First Evaluation of Drug-Resistant *Mycobacterium tuberculosis* Clinical Isolates from Congo Revealed Misdetection of Fluoroquinolone Resistance by Line Probe Assay Due to a Double Substitution T80A-A90G in GyrA

Alexandra Aubry¹,²,³, Wladimir Sougakoff¹,²,³, Pamela Bodzongo⁴, Guy Delcroix⁵, Sylvie Armand⁵, Gérald Millot³, Vincent Jarlier¹,²,³, René Courcol⁵,⁶,⁷,⁸, Nadine Lemaitre⁵,⁶,⁷,⁸.*

¹ UPMC Université, Paris, France, ² INSERM U1135, Paris, France, ³ Centre National de Référence des Mycobactéries et de la Résistance des Mycobactéries aux Antituberculeux, Paris, France, ⁴ Faculté des Sciences de la Santé, Brazzaville, Congo, ⁵ Laboratoire de Bactériologie-Hygiène du CHRU, Lille, France, ⁶ Université Lille Nord de France, Lille, France, ⁷ UDSL, F-59000 Lille, France, ⁸ INSERM U1019-UMR8204, Lille, France

**Abstract**

**Background:** Tuberculosis (TB) is one of the major public health problems in Congo. However, data concerning *Mycobacterium tuberculosis* drug resistance are lacking because of the insufficient processing capacity. So, the aim of this study was to investigate for the first time the resistance patterns and the strain lineages of a sample of *M. tuberculosis* complex (MTBC) isolates collected in the two main cities of Congo.

**Methods:** Over a 9-day period, 114 smear-positive sputa isolated from 114 patients attending centers for the diagnosis and treatment of TB in Brazzaville and Pointe Noire were collected for culture and drug susceptibility testing (DST). Detection of mutations conferring drug resistance was performed by using line probe assays (GenoType MTBDRplus and MTBDRsl) and DNA sequencing. Strain lineages were determined by MIRU-VNTR genotyping.

**Results:** Of the 114 sputa, 46 were culture positive for MTBC. Twenty-one (46%) were resistant to one or more first-line antiTB drugs. Of these, 15 (71%) were multidrug resistant (MDR). The most prevalent mutations involved in rifampin and isoniazid resistance, D516V (60%) in rpoB and S315T (87%) in katG respectively, were well detected by MTBDRplus assay. All the 15 MDR strains were susceptible to fluoroquinolone and injectable second-line drug. No mutation was detected in the *rrs* locus involved in resistance to amikacin and capreomycin by both the MTBDRsl assay and DNA sequencing. By contrast, 9 MDR strains belonging to the same cluster related to T-family were identified as being falsely resistant to fluoroquinolone by the MTBDRsl assay due to the presence of a double substitution T80A-A90G in GyrA.

**Conclusions:** Taken together, these data revealed a possible spread of a particular MDR clone in Congo, misidentified as fluoroquinolone resistant by MTBDRsl assay. Thus, this test cannot replace gold-standard culture method and should be interpreted carefully in view of the patient’s native land.

