
*Growth-based expected results determined by agar proportion, except for PZA which was determined by MGIT™. Molecular expected results determined by whole genome sequencing.

Rifampin

DNA sequence analysis of *rpoB* in Isolate 2025I revealed a C>T point mutation in codon 450 resulting in wild-type serine being replaced by leucine (Ser450Leu). Isolates with Ser450Leu mutations are associated with RIF resistance and should reliably test as resistant in growth-based assays [5, 13, 14, 17].

Figure 8. Isolate 2025I: Percent of laboratories reporting RIF resistance, by growth-based method



Note: RIF=rifampin, AP=agar proportion. Laboratories performing Sensititre® reported RIF MIC values as >8 µg/ml (n=1), 16 µg/ml (n=1), ≥16 µg/ml (n=1), and >16 µg/ml (n=1).

For internal comparison purposes, isolate 2025I was previously sent as MPEP 2024D. Similar RIF results were reported across all methods for MPEP 2025I and MPEP 2024D.

Complete first-line DST, second-line DST, and molecular results submitted by all participants for Isolate 2025I are listed in Tables 24–30.

Table 24. Isolate 2025I—Participant Results for First-Line DST by AP

Drug	Susceptible	Resistant	Total
Rifampin	0	10	10
Isoniazid—Low	10	0	10
Isoniazid—High	10	0	10
Ethambutol	10	0	10

Table 25. Isolate 2025I—Participant Results for First-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Rifampin	0	47	47
Isoniazid—Low	46	1	47
Isoniazid—High	17	0	17
Ethambutol	46	0	46
Pyrazinamide	0	0	0

Table 26. Isolate 2025I—Participant Results for First-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Rifampin	0	4	4
Isoniazid—Low	4	0	4
Isoniazid—High	3	0	3
Ethambutol	4	0	4

Table 27. Isolate 2025I—Participant Results for Second-Line DST by AP

Drug	Susceptible	Resistant	Total
Streptomycin	8	0	8
Ofloxacin	4	0	4
Ciprofloxacin	2	0	2
Moxifloxacin	4	0	4
Levofloxacin	4	0	4
Amikacin	6	0	6
Kanamycin	5	0	5
Capreomycin	6	0	6
Ethionamide	5	0	5
Rifabutin	0	5	5
Cycloserine	3	0	3
p-Aminosalicylic acid	3	0	3
Rifapentine	0	0	0
Bedaquiline	0	0	0
Linezolid	0	0	0
Clofazimine	0	0	0
Pretomanid	0	0	0

Table 28. Isolate 2025I—Participant Results for Second-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Streptomycin	17	0	17
Ofloxacin	2	0	2
Ciprofloxacin	1	0	1
Moxifloxacin	12	0	12
Levofloxacin	5	0	5
Amikacin	3	0	3
Kanamycin	1	0	1
Capreomycin	3	0	3
Ethionamide	3	0	3
Rifabutin	0	4	4
Cycloserine	0	0	0
p-Aminosalicylic acid	0	0	0
Rifapentine	0	0	0
Bedaquiline	1	0	1
Linezolid	2	0	2
Clofazimine	1	0	1
Pretomanid	0	0	0

Table 29. Isolate 2025I—Participant Results for Second-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Streptomycin	2	0	2
Ofloxacin	1	0	1
Ciprofloxacin	0	0	0
Moxifloxacin	1	0	1*†
Levofloxacin	1	0	1
Amikacin	2	0	2
Kanamycin	1	0	1
Capreomycin	1	0	1*
Ethionamide	1	0	1
Rifabutin	0	2	2*
Cycloserine	0	0	0*†
p-Aminosalicylic acid	2	0	2
Rifapentine	0	0	0*
Bedaquiline	0	0	0*
Linezolid	1	0	1*
Clofazimine	0	0	0*
Pretomanid	0	0	0*

*One additional laboratory reported 'No Interpretation' for MOX, CAP, RBT, CYS, RPT, BDQ, LZD, CFZ, and PTM by Sensititre®.

