



Department  
of Health

Wadsworth  
Center

# Perspectives from a Public Health Laboratory

July 1, 2015

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Wadsworth Center

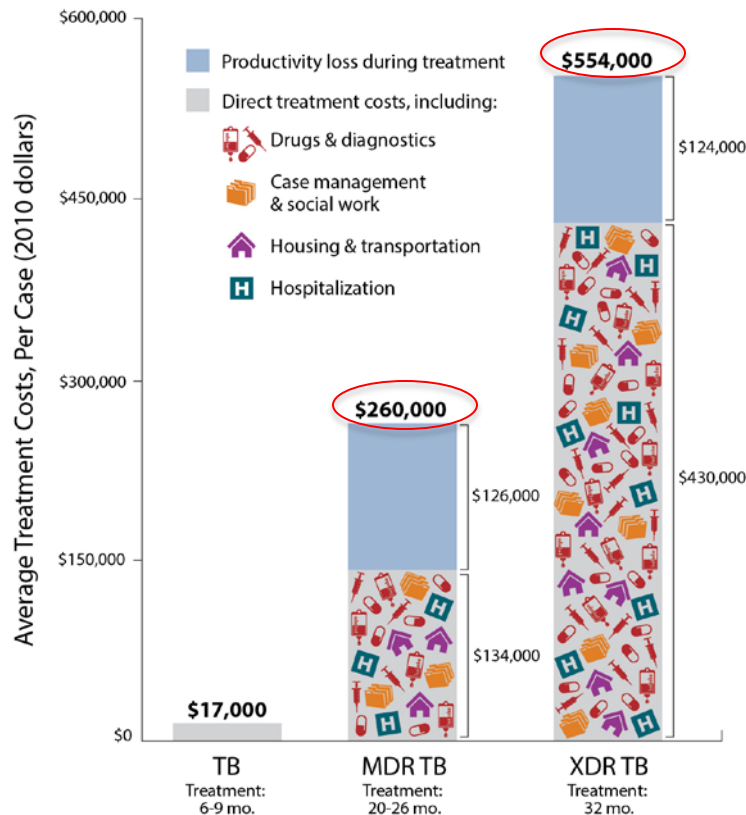
\*I have no disclosures.

# Drug Resistant Tuberculosis is a Global Health Concern

- **Multi-drug resistant TB (MDR):** resistant to at least rifampin and isoniazid
- **Extensively drug resistant TB (XDR):** resistant to rifampin and isoniazid plus any fluoroquinolone and at least one of three injectable second-line drugs (i.e., amikacin, kanamycin, or capreomycin).

## The Outsized Financial Toll of MDR and XDR TB

Cost increases with greater resistance:



## Preventing and Controlling MDR and XDR TB in the U.S. Requires:

**BETTER  
TREATMENT  
OPTIONS**

**RAPID  
DIAGNOSIS**

**EXPERT  
TREATMENT  
OF EVERY  
TB CASE**

**IMPROVING  
GLOBAL TB  
DIAGNOSIS AND  
TREATMENT**

<http://www.cdc.gov/nchstp/newsroom/2014/WorldTBDay-graphics.html>



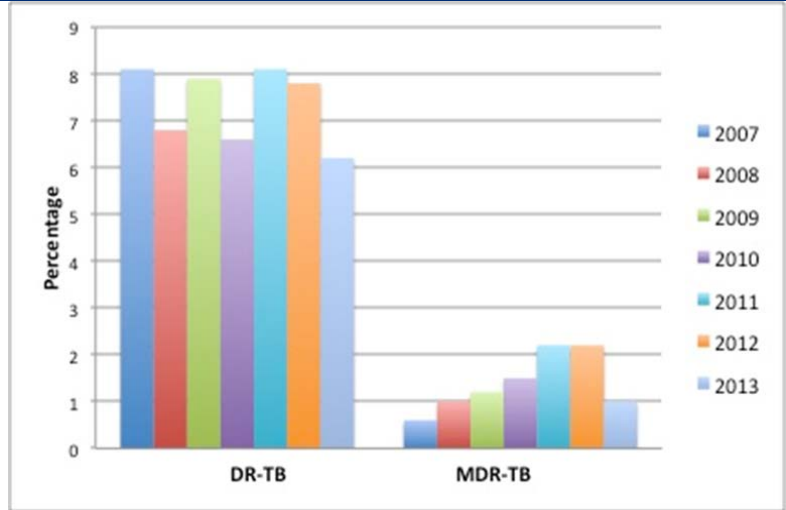
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# Why perform WGS on *Mycobacterium tuberculosis*?