---

Introduction

Tuberculosis (TB) remains an important cause of morbidity and mortality in 2012 with 8.6 million cases and 1.3 million deaths worldwide [1]. Sub-Saharan Africa is particularly affected with approximately 1.3 million new cases. Congo is a West Africa country with a population of ~4 million people. As in many sub Saharan Africa countries, TB is a major health problem in Congo despite the implementation of the Directly Observed Therapy Short course (DOTS) strategy in the mid-1990. The World Health Organization estimated the incidence of all forms of TB in Congo at 381/100,000 and mortality at 42/100,000 in 2012 [1]. Among the new TB cases, the rate of HIV patients reaches 33%. Thus, Congo is considered a “high burden” country for TB and HIV infection. The Global Plan to STOP TB (2006–2015) recommends knowing early the drug susceptibility status, especially in case of retreatment. During the past few years, several molecular techniques including reverse hybridization assay with DNA probes have been developed to quickly predict drug resistance in clinical
isolates of *Mycobacterium tuberculosis* complex (MTBC) and thereby to facilitate appropriate patient management. GenoType MTBDR*plus* demonstrated a good concordance with phenotypic drug susceptibility testing and has been approved by the WHO for rapid screening of patients at risk of MDR-TB. Unfortunately, routine drug susceptibility testing (DST) is not implemented in Congo due to the lack of laboratory capacity for mycobacterial culture, and molecular methods targeting drug resistance mutations. As in other African countries, smear microscopy is the primary method used for diagnosing TB in Congo, and if diagnosed, a standardized supervised treatment is set, with the following regimens: 2HRZE/4HR and 2HRZES/1HRZE/5HRE (H: isoniazid, R: rifampin, Z: pyrazinamide, E: ethambutol and S: streptomycin) for new and previously treated TB cases, respectively. Consequently, to date, no study has been conducted in this country to reflect the situation in terms of resistance phenotypes and molecular mechanisms of resistance. This study represents the first phenotypic and molecular study of tuberculosis in Congo with the goal to (i) determine drug susceptibility patterns in samples collected in the two main Congo’s cities (Brazzaville and Pointe-Noire) that account for two third of the population and (ii) characterize mutations prevalent in clinical isolates by using the commercially available GenoType MTBDR*plus* and GenoType MTBDR*i* assays, as well as DNA sequencing [2,3]. Furthermore, to gain an insight into the epidemiology of these MTBC isolates, a molecular typing by determination of the MIRU-VNTR patterns was also performed. Based on the results obtained, we report for the first time the presence of MDR but not XDR strains in Congo. We also showed that reverse hybridization assay with DNA probes falsely detected fluoroquinolones resistance in a predominant MDR clone harboring a double substitution T80A-A90G known to confer hypersusceptibility to fluoroquinolones [4,5,6]. This emphasized that detection of *gyrA* mutations by line probe assay should be interpreted with caution and cannot replace conventional drug susceptibility testing in countries such as Congo.

**Materials and Methods**

**Ehics statement**

Ethical approval for this study was obtained from the Faculty of Sciences de la Santé of Congo review committee. Informed written consent was waived by the IRB because all data and sampling were collected during the course of routine care in patients registered at the DOTs centers for suspicion of pulmonary TB or TB treatment. This study did not require any additional data, sampling and contact with participants. The outcome of the research data did not affect patient management. The objectives of the study were verbally explained to all participants. They were free to refuse that their sputum was transported to TB reference laboratories in France for processing and culture. No personal identifiers were recorded to maintain anonymity and confidentiality.

**Patients and specimens**

One smear-positive sputum per patient was collected over a 9-day period from 114 patients attending 6 centers for the diagnosis and treatment of TB of the two largest cities of Congo (5 located in Brazzaville and one located in Pointe Noire). Samples were studied anonymously in combination with the available clinical information including sex age, HIV status and past history of treatment. All patients included in this study were previously untreated or treated for less than a month at the time of collection of smear-positive sputum.

**Culture and antibiotic susceptibility testing**

The 114 refrigerated sputa were shipped to the laboratory of bacteriology from the teaching hospital at Lille (France) for culture and determination of first-line drug susceptibility of isolates as well as mutations profiles associated with the resistance to anti-TB drugs. Samples were processed by standard methods (N-acetyl L-cysteine-NaOH), followed by staining with auramine-rhodamine fluorochrome for microscopy and by culturing in a bactec MGIT 960 (Becton-Dickinson) non radiometric automatic isolation system [7–8]. Primary culture was characterized as belonging to MTBC using an immunochromatographic assay, based on detection of a specific MPT64 antigen (BIOCENTRIC, France). When the immunochromatographic assay was negative, identification of mycobacteria was done by 16S-23S rDNA internal transcribed spacers or Hsp65 sequencing [9,10]. A total of 46 samples were culture positive for MTBC and were used for determining the drug susceptibility profiles against the first-line drugs: isoniazid (0.1 μg/ml), rifampin (1.0 μg/ml), ethambutol (5 μg/ml) and streptomycin (1 μg/ml) by using the MGIT 960 system according to the manufacturer’s instructions [11]. Isolates resistant to at least to isoniazid and rifampin were considered as multidrug resistant (MDR) isolates and underwent drug susceptibility testing with ofloxacin, moxifloxacin and amikacin to identify extensively drug resistant (XDR) TB isolates. The breakpoint concentrations of ofloxacin, moxifloxacin and amikacin with MGIT 960 system were 2, 0.5 and 1 μg/ml, respectively [12,13]. Two concentrations of ofloxacin and moxifloxacin were tested (1 and 2 μg/ml, and 0.25 and 0.5 μg/ml, respectively).