†One additional laboratory reported 'No Interpretation' for MOX and CYS by Sensititre®.

Table 30. Isolate 2025I—Participant Results for Molecular Testing

Drug	Mutation Not Detected	Mutation Detected	Total
Rifamycins (Rifampin, Rifabutin, Rifapentine)	0	14*	14
Isoniazid	9	1†	10
Ethambutol	9	0	9
Pyrazinamide	9	0	9
Streptomycin	6	0	6
Fluoroquinolones (Ofloxacin, Ciprofloxacin, Moxifloxacin, Levofloxacin)	8	0	8
Amikacin	8	0	8
Kanamycin	8	0	8
Capreomycin	7	0	7
Ethionamide	6	0	6
Cycloserine	1	0	1
p-Aminosalicylic acid	1	0	1
Bedaquiline	6	0	6
Linezolid	7	0	7
Clofazimine	6	0	6
Delamanid	2	0	2
Pretomanid	2	0	2

*Nine of 14 laboratories noted the detection of *rpoB* Ser450Leu mutation (with one laboratory also noting an *rpoB* Arg522Ser mutation) and two laboratories performing Xpert® MTB/RIF assay noted Probe E.

† One laboratory noted the detection of an Arg463Leu mutation.

Isolate 2025J

Expected Results:

Drug	Growth-based*	Molecular*
RIF	S	*rpoB* wild-type
INH	R (high-level) †	*katG* Ser315Thr; *inhA & fabG1* wild-type
EMB	R¶	*embB* Tyr319Cys
PZA	N/A §	*pncA* wild-type
FQ	S	*gyrA & gyrB* wild-type
STR	R	*rpsL* Lys43Arg

Note: RIF=rifampin, INH=isoniazid, EMB=ethambutol, PZA=pyrazinamide, FQ=fluoroquinolones, STR=streptomycin, S=susceptible, R=resistant.

*Growth-based expected results determined by agar proportion, except for PZA which was determined by MGIT™. Molecular expected results determined by whole genome sequencing.

† Resistant at 0.2 µg/ml and 1.0 µg/ml by agar proportion. See Equivalent Critical Concentration table on page 8 for more information.

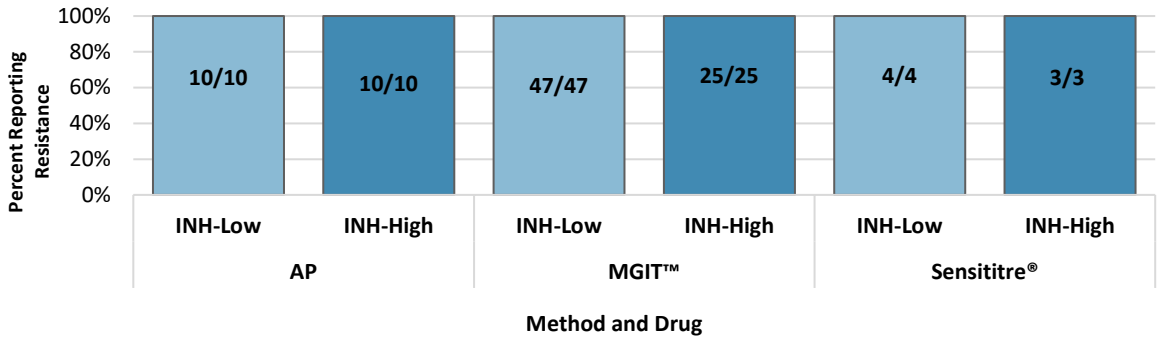
§ No growth-based result available. No mutation detected in *pncA*; consistent with likely PZA susceptible.

¶93% of participant results were EMB susceptible despite expected resistance by growth-based testing and the mutation's association with resistance [5]. The reason for the unexpected susceptible result is unknown; laboratories may consider excluding this isolate from quality assurance assessments for growth-based methods.

Isoniazid

DNA sequence analysis of *inhA, katG,* and *fabG1* of Isolate 2025J revealed a G>C point mutation in the *katG* locus resulting in wild-type serine being replaced by threonine at codon 315 (Ser315Thr); *inhA* and *fabG1* were wild-type (i.e., no mutations were detected). The *katG* Ser315Thr mutation is known to cause high-level isoniazid resistance [5, 11, 12].

