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Correction to: Molecular characterization of multidrug-resistant *Mycobacterium tuberculosis* (MDR-TB) isolates identifies local transmission of infection in Kuwait, a country with a low incidence of TB and MDR-TB

Noura M. Al-Mutairi, Suhail Ahmad^{*} and Eiman M. Mokaddas

Correction to: Eur J Med Res (2019) 24:38

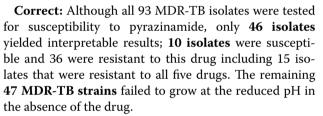
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The original publication of this article [1] contained few erroneous paragraphs and errors in Table 1 and Table 2. The first four paragraphs are in the 'Results' section while the last four paragraphs are in the 'Discussion' section. The errors in Table 1 involve the number of isolates tested for pyrazinamide and pyrazinamide susceptible isolates, ethambutol-susceptible isolates with a mutation and number of resistant isolates with a mutation for streptomycin. The error in Table 2 involves wrong codon number for a mutation in isolate KM17-01 in Cluster XII for *gidB* gene. The updated informations have been indicated in **bold** and also refer corrected Tables 1 and 2.

Incorrect: Although all 93 MDR-TB isolates were tested for susceptibility to pyrazinamide, only 47 isolates yielded interpretable results; 11 isolates were susceptible and 36 were resistant to this drug including 15 isolates that were resistant to all five drugs. The remaining 46 MDR-TB strains failed to grow at the reduced pH in the absence of the drug.

The original article can be found online at https://doi.org/10.1186/s4000 1-019-0397-2.

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Incorrect: The proportion of MDR-TB isolates exhibiting resistance conferring mutations in target genes varied for different anti-TB drugs, being highest for rifampicin and lowest for streptomycin (Table 1).

Correct: The proportion of MDR-TB isolates exhibiting resistance conferring mutations in target genes varied for different anti-TB drugs, being highest for rifampicin and lowest for streptomycin **among SIRE drugs** (Table 1).

Incorrect: PCR-sequencing of *pncA* identified mutations in 30 of 36 MDR-TB strains phenotypically resistant to pyrazinamide and 23 of 46 isolates for which phenotypic DST data for pyrazinamide was not available while all 11 isolates phenotypically susceptible to pyrazinamide contained wild-type sequence for *pncA*.

Correct: PCR-sequencing of *pncA* identified mutations in 30 of 36 MDR-TB strains phenotypically resistant to pyrazinamide and 23 of **47** isolates for which phenotypic DST data for pyrazinamide was not available while all **10** isolates phenotypically susceptible to pyrazinamide contained wild-type sequence for *pncA*.



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Table 1 Phenotypic resistance by MGIT 960 system to anti-TB drugs among 93 multidrug-resistant *M. tuberculosis* isolates and number of susceptible and resistant isolates with mutations in target genes for each drug

Anti-tuberculosis drug	No. of isolates tested	No. of susceptible isolates	No. of susceptible isolates with mutation ^a	No. of resistant isolates	No. (%) of resistant isolates with mutation ^a
Rifampicin	93	0	0	93	93 (100)
Isoniazid	93	0	0	93	92 (98.9)
Pyrazinamide	46	10	0	36	30 (83.3)
Ethambutol	93	52	39 ^b	41	38 (92.7)
Streptomycin	93	34	0	59	51 (86.4)

^a Resistance conferring mutations were detected in *rpoB* for rifampicin, *katG*+*inhA* for isoniazid, *pncA* for pyrazinamide, *embB* for ethambutol, and *rpsL*+rrs for streptomycin

Incorrect: Fifty isolates contained mutations at *embB306* (M306V, n=28; M306I, n=19 and M306L, n=3), 15 isolates contained a mutated *embB406* (G406D, n=8; G406A, n=4; G406C, n=2 and G406S, n=1), 10 isolates contained a mutated *embB497* (Q497R, n=6; Q497K, n=3 and Q497H, n=1) and one isolate contained a mutation (Y319S) at *embB319*.