**DNA extraction**

For DNA preparation, 1 ml of bacteria cultured in MGIT was used. Liquid cultures were centrifugated at 10,000 g for 15 min. and the mycobacterial pellets were resuspended in 300 μl distilled water and heat-killed at 95°C for 30 min. DNA used for amplification by PCR was obtained by heat shock extraction (3 cycles of freezing at ~80°C and boiling for 1 min.)

**Detection of mutations in drug target genes in MTBC isolates**

In order to screen for resistance to rifampin and isoniazid, the GenoType MTBDR*plus* assay was performed as recommended by the manufacturer (Hain LifeScience, GmbH, Germany). In addition, MTBC isolates found to be MDR were tested by GenoType MTBDR*i* assay, a line probe assay (LPA) that detects mutations associated with fluoroquinolone and injectable second-line drugs resistance. DNA sequencing in specific hot-spot target regions of the following genes: *rpoB* (rifampin resistance), *katG, inhA* and *inhB* promoter region (isoniazid resistance), *gyrA, gyrB* (fluoroquinolone resistance), *rpsL* and *rrs* (amino glycoside resistance) was performed to characterize more precisely the pattern of mutation or to resolve discrepancies between LPA and DST. The primers used for the DNA sequencing are listed in Table 1. The PCR products were purified using a Macherey-Nagel PCR purification kit according to the manufacturer’s instructions. The purified DNA was used for DNA sequencing with a 3500 Dx Genetic analyzer (Applied Biosystem) automated sequencer.

**MIRU-VNTR typing**

The MTBC culture positive isolates were further genotyped by PCR amplification of a panel of 24 MIRU-VNTR loci at the National Reference Centre for Mycobacteria (Pitié-Salpêtrière hospital, Paris, France), as previously described by Supply et al. [14]. Briefly, 2 μl of DNA extracted from cultures of the MTBC
null
Misdetection of Fluoroquinolone Resistance by LPA in MDR-TB Strains

Table 2. MTBC clinical isolates susceptibilities to antimicrobial drugs.

|                              | Sensitivity to all first-line drugs | Resistant to at least one drug but not to INH and RIF | MDR |
|------------------------------|------------------------------------|------------------------------------------------------|-----|
| New cases of TB              | 23                                 | 6                                                    | 8   |
| Recurrent or relapse cases of TB | 2                                 | 0                                                    | 7*  |

*p = 0.003 (patients with previous history of TB vs no previous history of TB).

doi:10.1371/journal.pone.0095083.t002

DST to fluoroquinolones (ofloxacin and moxifloxacin) and injectable second-line drug (amikacin), and by genotypic MTBDR-sl assay. All the 15 MDR strains were susceptible to amikacin and fluoroquinolones thus excluding the presence of XDR strains in the Congo’s isolates studied. The 15 MDR strains phenotypically susceptible to amikacin also harbored a wild-type nt 1400 region of rrs. In contrast, 9 of the 15 MDR strains, predicted by MGIT 960 to be susceptible to ofloxacin and moxifloxacin, were detected as potentially resistant to fluoroquinolones by MDRTB-sl assay by lack of hybridization with the WT2 probe while no hybridization was observed with all the mutation probes (MUT1, MUT2, MUT3 A→D) thus, indicating an unusual mutation in gyrA. A possible resistance to fluoroquinolones suggested by the MDRTB-sl results but remaining undetectable at the phenotypic level was unexpected since the second-line drug-based regimen has not yet been introduced in Congo. DNA sequencing of gyrA revealed that these 9 MDR strains harbored the same combination of GyrA T80A and A90G substitutions known to confer hypersusceptibility to fluoroquinolones [4–6]. We also sequenced gyrB because mutations in this gene that have been previously associated with fluoroquinolone resistance are not explored by the MTBDR-sl assay [20]. One MDR strain displayed the substitution G559A in GyrB but this mutation is not involved in fluoroquinolone resistance [21]. In our study, a GyrA T80A and A90G substitutions were also found in one strain susceptible to first-line drugs and the GyrB G559A substitution in three non MDR strains: two drug susceptible and one isoniazid mono-resistant strains (data not shown). GyrA T80A and A90G and GyrB G559A substitutions may represent natural variations of M. tuberculosis resulting in false-resistance to fluoroquinolones by LPA which can lead to a XDR-TB misdiagnosis and unnecessary restriction of active drugs. Natural variations in the genome especially in the gyrA gene at position 73, (T73A) and 95 (S95T) have been previously reported in MTBC isolates from other African countries [22,23] and emphasized that LPA assay should be used and interpreted with caution in patients originating from these countries. Finally, second-line DST may be more accurate for the detection of second drugs in these resource-limited TB settings. For this purpose, recent studies highlighted the usefulness of the sensititre MycoTB plate method in low-income countries such as Tanzania and Uganda [24,25]. This method is rapid (the turnaround time is 10–15 days when the test is valid on the first try), ready to use (lyophilized first and second-line drugs with several dilutions), and requires minimal instrumentation (mirror box) [26]. This method could be useful for DST surveillance in Congo especially among patients receiving empirical MDR regimen that could be introduced in this country because of the absence or low-prevalence of fluoroquinolone and injectable aminoglycoside resistance.

