

Reinfection and mixed infection cause changing *Mycobacterium tuberculosis* drug-resistance patterns.

Annelies van Rie (PhD), Thomas C. Victor (PhD), Madalene Richardson (MSc),
Rabia Johnson (MSc), Gian D. van der Spuy (MSc), Emma J. Murray
(BSocSci(Hon)), Nulda Beyers (PhD), Nico C. Gey van Pittius (PhD), Paul D. van
Helden (PhD), Robin M. Warren (PhD).

Online Data Supplement

MATERIALS AND METHODS.

Cloning of IS6110 insertion sites.

M. tuberculosis DNA from the respective strains were digested with RsaI and the resulting chromosomal fragments were ligated into EcoRV linearized and dephosphorylated pBluescript. The ligation reaction was then subjected to PCR amplification using the forward primer GCTCAACGCCAGAGACCAGC (complementary to the IS6110 element) in combination with the T3 primer CAATTAACCCTCACTAAAGG (complementary to the pBluescript vector). Amplification products were then subjected to a second round of amplification with a nested forward primer GGA CTCACCGGGGCGGTTC together with the T3 primer. These products were fractionated in 1% agarose and visualised after staining with ethidium bromide. The respective amplification products were extracted from the agarose and ligated into pGEM-Teasy (Promega) according to the manufacturers instructions. Positive clones were subjected to DNA sequencing to determine the points of IS6110 insertion. Primers complementary to the IS6110 insertion junctions were designed from the sequence data. Each IS6110 insertion junction primer was used together with the universal forward primer in a PCR amplification assay to determine the specificity of amplification by amplification of *M. tuberculosis* DNA from a panel of isolates representative of the 30 different strain families identified in the epidemiological field site (E1). IS6110 insertion junction primers which only produced an amplification product on amplification of the strain from which they were cloned were used in the PCR assay to determine the strain population in serial sputum cultures from patients with MDR-tuberculosis.

FIGURE LEGENDS.

Figure E1. Phenotypic and genotypic characterization of sputum cultures from patients 3, 4, 5, 6, 7 and 8.

Serial *M. tuberculosis* cultures were obtained from patients diagnosed with MDR tuberculosis. Phenotypic culture-based drug susceptibility testing was performed by the direct proportion method. Treatment regimen implemented at each visit is indicated, while adherence was measured for the period between each visit. Mutations conferring resistance were detected by DNA sequencing or PCR dot-blot (E2). All sputum cultures were genotyped by IS6110 DNA fingerprinting (E3) and the strain(s) present was randomly assigned an alphabetical designation according to their strain family classification. Presence of multiple strains in each culture was determined using strain-specific PCR amplification (1). Abbreviations: S drug sensitive; R drug resistant; nd not determined; Inh (isoniazid) ; Rif (rifampin); Pza (pyrazinamide); Emb (ethambutol); Eth (ethionamide); Kana (kanamycin); Inat (isoniazid & thiacetazone); Oflox (ofloxacin); Sm (streptomycin); Teri (terizidone); thia (thiacetazone); D default (stopped therapy for a period of > 2 months); U unknown; + mutation present; - mutation absent; * internal positive PCR control (Rv3875).

REFERENCES.

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- E3. van Embden, J. D., M. D. Cave, J. T. Crawford, J. W. Dale, K. D. Eisenach, B. Gicquel, P. Hermans, C. Martin, R. McAdam, and T. M. Shinnick. 1993. Strain identification of *Mycobacterium tuberculosis* by DNA fingerprinting: recommendations for a standardized methodology. *J.Clin.Microbiol.* 31:406-409.