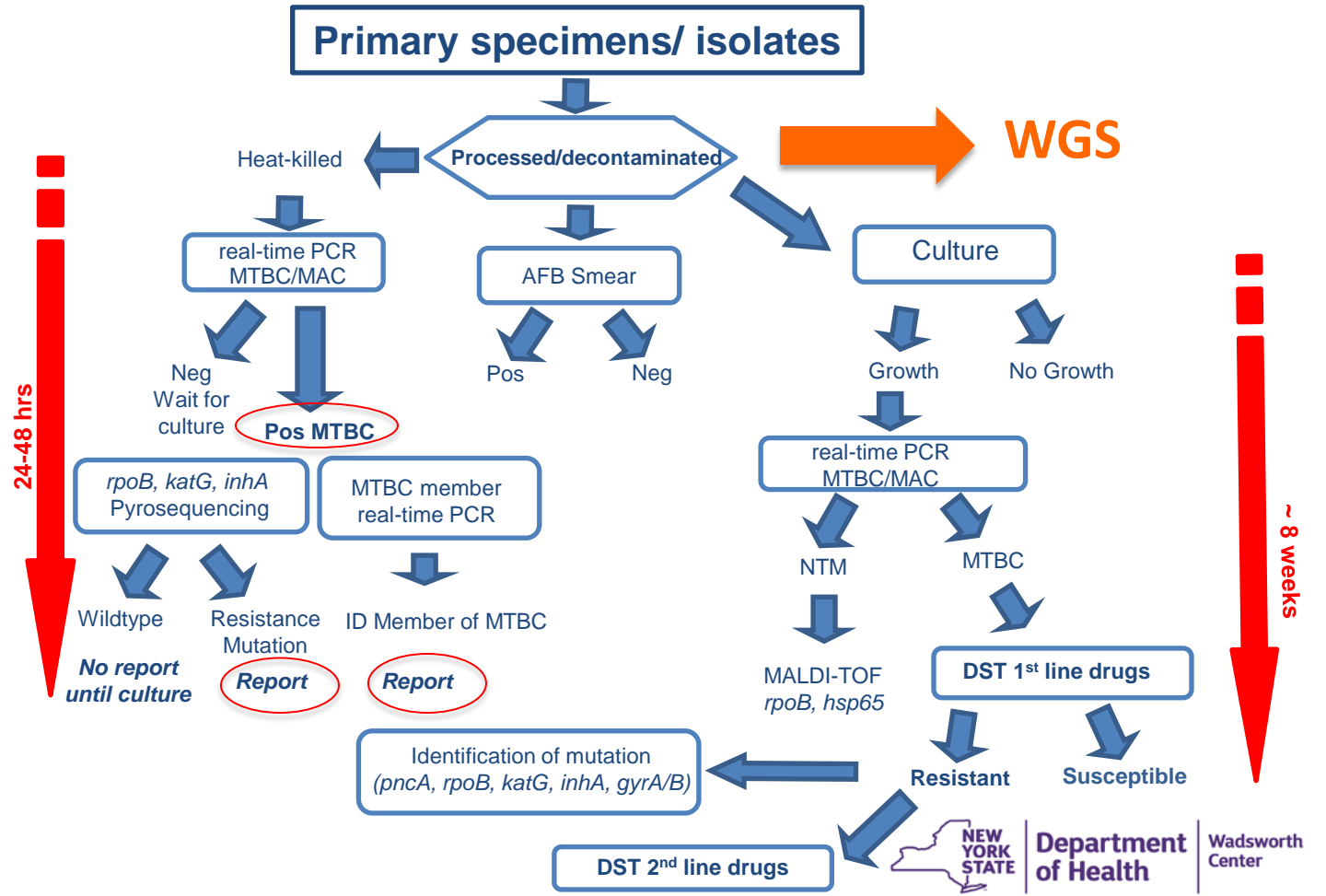
- **Faster turn-around time**
- **More comprehensive results**
  - **Detect mixed infections**
  - **Many predictors of drug resistance**
  - **Emerging resistance**
- **Cost effective**
  - **Replace existing assays (real-time PCR, pyrosequencing, spoligotyping)**
  - **Staff time savings**





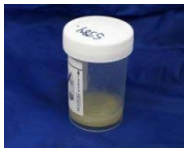
	2007	2008	2009	2010	2011	2012	2013	2014
TB Cases	1175	1200	1007	954	910	864	872	786





# Whole Genome Sequencing

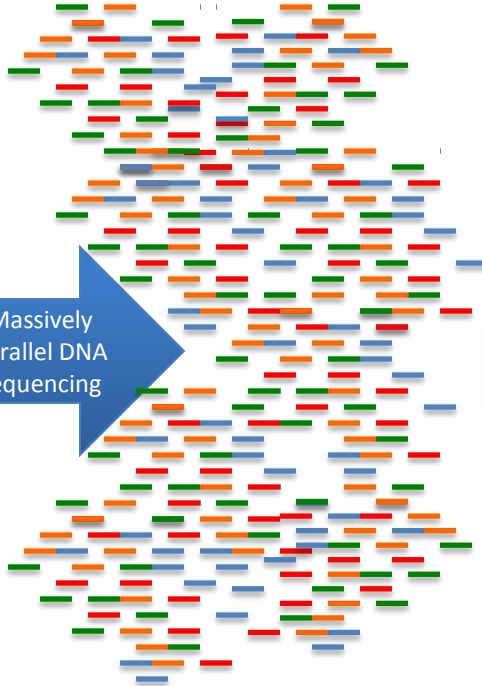
Next Generation Technologies



Extract TB  
DNA

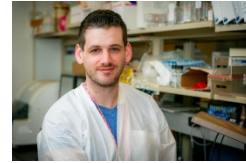


Massively  
Parallel DNA  
sequencing



Bioinformatics

# Validating a WGS assay for TB



Bacteriology/Myco  
bacteriology  
Laboratory

Selecting validation  
approach, culture,  
optimization of DNA  
preparation

Core Facilities

Library preparation and Miseq  
sequencing, optimizing, planning  
overall decisions for balancing runs  
(3 Illumina Miseqs)