Correct: Fifty isolates contained mutations at *embB306* (M306V, n=28; M306I, n=19 and M306L, n=3), **16** isolates contained a mutated *embB406* (G406D, n=8; G406A, n=5; G406C, n=2 and G406S, n=1), 10 isolates contained a mutated *embB497* (Q497R, n=6; Q497K, n=3 and Q497H, n=1) and one isolate contained a mutation (Y319S) at *embB319*.

Incorrect: Forty-nine of 59 MDR-TB strains additionally resistant to streptomycin contained a mutation in the target genes analysed (Table 1), many of which have been described previously [23, 28]. These included 44 isolates with a mutation in rpsL (K43R, n=33; K43T, n=1; K88R, n=5; K88T, n=4; K88M, n=1), four isolates with a mutation in rrs 500 or 900 region (A514C, n=1; C517T, n=1; G878A, n=1 and A906G, n=1) and one isolate with rpsL K88R+rrs C602A double mutation.

Correct: Fifty-one of 59 MDR-TB strains additionally resistant to streptomycin contained a mutation in the target genes analysed (Table 1), many of which have been described previously [23, 28]. These included 44 isolates with a mutation in rpsL (K43R, n=33; K43T, n=1; K88R, n=5; K88T, n=4; K88M, n=1), four isolates with a mutation in rrs 500 or 900 region (A514C, n=1; C517T, n=1; G878A, n=1 and A906G, n=1) and **three isolates with double mutation in** rpsL and rrs genes (rpsL K43R+rrs C527T, n=1; rpsL K88T+rrs C517T, n=1; rpsL K88R+rrs C602A, n=1).

Incorrect: Resistance conferring mutations in *rpsL* and/or *rrs* gene were detected in majority (49 of 59, 83%) of streptomycin-resistant but not in any streptomycin-susceptible MDR-TB strain while mutations in *embB*

gene were detected in both ethambutol-resistant and -susceptible MDR-TB strains, as described in our previous studies [23, 28].

Correct: Resistance conferring mutations in *rpsL* and/ or *rrs* gene were detected in majority (**51 of 59, 86.4%**) of streptomycin-resistant but not in any streptomycin-susceptible MDR-TB strain while mutations in *embB* gene were detected in both ethambutol-resistant and -susceptible MDR-TB strains, as described in our previous studies [23, 28].

Incorrect: Phenotypic DST results for pyrazinamide were available for only 47 of 93 MDR-TB strains while the remaining 46 isolates failed to grow at lower pH. No *pncA* mutation was detected in 50 pansusceptible strains. Analysis of 93 MDR-TB strains showed that 30 of 36 MDR-TB strains phenotypically resistant to pyrazinamide and 23 of 46 isolates for which DST data for pyrazinamide was not available contained a mutation in *pncA* while all 11 MDR-TB strains phenotypically susceptible to pyrazinamide contained wild-type sequence for *pncA*.

Correct: Phenotypic DST results for pyrazinamide were available for only **46** of 93 MDR-TB strains while the remaining **47** isolates failed to grow at lower pH. No *pncA* mutation was detected in 50 pansusceptible strains. Analysis of 93 MDR-TB strains showed that 30 of 36 MDR-TB strains phenotypically resistant to pyrazinamide and 23 of **47** isolates for which DST data for pyrazinamide was not available contained a mutation in *pncA* while all **10** MDR-TB strains phenotypically susceptible to pyrazinamide contained wild-type sequence for *pncA*.

Incorrect: The two isolates in Cluster XII were also very closely related, with the second isolate (KM17-01) displaying an additional mutation (L95F) in *gidB* which is considered as a hot-spot for mutations in the *M. tuberculosis* genome [21, 57].