Figure 9. Isolate 2025J: Percent of Laboratories Reporting INH-Low and INH-High Resistance, by Growth-based Method



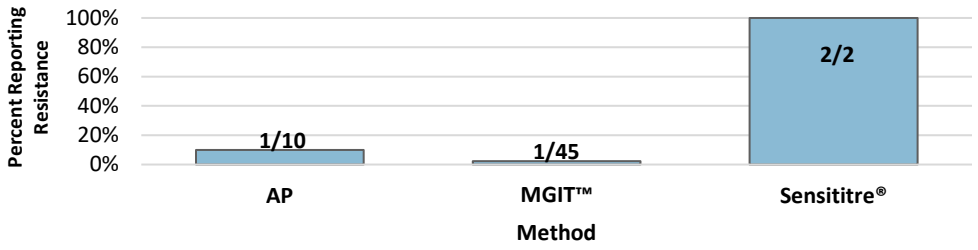
Note: INH-Low=isoniazid-low concentration, INH-High=isoniazid-high concentration, AP=agar proportion. Laboratories performing Sensititre® reported INH MIC values as 3.2 µg/ml (n=1) and 4 µg/ml (n=3).

Ethambutol

DNA sequence analysis of *embB* of Isolate 2025J revealed an A>G point mutation in the *embB* gene resulting in wild-type tyrosine being replaced by cysteine at codon 319 (Tyr319Cys). The Tyr319Cys mutation is associated with EMB resistance [5].

Resistance was expected by growth-based testing and the mutation's association with resistance [5]. The reason for the unexpected susceptible result by 93% of participant results is unknown. Laboratories may consider excluding this isolate from quality assurance assessments for growth-based methods.

Figure 10. Isolate 2025J: Percent of Laboratories Reporting EMB Resistance, by Growth-based Method

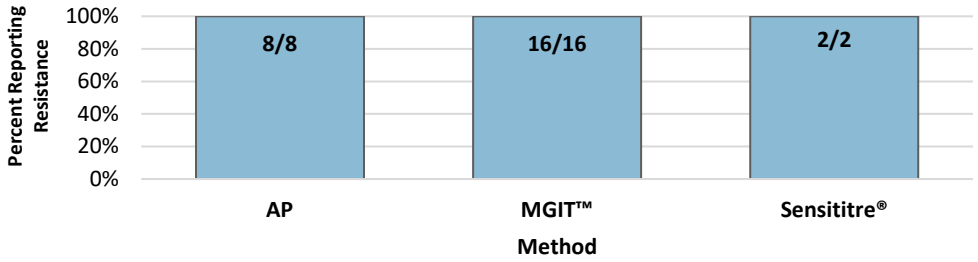


Note: EMB=ethambutol, AP=agar proportion. Laboratories performing Sensititre® reported EMB MIC values as 4 µg/ml (n=2), 8 µg/ml (n=1), and 10 µg/ml (n=1), although only two laboratories reported a categorical interpretation.

Streptomycin

DNA sequence analysis of *embB* of Isolate 2025J revealed an A>G point mutation in the *rpsL* gene resulting in wild-type lysine being replaced by arginine at codon 43 (Lys43Arg). The Lys43Arg mutation is associated with STR resistance [5].

Figure 11. Isolate 2025J: Percent of Laboratories Reporting STR Resistance, by Growth-based Method



Note: STR=streptomycin, AP=agar proportion. Laboratories performing Sensititre® reported STR MIC values as 32 µg/ml (n=1) and >32 µg/ml (n=1).

Complete first-line DST, second-line DST, and molecular results submitted by all participants for Isolate 2025J are listed in Tables 31–37.