Bioinformatics

Development, testing and continual  
improvements to pipeline, data storage

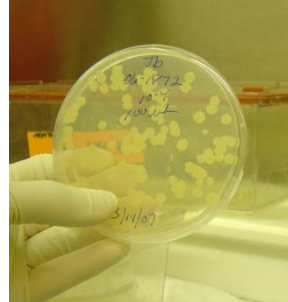




# What to validate first?

- Isolates
  - Solid
  - MGITs
- Primary specimens
  - sputum
  - other

Need to keep in mind available testing volumes, what is needed for other tests, archiving, etc...



# How Can We Mimic a Clinical Isolate?

- **Grow 2 different strains in MGIT tube**
  - *M. tuberculosis* : ATCC strain (ATCC)
  - *M. bovis* BCG : patient strain (BCG)
- **Aliquots made and heat-killed before leaving BSL-3**

MGIT



$10^5$  to  $10^6$  colony-forming units  
per milliliter (CFU/mL)

# Preparing TB DNA for WGS

- Assess methods used in lab
- Research TB WGS methods
- Assess worse case scenario
  - 1- 2 ml MGIT
  - early MGIT positive (Day 0-3 flagged positive)
- Ease of use, cost
- DNA concentration
- Ultimately- WGS 40X depth and close to 100% coverage



# Breaking TB Open is Critical for DNA Extraction

## Important TB Characteristics

- ~24 hour doubling time
- TB clumps together
- Unique cell wall
  - Rich in lipids (>60%)
  - Mycolic acids



## Initial Methods Tested

- Typical bacterial extraction
- Zymo Research Kit
  - Meant for tough to lyse fungi/ bacteria
- CTAB method
  - Ideal for plant cell nucleic acid extraction/ MTB

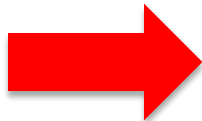


**DNA yield too low,  
labor intensive, WGS  
variable results**



# InstaGene Matrix and Tissue Homogenizer

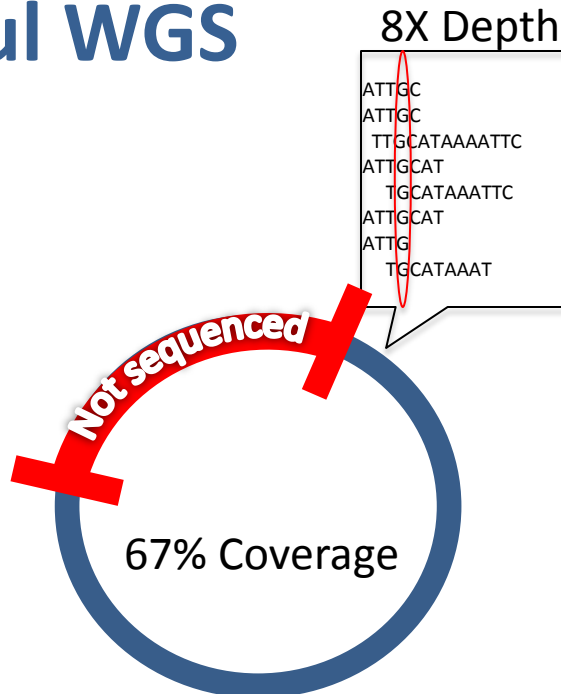
- **InstaGene matrix (Chelex resin)**
  - The Chelex matrix binds to PCR inhibitors rather than DNA, preventing DNA loss due to irreversible DNA binding.
- **Fastprep tissue homogenizer**
  - Good enough yield to provide reliable WGS data even with 0 day MGIT



**Success!**

# Successful WGS

- **Depth:** Essentially the number of times the base was read; measure of confidence in correct call
  - Can be given as a genome average
  - We are aiming for 40X
- **Coverage:** A percentage that describes how much of the genome was sequenced
  - Best 100%



# Library Preparation is Another Key Factor

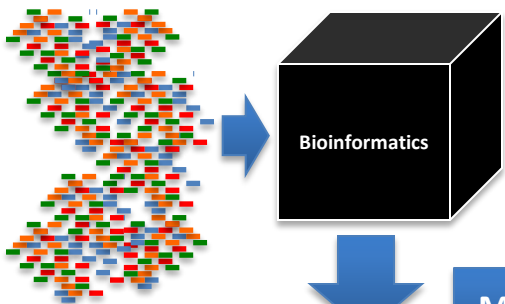
- **Votintseva *et al.* suggested using 15 cycle library preparation**
  - 2015 paper about WGS of early positive MGIT

			12 cycle library prep		15 cycle library prep	
			Nextera XT DNA Library Preparation Kit			
Sample	Method	stock ng/ul	Avg depth coverage %		Avg depth	coverage %
<i>M. bovis</i> BCG (0day)	InstaGene	0.268	FAIL	FAIL	27.66	97.23
	InstaGene	0.344	FAIL	FAIL	19.4	97.07
	InstaGene	0.346	FAIL	FAIL	14.22	96.78





