MYCOBACTERIUM TUBERCULOSIS GENOME SEQUENCING REPORT

NOT FOR DIAGNOSTIC USE

Patient Name	JOHN DOE	Barcode	
Birth Date	2000-01-01	Patient ID	12345678910
Location	SOMEPLACE	Sample Type	SPUTUM
Sample Source	PULMONARY	Sample Date	2016-12-25
Sample ID	A12345678	Sequenced From	MGIT CULTURED ISOLATE
Reporting Lab	LAB NAME	Report Date/Time	2017-01-01, 15:36
Requested By	REQUESTER NAME	Requester Contact	REQUESTER@EMAIL.COM

Summary

The specimen was positive for **Mycobacterium tuberculosis**. It is **resistant to isoniaizd and rifampin**. It belongs to a cluster, suggesting **recent transmission**.

Organism

The specimen was positive for ***Mycobacterium tuberculosis***, lineage 2.2.1 (**East-Asian Beijing**).

Drug Susceptibility

Resistance is reported when a high-confidence resistance-conferring mutation is detected. **"No mutation detected" does not exclude the possibility of resistance**.

☐ No drug resistance predicted
☐ Mono-resistance predicted
☑ Multi-drug resistance predicted
☐ Extensive drug resistance predicted

Drug class	Interpretation	Drug	Resistance Gene (Amino Acid Mutation)
First Line	Susceptible	Ethambutol	No mutation detected
		Pyrazinimide	No mutation detected
	Resistant	Isoniazid	katG (S315T)
		Rifampin	rpoB (S531L)
Second Line	Susceptible	Streptomycin	No mutation detected
		Ciprofloxacin	No mutation detected
		Ofloxacin	No mutation detected
		Moxifloxacin	No mutation detected
		Amikacin	No mutation detected
		Kanamycin	No mutation detected
		Capreomycin	No mutation detected

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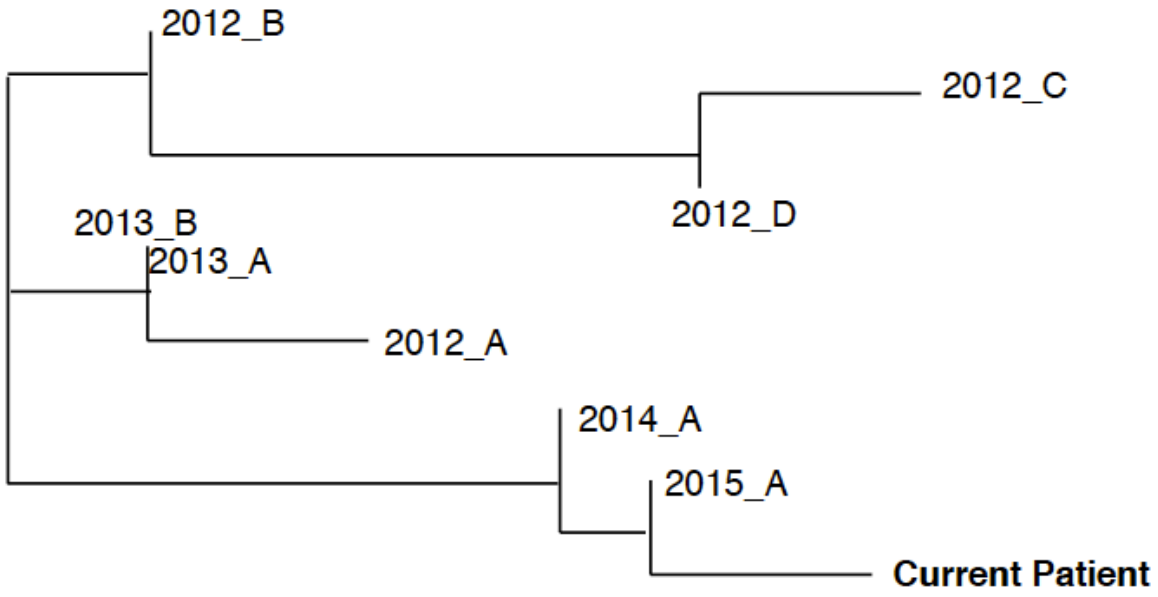
Cluster Detection

The current isolate was clustered with previously sequenced isolates, suggesting **recent transmission**.

Relatedness	Number of prior matching isolates
Closely Related (< 5 mutations apart)	**2** isolates
Related (6 to 30 mutations apart)	**6** isolates



Assay Details

Sample ID	A12345678	Barcode	
Sequencer	ILLUMINA HISEQ 2500	Method	WGS
Pipeline	RESEQTB V.3.2C	Reference	H37RV

Comments

No additional comments for this report

Standard Disclaimer: *Low frequency hetero-resistance below the limit of detection by sequencing may affect typing results. The interpretation provided is based on the current understanding of genotype-phenotype relationships.*

Authorised

Signature	Name
Position	Date