Correct: The two isolates in Cluster XII were also very closely related, with the second isolate (KM17-01) (Table 2) displaying an additional mutation (**L59F**) in

b M. tuberculosis isolates with embB mutations usually confer low level of resistance to ethambutol which are often missed by the MGIT 960 system [23, 28]

Table 2 Detailed clinical, demographic and molecular characteristics of 42 M. tuberculosis isolates in 16 (Cluster I to Cluster XVI) clusters

Chiefer	Chister no Clinica	Isolate no Year	Year	Patient's	Spoligotyping data	ing data	Genetic alterat	Genetic alteration detected in							
	specimen	201816	of isolation	nationality	d spoking do	1	ספוופור מונפוס	III detected III							
					SIT	Mtb family	rpoB	katG ii	inhA	pncA	етрВ	rpsL	rrs	gidB	rpsA
_	Sputum	KM06-153	2006	Indian	255	Beijing	TCG456TTG	ACG315ACC V	WT	WT	ATG306GTG	AAG43AGG		N. D.	N. D.
	CSF	KM09-22	2009	Indian	255	Beijing	TCG456TTG	ACG315ACC V	TW	WT	ATG306GTG	AAG43AGG	\vdash	N. D.	N. D.
	Sputum	KM13-37	2013	Indian	-	Beijing	TCG456TTG	ACG315ACC V	TW	WT	ATG306GTG	AAG43AGG	\perp	N.D.	N. D.
	FNA	KM16-06	2016	Nepalese	_	Beijing	TCG456TTG	ACG315ACC V	TW	WT	ATG306GTG	AAG43AGG	\perp	N. D.	N. D.
	FNA	KM17-03	2017	Indian	_	Beijing	TCG456TTG	ACG315ACC V	ΤW	WT	ATG306GTG	AAG43AGG	_ M	N.D.	N. D.
=	Sputum	KM14-58	2014	Nepalese	-	Beijing	TCG456TTG	ACG315ACC V	TW	GTG139GCG	ATG306GTG	AAG43AGG	$\stackrel{>}{\sim}$	GAA- 92GAC + GCA205GCG	CGA212CGC
	Sputum	KM14-69	2014	Indian	_	Beijing	TCG456TTG	ACG315ACC V	ΤW	GTG139GCG	ATG306GTG	AAG43AGG	TW.	GCA205GCG	WT
≡	Sputum	KM08-501	2008	Kuwaiti	⊢ I	Beijing	TCG456TTG	ACG315ACC V	TW	GGT139GTT	ATG306GTG	AAG43AGG		<u>GAA-</u> <u>92GAC + GCA205GCG</u>	CGA212CGC
	Sputum	KM08-502	2008	Kuwaiti	⊢ I	Beijing	TCG456TTG	ACG315ACC V	TM	GGT139GTT	ATG306GTG	AAG43AGG		<u>GAA-</u> 92GAC + G <i>CA205GCG</i>	CGA212CGC
	Sputum	KM09-207	<u>2009</u>	Indian	⊢ I	Beijing	TCG456TTG	ACG315ACC V	T _W	GGT139GTT	ATG306GTG	AAG43AGG	\bowtie	<u>GAA-</u> 92GAC + GCA205GCG	CGA212CGC