# TB Bioinformatics Pipeline



Map to Reference Genome

Kracken  
K-mer  
matching

Detect  
spacers

SNP calling  
with indels

SNP calling  
ignore indels

MTBC  
member ID

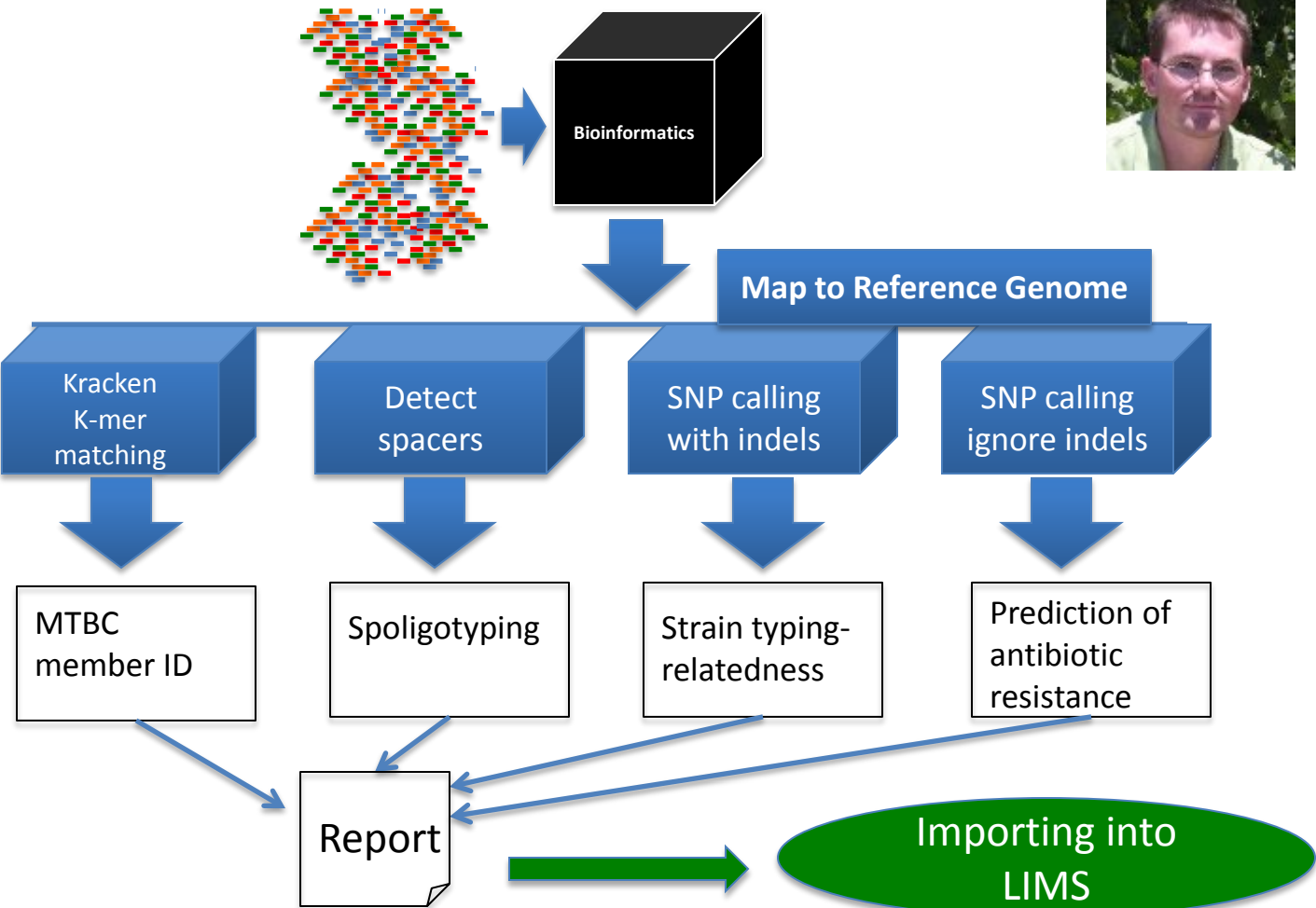
Spoligotyping

Strain typing-  
relatedness

Prediction of  
antibiotic  
resistance

Report

Importing into  
LIMS



# Example report excerpt

All Mutation in screened loci (except silent mutations):

