

Title: Spoligotyping results of *M.tuberculosis* strains isolated from individuals with PTB symptoms who attended HWSs and *M.tuberculosis* isolates accessed at regional public health research laboratory center, Bahir Dar, Ethiopia.

Summary Table (a): Spoligo-patterns, and *M.tuberculosis* lineages/sublineages among isolates from individuals with symptoms of PTB attending HWSs in the Amhara region, Ethiopia, 2019-2020 (n = 122).

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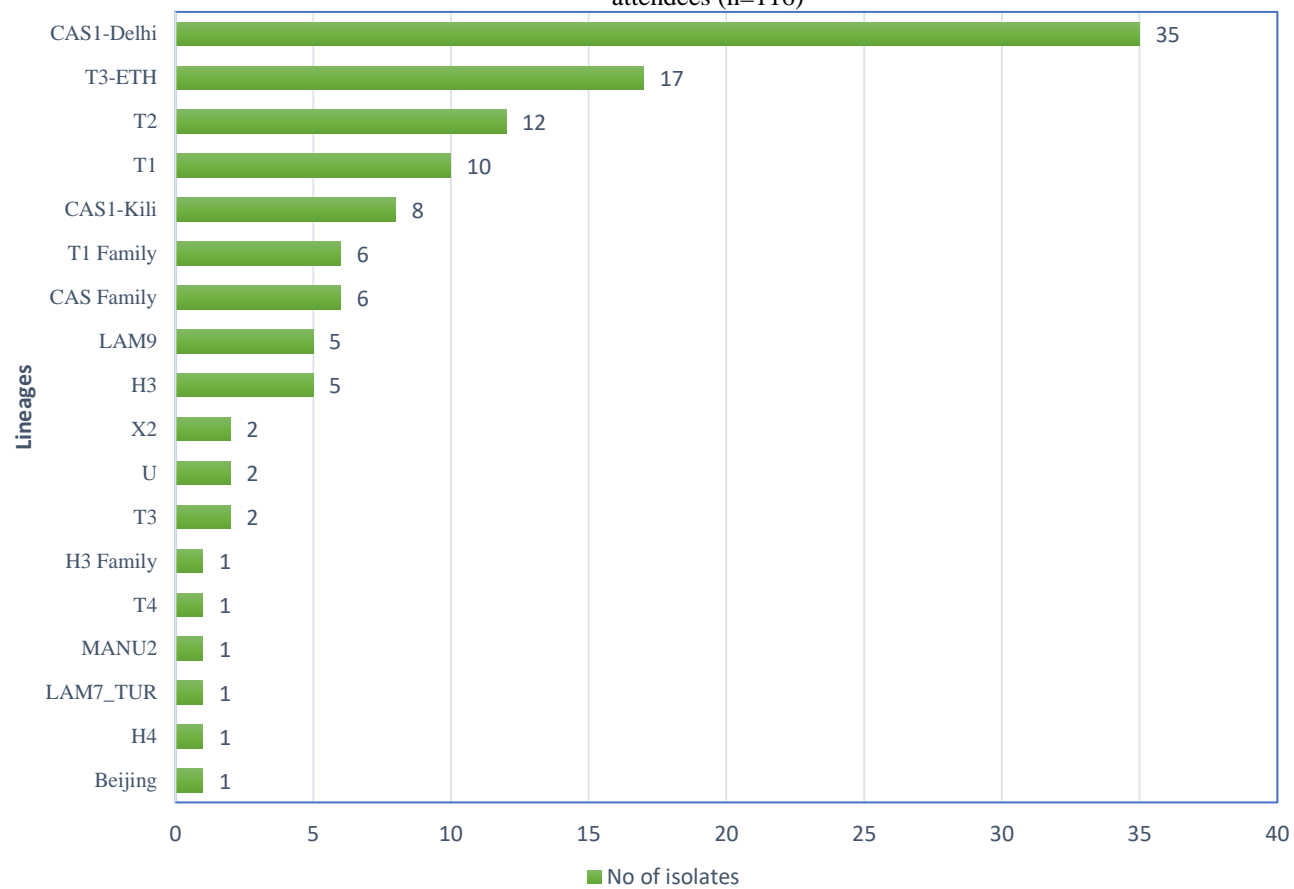
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NB: AZ: Awi zone; **CAS:** Central Asian; **CG:** Central Gondar; **EA*:** East Asian; **EA:** Euro-American; **EAI:** East African Indian; **EG:** East Gojam; **ETH:** Ethiopia; **HWS:** Holy water sites; **L:** Lineage; **LAM:** Latin-American; **MA**:** Mycobacterium africanum; **NA:** Not assigned; **NS:** North Shewa; **NW:** North Wello; **PTB:** pulmonary tuberculosis; **SG:** South Gondar; **SIT:** spoligo-international types; **SW:** South Wello; **WG:** West Gojam; **WH:** Wag-Hamra.