Table 31. Isolate 2025J—Participant Results for First-Line DST by AP

Drug	Susceptible	Resistant	Total
Rifampin	10	0	10
Isoniazid—Low	0	10	10
Isoniazid—High	0	10	10
Ethambutol	9	1	10

Table 32. Isolate 2025J—Participant Results for First-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Rifampin	47	0	47
Isoniazid—Low	0	47	47
Isoniazid—High	0	25	25
Ethambutol	44	1	45*
Pyrazinamide	0	0	0

*One additional laboratory reported 'No Interpretation' for EMB by MGIT™.

Table 33. Isolate 2025J—Participant Results for First-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Rifampin	4	0	4
Isoniazid—Low	0	4	4
Isoniazid—High	0	3	3
Ethambutol	0	2	2*

*One additional laboratory reported 'Intermediate' and one laboratory reported 'No Interpretation' for EMB by Sensititre®.

Table 34. Isolate 2025J—Participant Results for Second-Line DST by AP

Drug	Susceptible	Resistant	Total
Streptomycin	0	8	8
Ofloxacin	4	0	4
Ciprofloxacin	2	0	2
Moxifloxacin	3	0	3
Levofloxacin	4	0	4
Amikacin	6	0	6
Kanamycin	5	0	5
Capreomycin	6	0	6
Ethionamide	5	0	5
Rifabutin	5	0	5
Cycloserine	3	0	3
p-Aminosalicylic acid	3	0	3
Rifapentine	0	0	0
Bedaquiline	0	0	0
Linezolid	0	0	0
Clofazimine	0	0	0
Pretomanid	0	0	0

Table 35. Isolate 2025J—Participant Results for Second-Line DST by MGIT™

Drug	Susceptible	Resistant	Total
Streptomycin	0	16	16
Ofloxacin	2	0	2
Ciprofloxacin	1	0	1
Moxifloxacin	12	0	12
Levofloxacin	5	0	5
Amikacin	2	0	2
Kanamycin	1	0	1
Capreomycin	2	0	2
Ethionamide	2	0	2
Rifabutin	3	0	3
Cycloserine	0	0	0
p-Aminosalicylic acid	0	0	0
Rifapentine	0	0	0
Bedaquiline	1	0	1
Linezolid	2	0	2
Clofazimine	1	0	1
Pretomanid	0	0	0

Table 36. Isolate 2025J—Participant Results for Second-Line DST by Sensititre®

Drug	Susceptible	Resistant	Total
Streptomycin	0	2	2
Ofloxacin	1	0	1
Ciprofloxacin	0	0	0
Moxifloxacin	1	0	1*†
Levofloxacin	1	0	1
Amikacin	2	0	2
Kanamycin	1	0	1
Capreomycin	1	0	1*
Ethionamide	1	0	1
Rifabutin	2	0	2*
Cycloserine	1	0	1
p-Aminosalicylic acid	2	0	2
Rifapentine	0	0	0*
Bedaquiline	0	0	0*
Linezolid	1	0	1*
Clofazimine	0	0	0*
Pretomanid	0	0	0*

*One additional laboratory reported 'No Interpretation' for MOX, CAP, RBT, CYS, RPT, BDQ, LZD, CFZ, and PTM by Sensititre®.

†One additional laboratory reported 'No Interpretation' for MOX by Sensititre®.

Table 37. Isolate 2025J—Participant Results for Molecular Testing

Drug	Mutation Not Detected	Mutation Detected	Total
Rifamycins (Rifampin, Rifabutin, Rifapentine)	14	0	14
Isoniazid	0	10*	10
Ethambutol	1	8†	9
Pyrazinamide	9	0	9
Streptomycin	1	5§	6
Fluoroquinolones (Ofloxacin, Ciprofloxacin, Moxifloxacin, Levofloxacin)	8	0	8
Amikacin	8	0	8
Kanamycin	8	0	8
Capreomycin	7	0	7
Ethionamide	6	0	6
Cycloserine	1	0	1
p-Aminosalicylic acid	1	0	1
Bedaquiline	6	0	6
Linezolid	7	0	7
Clofazimine	6	0	6
Delamanid	2	0	2
Pretomanid	2	0	2

*Nine of 10 laboratories noted the detection of *katG* Ser315Thr mutation.