7362	21	GAG -> CAG	Glu -> <u>Gln</u>	Rv0006	<u>gyrA</u>	<u>Fluoroquinolones</u>
7584	95	AGC -> ACC	Ser -> <u>Thr</u>	Rv0006	<u>gyrA</u>	<u>Fluoroquinolones</u>
9303	668	GGC -> GAC	<u>Gly</u> -> Asp	Rv0006	<u>gyrA</u>	<u>Fluoroquinolones</u>
9555	752	ACG -> ACC	<u>Thr</u> -> <u>Thr</u>	Rv0006	<u>gyrA</u>	<u>Fluoroquinolones (Silent)</u>
761154	450	TCG -> TTG	Ser -> <u>Leu</u>	Rv0667	<u>rpoB</u>	Rifampicin
764816	483	GTG -> GCG	Val -> Ala	Rv0668	<u>rpoC</u>	Rifampicin compensatory
765149	594	GGG -> GAG	<u>Gly</u> -> Glu	Rv0668	<u>rpoC</u>	Rifampicin compensatory
775639	948	ATT -> GTT	Ile -> Val	Rv0676c	<u>mmpL5</u>	<u>Clofazimine/Bedaquiline</u>
1416234	372	TGT -> GGC	<u>Cys</u> -> <u>Gly</u>	Rv1267	<u>embR</u>	Ethambutol
1416222	376	TTC -> CTC	<u>Phe</u> -> Leu	Rv1267	<u>embR</u>	Ethambutol
1674046	203	CTG -> CTA	Leu -> Leu	Rv1483	<u>mabA</u>	Isoniazid (Silent)
1917970	11	CTA -> CTG	Leu -> Leu	Rv1694	<u>tlyA</u>	<u>Aminoglycosides (Silent)</u>
2155169	315	AGC -> ACC	Ser -> <u>Thr</u>	Rv1908c	<u>katG</u>	Isoniazid
2280896	116	CTG -> CGG	Leu -> Arg	Rv2043c	<u>pncA</u>	<u>Pyrazinamide</u>
3336825	365	ACA -> GCA	<u>Thr</u> -> Ala	Rv2981c	<u>ddlA</u>	<u>D-Cycloserine</u>
4242641	927	CGC -> CGT	Arg -> Arg	Rc3793	<u>embC</u>	Ethambutol (Silent)
4242803	981	GTG -> CTG	Val -> Leu	Rc3793	<u>embC</u>	Ethambutol
4243221	-12	C -> T	<u>intergenic</u>	<u>embC-embA</u>		Ethambutol
4247429	306	ATG -> ATA	Met -> Ile	Rv3795	<u>embB</u>	Ethambutol
4407968	79	TTG -> TCG	Leu -> Ser	RV3919c	<u>gidB</u>	Streptomycin

High confidence mutations detected :

<u>embB</u>	306	ATG -> ATA	Met -> Ile	Ethambutol
<u>katG</u>	315	AGC -> ACC	Ser -> <u>Thr</u>	Isoniazid
<u>mabA</u>	203	CTG -> CTA	Leu -> Leu	Isoniazid
<u>pncA</u>	116	CTG -> CGG	Leu -> Arg	<u>Pyrazinamide</u>
<u>rpoB</u>	450	TCG -> TTG	Ser -> Leu	Rifampicin

-----  
Resistance Report:

Ethambutol	PASS	Resistant
<u>Fluoroquinolones</u>	PASS	Sensitive
Isoniazid	PASS	Resistant
<u>Pyrazinamide</u>	PASS	Resistant
Rifampicin	PASS	Resistant
Streptomycin	PASS	Sensitive

# Validation of TB WGS

- SOP, reports, interpretation, QC, assay controls, metrics
- Specificity, intra-assay and inter-assay reproducibility
- Retrospective testing
- Prospective testing
- Evaluate each drug



# TB WGS Reports

<b>Concentrated Smear (Ziehl - Neelsen/1,000 X)</b> (03/13/14):	<b>Numerous (&gt;9 acid-fast bacilli per field)</b>
<b>Direct Molecular Detection - Real-time PCR</b>	
Mycobacterium tuberculosis complex DNA by real-time PCR:	<b>DETECTED</b>
Mycobacterium avium complex DNA by real-time PCR:	<b>Not Detected</b>
<b>Molecular Identification - Real-time PCR</b>	
Mycobacterium tuberculosis complex species DNA identified:	<b>Mycobacterium tuberculosis</b>
<b>Culture</b> (03/25/14):	<b>acid-fast bacillus was isolated</b>
<b>Direct Molecular Drug Susceptibility Detection- Pyrosequencing</b>	
Rifampin (rpoB):	<b>Mutation present (Ser531Leu) suggests Rifampin resistance. Result must be confirmed by culture based susceptibility testing.</b>
Isoniazid (katG):	<b>Mutation absent. Culture must be performed for final susceptibility result.</b>
Isoniazid (inhA):	<b>Mutation absent. Culture must be performed for final susceptibility result.</b>
<b>Identification</b> (03/26/14):	<b>Mycobacterium tuberculosis was identified by culture and molecular analysis.</b>
<b>Susceptibility Testing for M. tuberculosis complex (MGIT)</b>	
Streptomycin [1.0 ug/ml]:	<b>Susceptible</b>
Isoniazid [0.1 ug/ml]:	<b>Susceptible</b>
Rifampin [1.0 ug/ml]:	<b>RESISTANT</b>
Ethambutol [5.0 ug/ml]:	<b>Susceptible</b>
Pyrazinamide [100 ug/ml]:	<b>Susceptible</b>

Whole genome sequencing



# Whole Genome Sequencing of TB: A “One Stop Shop”

## WGS

Single assay

Species identification

Genotyping (more accurate)

Drug resistance mutations

(more comprehensive)