Figure E1a

Patient 3 (HIV neg)

Patient 4 (HIV neg)

		A	B	C	D	E	F	G	H	I	J	K	L	M	A	B	C	D	E	F	G	H
Date	Dav	U	25	20	16	29	05	09	31	29	04	15	05	14	U	14	09	20	21	28	05	08
	Month	11	05	07	08	09	10	11	01	02	04	10	02	08	11	04	06	06	07	07	01	06
	Year	94	95	95	95	95	95	95	96	96	96	96	98	98	93	94	94	94	94	94	95	95
Susceptibility -	isoniazid	nd	nd	R	R	R	R	R	S	R	R	S	R	R	R	R	S	R	R	S	R	R
	- rifampin	nd	nd	R	R	R	R	R	S	R	R	S	R	R	R	R	S	R	R	S	R	R
	- streptomycin	nd	nd	R	R	R	R	R	nd	R	R	nd	R	R	nd	nd	nd	R	nd	nd	S	R
	- ethambutol	nd	nd	S	S	S	S	S	nd	S	S	nd	S	S	nd	nd	nd	S	nd	nd	S	R
Treatment -	Rifafour (Inh, Rif, Pza, Emb)	U	X	X	X	X	X															
	- Rifater (Inh, Rif, Pza)														X							
	- Emb, Eth, Inat, Kana								X	X	X	X	X	X								
	- Emb, Eth, Inat, Kana, Teri															X						
	- Eth, Inat, Kana, Teri																X	X	X	X		
	- Emb, Eth Inat,																					X
	- Emb, Eth, Inat, Teri, Pza																					
Adherence (%)		87	79	90	90	95	99	71	79	53	49	D	U		83	80	82	100	100	68	57	
Point mutations - <i>KatG315</i>		nd	nd	+	+	+	+	+	+	+	-	+	+	nd	+	-	+	+	+	+	+	
	- <i>rpoB531</i>	nd	nd	-	nd	nd	nd	nd	nd	nd	-	-	-	nd	+	-	+	+	+	+	+	
	- <i>rpoB516</i>	nd	nd	+	+	+	+	+	+	+	-	+	+	nd	nd	-	nd	nd	nd	nd	nd	
	- <i>rpsL43</i>	nd	nd	+	+	+	+	+	+	+	-	+	+	nd	-	-	-	-	-	-	-	
	- <i>rrs513</i>	nd	nd	-	-	-	-	-	-	-	-	-	-	nd	-	nd	nd	+	+	+	+	
- <i>emb306</i>	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	-	-	-	nd	+	-	+	+	+	+	+	
Strain designation		b	b	b	b	b	b	b	b	b	e	b	b		d	f	d	d	d	d	d	
IS6110 DNA fingerprinting																						
	PCR (strain b)														PCR (strain d)							
	Strain-specific PCR														Strain-specific PCR							

Figure E1b

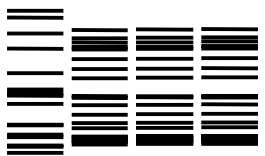
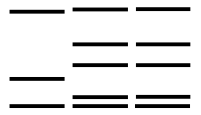
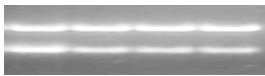
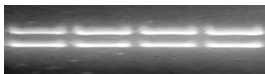
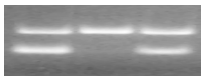
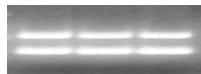
		Patient 5 (HIV nd)				Patient 6 (HIV nd)		
		A	B	C	D	A	B	C
Date	Day	03	26	05	05	17	23	10
	Month	06	11	01	01	06	09	10
	Year	93	93	95	95	93	93	93
Susceptibility	- isoniazid	S	nd	R	R	R	R	R
	- rifampin	S	nd	R	R	R	R	R
	- streptomycin	S	nd	R	R	nd	R	R
	- ethambutol	S	nd	R	R	nd	nd	nd
Treatment	- Rifater (Inh, Rif, Pza)	X				X	X	X
	- Emb, Eth, Kana, Inat, Oflox, Sm, Teri, Pza		X	X	X			
Adherence (%)			U	78	78		97	U
Point mutations	- <i>KatG315</i>	-	+	+	+	-	+	+
	- <i>rpoB531</i>	-	+	+	+	-	+	+
	- <i>rpsL43</i>	-	-	-	-	-	+	+
	- <i>rrs513</i>	-	+	+	+	-	-	-
	- <i>emb306</i>	-	+	+	+	-	-	-
Strain designation		g	d	d	d	h	b	b
IS6110 DNA fingerprinting								
Strain-specific PCR		<p>PCR (strain g)</p>  <p>PCR (strain d)</p> 				<p>PCR (strain h)</p>  <p>PCR (strain b)</p> 		

Figure E1c