†Eight laboratories noted the detection of *embB* Tyr319Cys mutation.

§ Five laboratories noted the detection of *rpsL* Lys43Arg mutation.

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Appendix 1: Accessible Explanations of Figures

Figure 1. **The primary classification of the 53 laboratories participating in the August 2025 MPEP panel is shown in this pie chart.** The largest slice represents 41 laboratories, or 77%, of the 53 that have self-classified as a health department laboratory. The next major slice signifies 5 laboratories, or 9%, of the 53 that self-classified as hospital laboratories. The remaining two slices of the pie chart represent 4, or 8%, of the 53 that self-classified as independent laboratories; and 3, or 6%, of the 53 that self-classified as federal government laboratories.

Figure 2. The annual volume of MTBC isolates tested for drug susceptibility by participating laboratories (N=53) in 2024 is displayed in this vertical bar graph. The vertical y–axis is the number of laboratories responding and ranges from 0 to 16 using increments of 2. Along the horizontal x-axis are eight vertical bars representing the number of isolates tested per year. From left to right, 13 laboratories tested less than or equal to 50 isolates per year; 14 laboratories tested between 51 to 100 isolates per year; 4 laboratories tested between 101 to 150 isolates per year; 5 laboratories tested between 151 to 200 isolates per year; 5 laboratories tested between 201 to 300 isolates per year; 2 laboratories tested between 301 to 500 isolates per year; 6 laboratories tested between 501 to 1000 isolates per year; and 4 laboratories tested greater than or equal to 1,001 isolates per year.

Figure 3. The drug susceptibility testing methods performed by MPEP participants (N=80) are displayed in this vertical bar graph. The vertical y-axis is the number of laboratories reporting with ranges from 0 to 60, by increments of 10, and the horizontal x- axis lists the susceptibility testing methods. Each bar represents the number of reporting laboratories performing a particular drug susceptibility test method. From left to right: 48 performed MGIT™, 12 performed agar proportion, 4 performed Sensititre®, 0 performed VersaTREK™, and 16 performed molecular methods.

Figure 4. The molecular methods performed by MPEP participants (N=16) are displayed in this pie chart. The two largest slices represent the 5 laboratories, or 31.5%, of the 16 laboratories, that performed targeted DNA sequencing and the 5 laboratories, or 31.5%, of the 16 laboratories, that performed whole genome sequencing. The next three slices represent 4 laboratories, or 25%, of the 16 laboratories, that performed the Cepheid Xpert® MTB/RIF assay; 1 laboratory, or 6%, of the 16 laboratories, that performed the Deeplex Myc-TB assay; and 1 laboratory, or 6%, of the 16 laboratories, that performed the Bruker line probe assay.

Figure 5. The antituberculosis drugs tested by growth-based method by MPEP participants are displayed in a horizontal bar graph. The vertical y -axis contains a list of each drug tested and the horizontal x-axis contains the number of laboratories with ranges from 0 to 60, by increments of 10. There are 22 horizontal bars with each bar representing the number of laboratories reporting a result for a particular drug for susceptibility testing. 52 laboratories tested rifampin; 52 laboratories tested isoniazid; 52 laboratories tested ethambutol; 0 laboratories tested pyrazinamide; 25 laboratories tested streptomycin; 7 laboratories tested ofloxacin; 16 laboratories tested moxifloxacin; 3 laboratories tested ciprofloxacin; 10 laboratories tested levofloxacin; 11 laboratories tested capreomycin; 7 laboratories tested kanamycin; 11 laboratories tested amikacin; 9 laboratories tested ethionamide; 5 laboratories tested p-Aminosalicylic acid; 12 laboratories tested rifabutin; 5 laboratories tested cycloserine; 1

laboratory tested rifapentine; 2 laboratories tested bedaquiline; 4 laboratories tested linezolid; 2 laboratories tested clofazimine; 0 laboratories tested delamanid; and 1 laboratory tested pretomanid.