## COST

Estimated around \$100 per sample

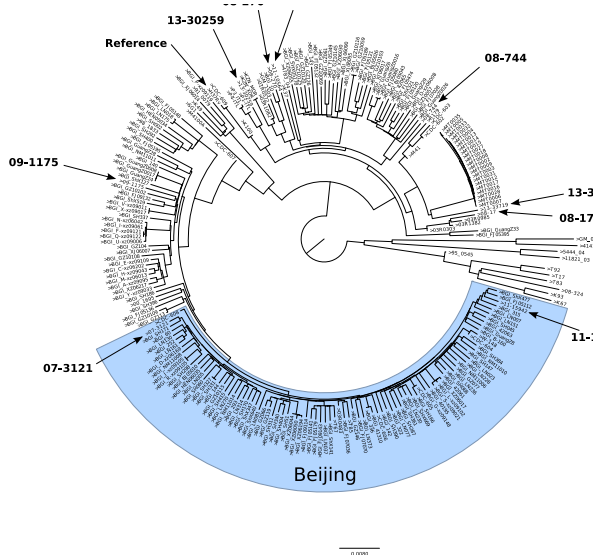
## TURNAROUND TIME

DNA preparation (1 days)

WGS result (4-5 days)



# WGS prediction spoligotypes and genotyping with increased resolution



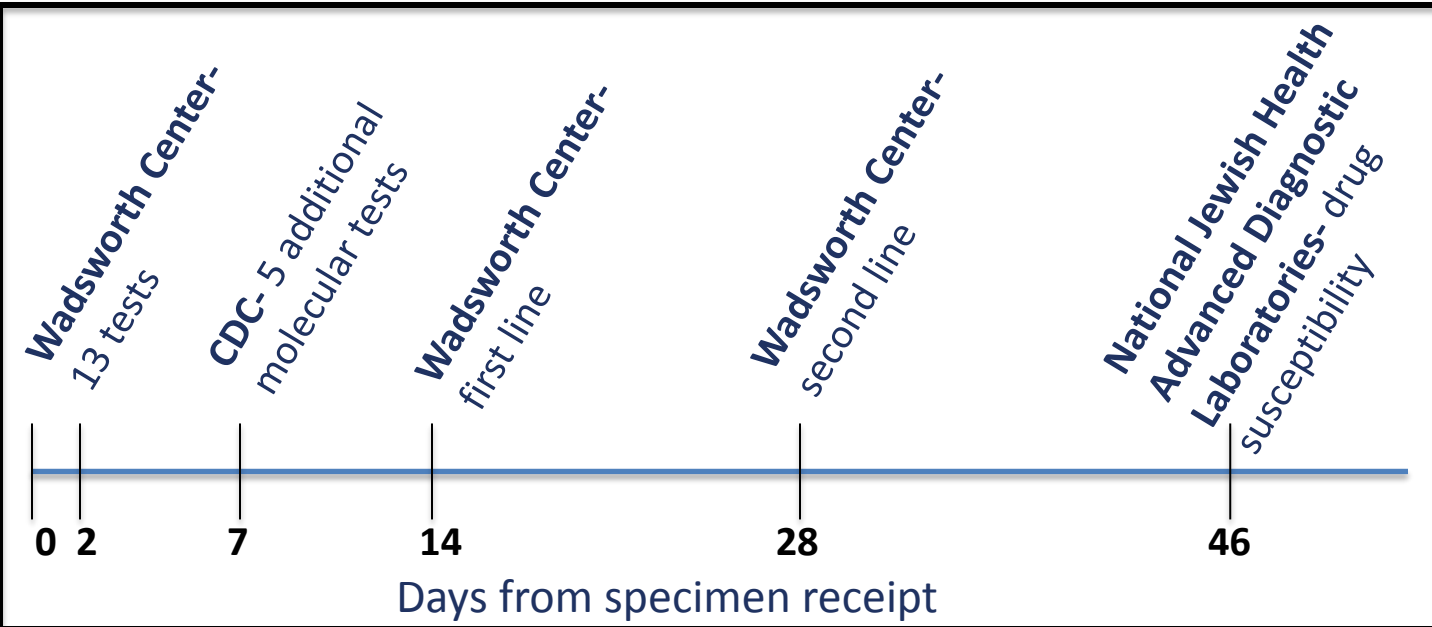
Sample #	Extraction	Accid.	Phenotype (DST)	Resistance Associated mutations (WGS)	Other mutations noted (WGS)	WGS Spoligotype	CLIMS spoligo. NYS	Do results correlate?
21	CTAB	14-7386	SM (low level in 2 <sup>nd</sup> line), INH, RIF, RBT	<b>rrs</b> .aa 450 (RIF) <b>tpsl</b> .aa 88 (SM) <b>katG</b> .aa 315 (INH)		S00034	Scheduled 12/15/14	Yes
22	CTAB	14-7387	INH (low level), RIF, RBT	<b>rrs</b> .aa 445 (RIF) <b>intergenic hyp-fabG1</b> aa. -15 (INH)		S00197	S00197	Yes
23	CTAB	14-7388	SM, INH, PZA, EMB (2 <sup>nd</sup> line only), KM, AN,	<b>rrs</b> .aa 450 (RIF) <b>tpsl</b> .aa 43 (SM) <b>katG</b> .aa 315 (INH) <b>embB</b> .aa 306 (EMB/INH)	<b>rrs</b> (AN/SM) <b>pncA</b> .aa 119 (PZA)	S00034	S00034	Yes
24	CTAB	14-7391	SM, EMB, CAP, KM, AN	<b>rrs</b> (AN/SM)	<b>embC</b> aa 981 (EMB) <b>gid</b> aa 97 (SM)	S00241	S00241	Yes
25	CTAB	14-7392	SM, RIF, EMB, PZA, KM, RBT, FLQ	<b>gyrA</b> .aa 94 (FLQ) <b>rrs</b> .aa 450 (RIF) <b>tpsl</b> .aa 452 (RIF) <b>embB</b> .aa 306 (EMB/INH) <b>embI</b> .aa 497 (EMB/INH)	<b>gid</b> aa 92 (SM) <b>rrs</b> (AN/SM) <b>tpsl</b> .aa 43 (SM) <b>pncA</b> TG-TGG (PZA) <b>eis</b> .promoter (AN/KM)	S00034	S00034	Yes
26	CTAB	14-7393	INH, RIF, PZA, EMB 5.0 (2 <sup>nd</sup> line only), ETA, RBT,	<b>rrs</b> .aa 450 (RIF) <b>intergenic hyp-fabG1</b> aa. -15 (INH/ETA) <b>embB</b> .aa 306 (EMB/INH)		S00002	S00002	Yes
27	CTAB	14-7395	SM, INH, RIF, EMB, PZA, RBT	<b>rrs</b> .aa 450 (RIF) <b>tpsl</b> .aa 43 (SM) <b>katG</b> .aa 315 (INH) <b>pncA</b> .aa 12 (PZA) <b>embB</b> .aa 306 (EMB/INH)		S00034	S00034	Yes
28	CTAB	14-7396	SM, INH, RIF, PZA, EMB (2 <sup>nd</sup> line only), RBT	<b>rrs</b> .aa 450 (RIF) <b>tpsl</b> .aa 43 (SM) <b>katG</b> .aa 315 (INH) <b>embB</b> .aa 306 (EMB/INH)	<b>pncA</b> .aa 151 (PZA)	S00034	S00034	Yes