Analysis of the dendrogram drawn from the MIRU-VNTR codes confirmed that the 9 MDR strains exhibiting the double mutation GyrA T80A and A90G, as well as the same mutations in rpoB and katG, were gathered into a unique cluster related to the T-family. All except one of the 9 strains displayed an identical MIRU-VNTR. The last strain differed at the level of one locus among the 24 loci analyzed (Table 3) thus, suggesting a possible focal outbreak in Pointe Noire district since 6 strains of this clone were isolated from patients attending the DOTS center of Pointe-Noire. The one susceptible strain harboring the double mutation in gyrA was also related to the T-family too but was not included in the same cluster encompassing the nine T80A-A90G MDR strains. One MDR strain and the three non MDR strains displaying the GyrB G559A substitution were linked in the MIRU-VNTR dendrogram and were related to the T lineage suggesting that this substitution could be a marker of a subgroup of strains in the T family. Only 4 MTBC (3 MDR and one susceptible) isolates belonged to the Beijing family in our study. A similar low prevalence of Beijing family among MTBC isolates was previously reported in the West Africa countries [15,27,28], contrarily to Asia, Russia, and the United States where the Beijing family predominates [29–32]. The 3 MDR Beijing strains that were closely related at the level of their MIRU-VNTR profile (Table 3) shared a D516Y substitution in RpoB and two of these had additional rpoB mutations at position 511. The two remaining MDR strains characterized by a S531 substitution in RpoB, were found to be related to the LAM family but had unique MIRU-VNTR codes, indicating that they were not related to any of the other MDR isolates (Table 3). Finally, MIRU-VNTR analysis revealed that a majority of the MTBC isolates included in our study (30 of 46, 65%) were related to the ill-defined T family which represents a group of strains showing a high degree of genetic diversity frequently encountered in Africa. The other genotypes found in the 46 strains analyzed were LAM (17%), Cameroon (9%) and Beijing (9%). The distribution of MIRU-VNTR families was similar between strains isolated in Pointe Noire and Brazzaville areas and between MDR and non MDR strains. No significant statistical link was found between lineages and epidemiological data such as age, sex and HIV status.

Conclusions

By conducting the first phenotypic and molecular investigation of M. tuberculosis clinical isolates in circulation in Congo we have revealed the presence of MDR-TB in this country as well as the probable spread of a particular clone of double mutant GyrA T80A and A90G hypersusceptible to fluoroquinolones among MDR strains in this region of Africa. The presence of MDR-TB emphasizes the urgent need to perform molecular assays to rapidly detect drug resistance in order to start an appropriate anti-TB treatment with second-line drugs in Congo. However, line probe assay may have limitation in detecting fluoroquinolone resistance in Congo since strains harboring specific mutations such as T80A-A90V in GyrA lead to false diagnosis of fluoroquinolone resistance. Therefore, a lack of hybridization with the wild type WT2 probe should not be interpreted as fluoroquinolone resistance until DNA sequencing and/or DST were performed.
Table 3. Characteristics of mutations in drug target genes from the 15 MDR-TB isolates.

