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

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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.

**Correct:** Although all 93 MDR-TB isolates were tested for susceptibility to pyrazinamide, only **46 isolates** yielded interpretable results; **10 isolates** were susceptible and 36 were resistant to this drug including 15 isolates that were resistant to all five drugs. The remaining **47 MDR-TB strains** failed to grow at the reduced pH in the absence of the drug.

**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*.
### 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 | No. of resistant isolates | No. (%) of resistant isolates with mutation |
|------------------------|------------------------|-----------------------------|------------------------------------------|--------------------------|------------------------------------------|
| 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                                      | 41                       | 38 (92.7)                                |
| Streptomycin           | 93                     | 34                          | 0                                        | 59                       | 51 (86.4)                                |
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| Streptomycin           | 93                     | 34                          | 0                                        | 59                       | 51 (86.4)                                |

| Anti-tuberculosis drug | No. of isolates tested | No. of susceptible isolates | No. of susceptible isolates with mutation | No. of resistant isolates | No. (%) of resistant isolates with mutation |
|------------------------|------------------------|-----------------------------|------------------------------------------|--------------------------|------------------------------------------|
| 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                                      | 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 addition ally 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].
Table 2 Detailed clinical, demographic and molecular characteristics of 42 *M. tuberculosis* isolates in 16 (Cluster I to Cluster XVI) clusters