# A Glimpse of the One Stop Shop in Action

Sample	# Day Pos	Qubit stock []	Clms				Whole Genome Sequencing							
			species	DST	Pyro/Sanger results	spoligotype	Depth	%Coverage	spoligotype	HC mutations	large deletions	other notable mut's	spoligo / speciation match?	DR match?
15-5031	1	1.16	<i>M. africanum?</i>	NOT DONE	NOT DONE	S01519 (700740007 774671)	173.30	97.80%	S01519 6(7)00740007774671	none	~13Kb deletion at RD12 region		YES: SNP in #3 & africanum on tree	
14-26616	0	0.378	<i>M. tuberculosis</i>	SM, INH, ETA	inhA C-15T (INH)	S00034	125.593	98.69	S00034	rpsL 88 (SM); mabA -15 (INH/ETA)	In-frame deletion iniB (INH)		YES	YES
15-6146	1	1.1	<i>M. tuberculosis</i>	SM, INH, FLQ(OFL)	katG Ser315Thr (INH), gyrA Asp94Gly (FLQ)	S00034	79.9	98.4	S00034	gyrA 94 Asp-Gly (FLQ), katG 315 (INH); rpsL 88 (SM)	None		YES	YES
14-7137	1	0.552	<i>M. tuberculosis</i>	SM, INH, RIF(MGIT only), ETA	rpoB Asp516Val (RIF), katG Ser315Leu (INH)	not done	168.6	99	S00035	katG 315 (INH); rpoB Asp-Val (RIF); rpsL 43 (SM)	None	ethA 329, ethA 403 (ETA)	YES	No for ETA



# XDR Case (November 2014)



Can we develop one assay capable of generating the same results...and more?  
Can we do it in <1 week?