Figure 6. The percent of laboratories reporting resistance to isoniazid (low and high concentrations), by growth-based method, for isolate 2025F is displayed in this vertical bar graph. The vertical y-axis is the percent of laboratories reporting resistance with ranges from 0% to 100%, by increments of 20, and the horizontal x-axis lists the method and drugs. Each bar represents the percent of laboratories reporting resistance. From left to right: laboratories performing agar proportion for INH-Low is 10 of 10 (100%) reporting resistance and INH-High is 10 of 10 (100%) reporting resistance; laboratories performing MGIT™ for INH-Low is 47 of 47 (100%) reporting resistance and INH-High is 25 of 25 (100%) reporting resistance; and laboratories performing Sensititre® for INH-Low is 4 of 4 (100%) reporting resistance and INH-High is 3 of 3 (100%) reporting resistance.

Figure 7. The percent of laboratories reporting resistance to rifampin, by growth-based method, for isolate 2025G is displayed in this vertical bar graph. The vertical y-axis is the percent of laboratories reporting resistance with ranges from 0% to 100%, by increments of 20, and the horizontal x-axis lists the method. Each bar represents the percent of laboratories reporting resistance. From left to right: laboratories performing agar proportion for rifampin is 5 of 9 (56%) reporting resistance; laboratories performing MGIT™ for rifampin is 12 of 46 (26%) reporting resistance; and laboratories performing Sensititre® for rifampin is 2 of 3 (67%) reporting resistance.

Figure 8. The percent of laboratories reporting resistance to rifampin, by growth-based method, for isolate 2025I is displayed in this vertical bar graph. The vertical y-axis is the percent of laboratories reporting resistance with ranges from 0% to 100%, by increments of 20, and the horizontal x-axis lists the method. Each bar represents the percent of laboratories reporting resistance. From left to right: laboratories performing agar proportion for rifampin is 10 of 10 (100%) reporting resistance; laboratories performing MGIT™ for rifampin is 47 of 47 (100%) reporting resistance; and laboratories performing Sensititre® for rifampin is 4 of 4 (100%) reporting resistance.

Figure 9. The percent of laboratories reporting resistance to isoniazid (low and high concentrations), by growth-based method, for 2025J is displayed in this vertical bar graph. The vertical y-axis is the percent of laboratories reporting resistance with ranges from 0% to 100%, by increments of 20, and the horizontal x-axis lists the method and drugs. Each bar represents the percent of laboratories reporting resistance. From left to right: laboratories performing agar proportion for INH-Low is 10 of 10 (100%) reporting resistance and INH-High is 10 of 10 (100%) reporting resistance; laboratories performing MGIT™ for INH-Low is 47 of 47 (100%) reporting resistance and INH-High is 25 of 25 (100%) reporting resistance; and laboratories performing Sensititre® for INH-Low is 4 of 4 (100%) reporting resistance and INH-High is 3 of 3 (100%) reporting resistance.

Figure 10. The percent of laboratories reporting resistance to ethambutol, by growth-based method, for 2025J is displayed in this vertical bar graph. The vertical y-axis is the percent of laboratories reporting resistance with ranges from 0% to 100%, by increments of 20, and the horizontal x-axis lists the method. Each bar represents the percent of laboratories reporting resistance. From left to right:

laboratories performing agar proportion for ethambutol is 1 of 10 (10%) reporting resistance; laboratories performing MGIT™ for ethambutol is 1 of 45 (2%) reporting resistance; and laboratories performing Sensititre® for ethambutol is 2 of 2 (100%) reporting resistance.

Figure 11. The percent of laboratories reporting resistance to streptomycin, by growth-based method, for 2025J is displayed in this vertical bar graph. The vertical y-axis is the percent of laboratories reporting resistance with ranges from 0% to 100%, by increments of 20, and the horizontal x-axis lists the method. Each bar represents the percent of laboratories reporting resistance. From left to right: laboratories performing agar proportion for streptomycin is 8 of 8 (100%) reporting resistance; laboratories performing MGIT™ for streptomycin is 16 of 16 (100%) reporting resistance; and laboratories performing Sensititre® for streptomycin is 2 of 2 (100%) reporting resistance.