≥	Sputum	KM12-05	2012	Ethiopian	21	CAS1-Kili	TCG456TTG	ACG315ACC V	L/M	Ins193A (FS) + 7CC65TCT	ATG306GTG	AAG88AGG	\bowtie	N.D.	N. D.
	Sputum	KM12-17	2012	Ethiopian	1144	F	TCG456TTG	ACG315ACC V	TW	Ins193A (FS) + 7CC65TCT	ATG306GTG	AAG88AGG	\vdash	N.D.	N. D.
	Sputum	KM15-08	2015	Ethiopian	21	CAS1-Kili	TCG456TTG	ACG315ACC V	TW	Ins193A (FS) + TCC65TCT	ATG306GTG	AAG88AGG	\succeq	N. D.	Ö ;
>	Sputum	KM07-333	2007	Indonesian	Orphan	Ä.	TCG456TTG	ACG315ACC V	TW	WT	WT	WT	\perp	N.D.	N. D.
	Sputum	KM10-23	2010	Indian	355	EAI3-IND	TCG456TTG	ACG315ACC V	TW	WT	WT	WT	_ M	N.D.	N. D.
>	Sputum	KM07-293	2007	Filipino	194	LAM2	TCG456TTG	ACG315ACC V	ΜT	WT	CAG497CGG	WT	\vdash	N. D.	N. D.
	Sputum	KM12-01	2012	Filipino	25	CAS1-Delhi	TCG456TTG	ACG315ACC V	ΜT	WT	CAG497CGG	TW		N. D.	N. D.
₹	Sputum	KM09-202	2009	Ethiopian	47	Ξ	GTC176TTC	ACG315ACC V	ΜT	WT	WT	TW		N. D.	N. D.
	Sputum	KM15-17	2015	Indian	47	Ξ	GTC176TTC	ACG315ACC V	WT	WT	WT	WT	_ ∖	N.D.	N. D.
\parallel	Sputum	KM14-67	2014	Ethiopian	149	T3-ETH	TCG456TTG	ACG315ACC V	TW.	<u> – 11 A/G</u>	ATG306ATC	WI	M	GGT69GAT	<u>IM</u>
	Sputum	KM15-21	2015	Ethiopian	149	T3-ETH	TCG456TTG	ACG315ACC V	MT	<u> </u>	ATG306ATC	WT	×	GGT69GAT	<u>IM</u>
×	Sputum	KM07-283	2007	Indian	26	CAS1-Delhi	TCG456TTG	ACG315ACC V	MT	TCC65TCT	ATG306ATA	WT	\vdash	N.D.	N. D.
	Sputum	KM14-68	2014	Indian	Orphan	Ä.	TCG456TTG	ACG315ACC V	TW	TCC65TCT	ATG306ATA	WT	\perp	N.D.	N. D.
	Sputum	KM17-20	2017	Kuwaiti	-	Beijing	TCG456TTG	ACG315ACC V	MT	— 11 A/G	CAG497CGG	AAG43AGG	\mathbb{A}	GAA- 92GAC + G <i>CA205GCG</i>	Μ
×	Sputum	KM17-22	2017	Kuwaiti	-	Beijing	TCG456TTG	ACG315ACC V	TW	- 11 A/G	CAG497CGG	AAG43AGG	M M	GAA- 92GAC + <i>GCA205GCG</i>	CGA212CGC
	Sputum	KM17-73	2017	Indian	-	Beijing	TCG456TTG	ACG315ACC V	TW	— 11 A/G	CAG497CGG	AAG43AGG	\mathbb{M}	GAA- 92GAC + <i>GCA205GCG</i>	CGA212CGC
	Pus	KM11-503	2011	Kuwaiti	⊢ I	Beijing	TCG456TTG	ACG315ACC V	TW.	11 A/G	GGC406GAC	AAG43AGG	TW.	GAA- 92GAC + GCA205GCG	CGA212CGC
	Sputum	KM14-56	2014	Kuwaiti	← I	Beijing	TCG456TTG	ACG315ACC V	MT	11 A/G	GGC406GAC	AAG43AGG	\mathbb{A}	<u>GAA-</u> 92GAC + GCA205GCG	CGA212CGC