Summary Table (b-1): Frequency of <i>M.tuberculosis</i> spoligotypes isolated from PTB symptomatic HWS attendees (n=116)		
Lineage, families	Spoligotyping result	
	SIT No.	n (%)
East-Asian (L2)		
Beijing	1	1 (0.9)
East-African-Indian (L3)		
CAS Family	NEW	6 (5.2)
CAS1-Delhi	25	12 (10.3)
"	26	16 (13.8)
"	1198	7 (6.0)
CAS1-Kili	21	8 (6.9)
Euro-American (L4)		
H3	50	1 (0.9)
"	134	4 (3.4)
H3 Family	NEW	1 (0.9)
H4	817	1 (0.9)
LAM9	42	2 (1.7)
"	1074	2 (1.7)
"	1933	1 (0.9)
MANU2	54	1 (0.9)
T4	40	1 (0.9)
T1	53	8 (6.9)
T2	118	1 (0.9)
T1	196	1 (0.9)
T2	52	11(9.5)
T1	117	1 (0.9)
T3	37	2 (1.7)
T1 Family	NEW	6 (5.2)
T3-ETH	149	17 (14.7)
LAM7-TUR	41	1 (0.9)
X2	137	2 (1.7)
<i>M.africanum</i> (L5/6)		
U	1729	2(1.7)
<i>SIT= spoligo international types; LAM = Latin-American; CAS =Central Asian.</i>		

Figure (b-2): Frequency of *M.tuberculosis* spoligotypes isolated from PTB symptomatic HWSs attendees (n=116)



Drug resistance profiles of *M.tuberculosis* lineages/sublineage/families isolated from PTB-symptomatic HWS attendees.

Summary Table (c): INH-Resistant (mono-hetro-multi/-) *M.tuberculosis* lineage/sublineages/families (n=20).

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NB: CAS: Central Asian; EA: Euro-American; EAI: East African Indian; **INH-HR**: Isoniazid hetero-resistant; **INH-MR**: Isoniazid-mono-resistant; **INHr**: Isoniazid resistant; **L**: Lineage; **NA**: Not assigned; **SIT**: spoligo-international types.

Summary Table (f): Drug-resistance patterns, drug resistance-conferring gene mutations associated with RIF, INH, and FLQ resistance, and *M.tuberculosis* lineages/sublineages/families (n=20).

Antibiotics (# of resistant isolates)	Resistant gene	Patterns of the gene mutation (Δ WT/MUT)	Amino-Acid (codon) change	Resistance pattern	SIT No	Lineages/subfa milies (n)
RIF (15)	<i>rpoB</i>	Δ rpoBWT8/ <i>rpoB</i> MUT3	S531L	RIF-R	SIT149	T3-ETH (6)
					SIT21	CAS1-Kili (5)
					NA	CAS Family (1)
		Δ rpoBWT7/ <i>rpoB</i> MUT2A	H526Y	RIF-R	SIT149	T3-ETH (1)
		Δ rpoBWT6/-	-	RIF-R	SIT54	MANU2 (1)
INH (20)	<i>katG</i>	Δ katGWT/ <i>katG</i> MUT1	S315T1	INH-R	SIT149	T3-ETH (12)
					SIT21	CAS1-Kili (5)
					SIT25	CAS1-Delhi (1)
					SIT54	MANU2 (1)
	<i>inhA</i>	ND	ND	ND	NA	CAS Family (1)
RIF & INH (15)	<i>rpoB/katG/inhA</i>	Δ rpoBWT8/ <i>rpoB</i> MUT3 & Δ katGWT/ <i>katG</i> MUT1	S531L & S315T1	MDR	-	-
					SIT149	T3-ETH (6)
					SIT21	CAS1-Kili (5)
					NA	CAS Family (1)
		Δ rpoBWT7/- & -/ <i>katG</i> MUT1	S315T1	MDR	SIT149	T3-ETH (1)
FLQ (5)	<i>gyrA, rpoB & katG</i>	Δ gyrAWT3/ <i>gyrA</i> MUT3A, Δ rpoBWT8/ <i>rpoB</i> MUT3, Δ katGWT/ <i>katG</i> MUT1	Asp94Ala (D/A), S531L & S315T1	Pre-XDR	SIT149	T3-ETH (1)
		Δ gyrAWT3/ <i>gyrA</i> MUT3A, Δ rpoBWT8/ <i>rpoB</i> MUT3, Δ katGWT/ <i>katG</i> MUT1	H526Y & S315T1	MDR	SIT149	T3-ETH (1)
	<i>gyrB</i>	Δ rpoBWT6/- & Δ katGWT/ <i>katG</i> MUT1	S315T1	MDR	SIT54	MANU2 (1)
					SIT21	CAS1-Kili (4)
	<i>inhA</i>	ND	ND	ND	NA	CAS Family (1)
	<i>gyrB</i>	ND	ND	ND	-	-
	<i>inhA</i>	ND	ND	ND	-	-

NB: Δ deletion; **FLQ:** Fluoroquinolone; **INH-R:** Isoniazid-resistant; **MDR:** Multidrug-resistant; **MUT:** Mutant; **ND:** no mutation detected at both wild-type and mutant probe; **Pre-XDR:** Pre-Extensively drug-resistant; **RIF-R:** Rifampicin-resistant; **SIT:** spoligotype international types; **WT:** Wild-type.