| Cluster no. | Clinical specimen | Isolate no. | Year of isolation | Patient's nationality | Spoligotyping data | Genetic alteration detected in SIT Mtb family |
|-------------|------------------|-------------|-------------------|----------------------|-------------------|---------------------------------------------|
| I Sputum    | KM06-153         | 2006        | Indian            | 255 Beijing          | TCG456TTG         | ACG315ACC WT                                      |
|            | KM09-22          | 2009        | Indian            | 255 Beijing          | TCG456TTG         | ACG315ACC WT                                      |
|            | KM13-37          | 2013        | Indian            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
|            | KM16-06          | 2016        | Nepalese          | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
|            | KM17-03          | 2017        | Indian            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
| II Sputum   | KM14-58          | 2014        | Nepalese          | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
|            | KM14-69          | 2014        | Indian            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
| III Sputum  | KM08-501         | 2008        | Kuwait            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
|            | KM08-502         | 2008        | Kuwait            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
|            | KM09-207         | 2009        | Indian            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
| IV Sputum   | KM12-05          | 2012        | Ethiopian         | 21 CAS1-Kili         | TCG456TTG         | ACG315ACC WT                                      |
|            | KM12-17          | 2012        | Ethiopian         | 1144 T1              | TCG456TTG         | ACG315ACC WT                                      |
|            | KM15-08          | 2015        | Ethiopian         | 21 CAS1-Kili         | TCG456TTG         | ACG315ACC WT                                      |
| V Sputum    | KM07-333         | 2007        | Indonesian        | Orphan N. A.         | TCG456TTG         | ACG315ACC WT                                      |
|            | KM10-23          | 2010        | Filipino          | 355 EA3-INID         | TCG456TTG         | ACG315ACC WT                                      |
|            | KM07-293         | 2007        | Filipino          | 194 LAM2             | TCG456TTG         | ACG315ACC WT                                      |
|            | KM12-01          | 2012        | Filipino          | 25 CAS1-Delhi        | TCG456TTG         | ACG315ACC WT                                      |
| VI Sputum   | KM09-202         | 2009        | Ethiopian         | 47 H1                | TCG456TTG         | ACG315ACC WT                                      |
|            | KM15-17          | 2015        | Indian            | 47 H1                | TCG456TTG         | ACG315ACC WT                                      |
| VII Sputum  | KM14-67          | 2014        | Bhutanese         | 149 T3-ETH           | TCG456TTG         | ACG315ACC WT                                      |
|            | KM15-23          | 2015        | Bhutanese         | 149 T3-ETH           | TCG456TTG         | ACG315ACC WT                                      |
| VIII Sputum | KM07-283         | 2007        | Filipino          | 26 CAS1-Delhi        | TCG456TTG         | ACG315ACC WT                                      |
|            | KM14-68          | 2014        | Indian            | Orphan N. A.         | TCG456TTG         | ACG315ACC WT                                      |
|            | KM17-20          | 2017        | Kuwait            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
| IX Sputum   | KM17-22          | 2017        | Kuwait            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
|            | KM17-73          | 2017        | Indian            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
|            | KM11-503         | 2011        | Kuwait            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
| X Sputum    | KM14-56          | 2014        | Kuwait            | 1 Beijing            | TCG456TTG         | ACG315ACC WT                                      |
| Cluster no. | Clinica specimen | Isolate no. | Year of isolation | Patient's nationality | Spoligotyping data | Genetic alteration detected in |
|-------------|-----------------|-------------|-------------------|----------------------|-------------------|------------------------------|
| XI | Sputum KM15-33 | 2015 | Kuwaiti | Beijing | TCG346TTG ACG315ACC WT | -11 A/G GCC406GAC AAG434AC WT GAA395AC + GGA205CG CGA212GC |
| | Sputum KM15-26 | 2015 | Kuwaiti | Beijing | TCG346TTG ACG315ACC WT | -11 A/G GCC406GAC AAG434AC WT GAA395AC + GGA205CG CGA212GC |
| | Sputum KM17-02 | 2015 | Kuwaiti | Beijing | TCG346TTG ACG315ACC WT | -11 A/G GCC406GAC AAG434AC WT GAA395AC + GGA205CG CGA212GC |
| | Sputum KM17-69 | 2017 | Kuwaiti | Beijing | TCG346TTG ACG315ACC WT | -11 A/G GCC406GAC AAG434AC WT GAA395AC + GGA205CG CGA212GC |
| XII | Sputum KM16-32 | 2016 | Egyptian | 19 | EAI2-Manila CAC451TAC ACG315ACC WT -15 C/T GAA37AAA CTC355CTA + GAG378GCC WT WT GGC100GCG CTG100GCG CGA212GC |
| | Sputum KM17-01 | 2017 | Filipino | 19 | EAI2-Manila CAC451TAC ACG315ACC WT -15 C/T GAA37AAA CTC355CTA + GAG378GCC WT WT GGC100GCG CTG100GCG CGA212GC |
| XIII | Pus KM07-297 | 2007 | Indian | Orphan | CAC451GAC WT | -15 C/T TCC355CTA + Ins 45 ST (FS) ARG306CTG WT WT N.D. N.D. |
| | FNA KM11-502 | 2015 | Indian | 3361 | T1 CAC451GAC WT | -15 C/T TCC355CTA + Ins 45 ST (FS) ARG306CTG WT WT N.D. N.D. |
| XIV | Sputum KM06-48 | 2006 | Egyptian | 53 | T1 TCG346TTG WT | -15 C/T WT WT WT WT N.D. N.D. |
| | Tissue KM06-277 | 2006 | Filipino | 19 | EAI2-Manila TCG346TTG WT | -15 C/T WT WT WT WT N.D. N.D. |
| XV | Sputum KM16-33 | 2016 | Indian | 8 | EAI3/EAI5 CAC451TAC ACG315ACC WT CTG355CCG ATG306GTG + GAG378GCC WT WT GGC100GCG CTG100GCG CGA212GC |
| | Sputum KM17-06 | 2017 | Filipino | 8 | EAI3/EAI5 CAC451TAC ACG315ACC WT CTG355CCG ATG306GTG + GAG378GCC WT WT GGC100GCG CTG100GCG CGA212GC |
| XVI | Sputum KM07-231 | 2007 | Indian | Orphan | CAS1-Delhi ATG440ATA + GAC441TAC | -15 C/T TCC355CTA GCC406GCC WT WT GCC100GCC + Del 350G WT |
| | Sputum KM07-252 | 2007 | Syrian | Orphan | CAS1-Delhi ATG440ATA + GAC441TAC | -15 C/T TCC355CTA GCC406GCC WT WT GCC100GCC + Del 350G WT |

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.

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

* Both isolates displayed identical spoligotyping pattern
gidB which is considered as a hot-spot for mutations in the *M. tuberculosis* genome [21, 57].

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Reference
1. Al-Mutairi NM, Ahmad S, Mokaddas EM. 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. Eur J Med Res. 2019;24:38. https://doi.org/10.1186/s40001-019-0397-2.

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