Table 2 (continued)

Cluster no. Clinica	. Clinica	Isolate no. Year	Year	Patient's	Spoligotyping data	ng data	Genetic alteration detected in	on detected in						
	decillien		O ISOIAUOI	nationality	SIT	Mtb family	rpoB	katG	inhA	pncA	етьв	rpsL	rrs gidB	rpsA
\bowtie	Sputum	<u>KM15-13</u>	2015	Kuwaiti	⊢ I	Beijing	TCG456TTG	ACG315ACC	T/M	<u> </u>	GGC406GAC	AAG43AGG	WT GAA- 92GAC+GCA205GCG	CGA212CGC
	Sputum	KM15-26	2015	Kuwaiti	← I	Beijing	TCG456TTG	ACG315ACC	WI	— 11 A/G	GGC406GAC	AAG43AGG	WI GAA- 92GAC+GCA205GCG	CGA212CGC
	Sputum	KM17-02	2015	Kuwaiti	⊢ I	Beijing	TCG456TTG	ACG315ACC	WI	11 A/G	GGC406GAC	AAG43AGG	WI GAA- 92GAC+GCA205GCG	CGA212CGC
	Sputum	KM17-69	2017	Kuwaiti	⊢	Beijing	TCG456TTG	ACG315ACC	TWT	11 A/G	GGC406GAC	AAG43AGG	WI GAA- 92GAC+GCA205GCG	CGA212CGC
≅	Sputum	KM16-32	2016	Egyptian	19	EAI2-Manila CAC451TAC	CAC451TAC	ACG315ACC	- 15 CT	GAA37AAA	CTG355CTA+ GAG378GCG	TW	WT GTG- 110GTT+GCA205GCG	WT
	Sputum	KM17-01	2017	Filipino	19	EAI2-Manila CAC451TAC	CAC451TAC	ACG315ACC	- 15 C/T	GAA37AAA	<i>CTG355CTA</i> + GAG- WT 378GCG	WT	WT CTCS9TTC + GTG- 110GTT+ GCA205GCG	WT
₹	Pus	KM07-297	2007	Indian	Orphan	∢ Ż	CAC451GAC	WT	- 15 C/T	<i>TCC65TCG</i> + Ins 453T (FS)	ATG306CTG	TW	WT N.D.	N. D.
	FNA	KM11-502	2015	Indian	3361	Ι	CAC451GAC	WT	- 15 CA	TCC65TCG+Ins 453T (FS)	ATG306CTG	TW	WT N.D.	N. D.
≥ ×	Sputum	KM06-48	2006	Egyptian	53	F	TCG456TTG	WT	- 15 C/T	WT	WT	TW	WT N.D.	N. D.
	Tissue	KM06-277	2006	Filipino	19	EAI2-Manila TCG456TTG	TCG456TTG	WT	- 15 CT	WT	WT	TW	WT N.D.	N. D.
\geqslant	Sputum	KM16-33	2016	<u>Indian</u>	∞I	EAI3/EAI5	CAC451TAC	ACG315ACC	M	CTG35CCG	<u>ATG306GTG + GAG-</u> AAG43AG <u>G</u> <u>378GCG</u>	AAG43AGG	WI GTG- 110GTT+GCA205GCG	WI
	Sputum	KM17-06	2017	Filipino	∞I	EAI3/EAI5	CAC451TAC	ACG315ACC	TM	CTG35CCG	ATG306GTG+ G78GCG	AAG43AGG	WI <u>GTG-</u> 110GTT+GCA205GCG	TW.
፟፟፠፟	Sputum	KM07-231	2007	<u>Indian</u>	<u>Orphanª</u>	CAS1-Delhi	ATG440ATA ± GAC441TAC	ACG315ACC	TW.	ICC65TCT	GGC406TGC	WI	WI GCA205GCG+Del 350G. (ES)	TW.
	Sputum	KM07-252	2007	Syrian	<u>Orphan</u> ª	CAS1-Delhi	ATG440ATA ± GAC441TAC	ACG315ACC	IW.	ICC65TCT	<u>GGC406TGC</u>	M	WI GCA205GCG + Del 350G. (FS)	TW.

N. A., not applicable; N. D., not done; CSF, cerebrospinal fluid; FNA, fine needle aspirate; SIT, shared international type; Mtb family, M. tuberculosis family; WT, wild-type sequence; Ins, insertion mutation; (FS), frame shift mutation, fine needle aspirate Clusters containing MDR-TB strains with identical patterns and isolated within a period of nearly 2 years are shown as underlined. Synonymous mutations are italicized

^a Both isolates displayed identical spoligotyping pattern

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gidB which is considered as a hot-spot for mutations in the *M. tuberculosis* genome [21, 57].

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Reference

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