# XDR Case (November 2014)

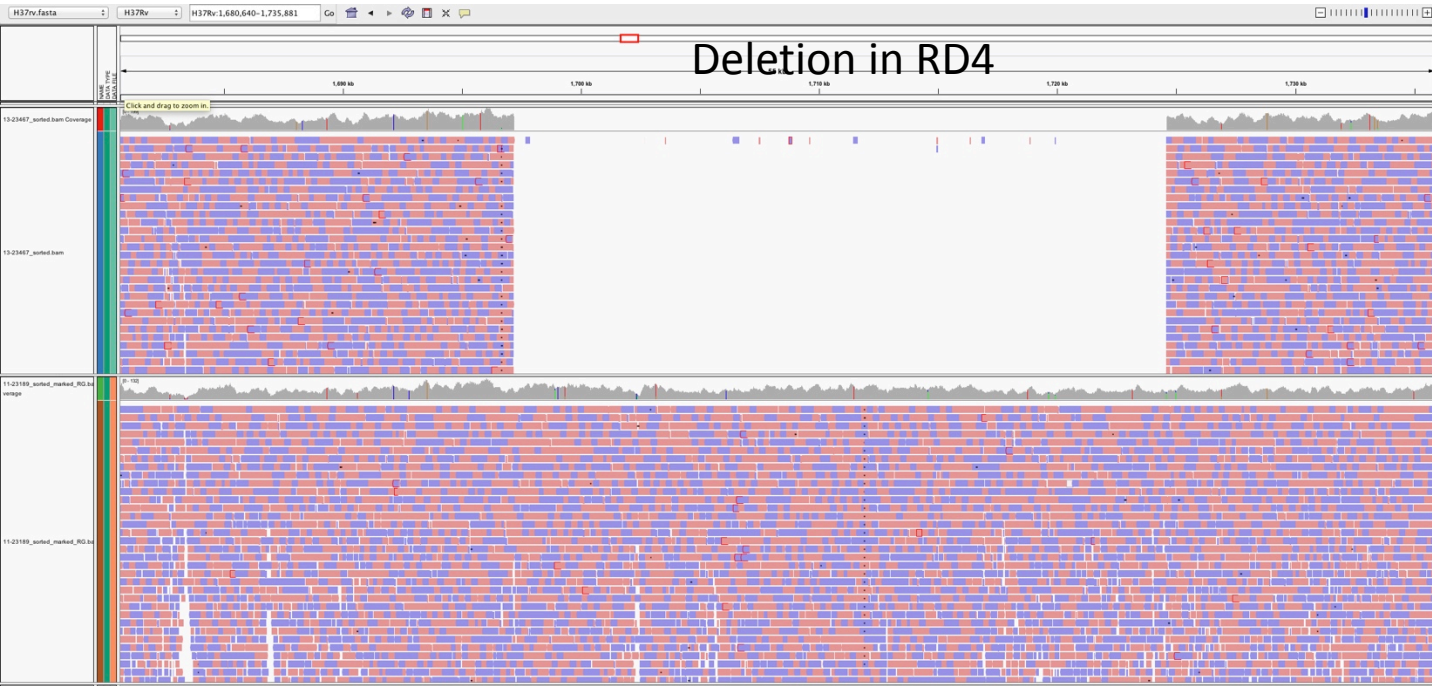
Spoligotype: S00062 (77774077760771)

Gene change	Genome position	Gene Position	SNP	Res. associated	Codon AA
<b>rrs</b> 1473246	1400	A -> G	AMI/SM		Putative
mutation*					
gyrA 7362 61		G -> C	FLQ 21	Glu/Gln	No GAG -> CAG
<b>gyrA</b> 7582 281		A -> G	<b>FLQ 94</b>	<b>Asp/Gly</b>	<b>HC mutation GAC -&gt; GGC</b>
gyrA 7585 284		G -> C	FLQ 95	Ser/Thr	No AGC -> ACC
gyrA 9304 2003		G -> A	FLQ 668	Gly/Asp	No GGC -> GAC
<b>rpoB</b> 761155	1349	C -> T	<b>RIF 450</b>	<b>Ser/Leu</b>	<b>HC mutation TCG</b>
-> TTG					
rpoC 764948	1579	T -> G	RIF 527	Leu/Val	No TTG -> GTG
rpoC 765150	1781	G -> A	RIF 594	Gly/Glu	No GGG -> GAG
tlyA 1917972	33	A -> G	AMI 11	Leu/Leu	No Silent
CTA -> CTG					
katG 2154678	1434	G -> C	INH 478	Ala/Ala	No Silent
GCG -> GCC					
<b>katG</b> 2155168	944	G -> C	<b>INH 315</b>	<b>Ser/Thr</b>	<b>HC mutation AGC</b>
-> ACC					
<b>pncA</b> 2289049	193	T -> TA	<b>PZA</b>	<b>Insertion</b>	<b>Frameshift No</b>
ahpC 2726409	217	G -> C	INH 73	Asp/His	No GAC -> CAC
embC 4242643	2781	C -> T	EMB 927	Arg/Arg	No Silent
CGC -> CGT					
embC 4242803	2941	G -> C	EMB 981	Val/Leu	No GTG -> CTG
<b>embB</b> 4247730	1217	G -> C	<b>EMB/INH 406</b>	<b>Gly/Ala</b>	<b>HC</b>
mutation GGC -> GCC					
embB 4249408	2895	G -> A	EMB/INH 965	Pro/Pro	No
Silent CCG -> CCA					
embB 4249678	3165	C -> A	EMB/INH 1055	Arg/Arg	No
Silent CGC -> CGA					
ethA 4326718	756	CCGCG ->	CGCGCG ETH	Insertion	Frameshift No
gid 4407934	269	T -> G	SM 90	Leu/Arg	No CTC -> CGC

Lineage Euro-American  
*M. tuberculosis* X1 family

Drug Resistant phenotype:  
**FLQ (OFL, LVX, MX)**  
**RIF**  
**INH**  
**SM**  
**EMB**  
**PZA**  
**RBT**  
**KAN**  
**AMI**  
**CAP (11%)**

# Evolving Pipeline



- Bedaquiline mutations detected



# Future Directions WGS TB

- Finalize validation and implement WGS for TB MGIT testing
- Refining pipeline and data interpretation
- TB Primary specimens
- LIMS importing
- NCBI
- Data Storage



**Wadsworth Center**  
NEW YORK STATE DEPARTMENT OF HEALTH

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STD, and TB Prevention



R03 NIH- Use of whole genome sequencing for  
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# Questions?