| No. of isolates | Drug target genes | MIRU-VNTR patterns | Spoligotyping based defined clades |
|-----------------|-------------------|--------------------|-----------------------------------|
|                 | N = 8             | D516V              | wt                                |
|                 |                   | S315T              | T80A+A90G                         |
|                 |                   |                    | 253332525322322752314423 T        |
|                 | N = 1             | D516V              | wt                                |
|                 |                   | S315T              | T80A+A90G                         |
|                 |                   |                    | 254332523223237252314423 T        |
|                 | N = 1             | S531L+V577M        | H270P wt                          |
|                 |                   |                    | 255332526235262213423 T           |
|                 | N = 1             | D516Y              | S315T K43R                        |
|                 |                   |                    | 2733354444324525231423 Beijing     |
|                 | N = 1             | L511+D516Y         | S315T K43R                        |
|                 |                   |                    | 2733354444326525231423 Beijing     |
|                 | N = 1             | S531L              | S315T K43R                        |
|                 |                   |                    | 251313542122437262211245 LAM       |
|                 | N = 1             | S531Q              | Del w                            |
|                 |                   |                    | 2513231421222342622213523 LAM      |

Acknowledgments
The authors thank the entire staff of the centers for the diagnosis and treatment of TB of Brazzaville and Pointe-Noire for their help in this study.

Author Contributions
Conceived and designed the experiments: AA WS NL. Performed the experiments: PB GD SA GM. Analyzed the data: AA WS PB NL. Contributed reagents/materials/analysis tools: VJ RC. Wrote the paper: AA WS NL.

References
1. WHO (2013) Global tuberculosis report. World Health Organization, Geneva, Switzerland.
2. Hofmann D, Rusch-Gerdes S, Richter E (2007) Evaluation of the GenoType MBTDRplus assay for rifampin and isoniazid susceptibility testing of Mycobacterium tuberculosis strains and clinical specimens. J Clin Microbiol 45:2635–2640.
3. Brosset F, Veirin N, Aubry A, Jarlier V, Sougakoff W (2010) Detection by GenoType MBTDR test of complex mechanisms of resistance to second-line drugs and ethambutol in multidrug-resistant Mycobacterium tuberculosis complex isolates. J Clin Microbiol 48:1683–1689.
4. Aubry A, Veirin N, Cambau E, Truffot-Pernot C, Jarlier V, et al. (2006) Novel gyrA mutations in quinolone-resistant and -hypersusceptible clinical isolates of Mycobacterium tuberculosis: functional analysis of mutant enzymes. Antimicrob Agents Chemother 50:104–112.
5. Malik S, Willby M, Sikes D, Tsolikov OV, Posey JJ (2012) New insights into fluoroquinolone resistance in Mycobacterium tuberculosis: functional genetic analysis of gyr and gyrB mutations. PLoS One 7:e97934.
6. Von Grell A, Martin A, Jureen P, Hoffner S, Vandamme P, et al. (2009) Multicenter evaluation of the Repetitive Unit-Variable-Number Tandem Repeat Typing of Mycobacteria decontamination with N-acetyl-L-cysteine-sodium hydroxide for culture of Mycobacteria using genus-specific PCR assay. J Clin Microbiol 47:3501–3506.
7. Kubica GP, Dye WE, Colin ML, Middlebrook G (1963) Spuismutagen and decontamination with N-acetyl-L-cysteine-sodium hydroxide for culture of mycobacteria. Am Rev Dis Resp 7:775–779.
8. Silver H, Sonnenwirth AC, Alex N (1966) Modifications in the fluorescence microscopy technique as applied to identification of acid-fast bacilli in tissue and bacteriological material. J Clin Path 19:581–588.
9. Brunello F, Ligozzi M, Cristelli E, Bonora S, Tortoli E, et al. (2001) Detection of the 23S rRNA mutations in quinolone-resistant and -hypersusceptible clinical isolates of Mycobacterium tuberculosis. J Antimicrob Chemother 47:123–138.
10. Roth A, Reisich U, Streubel A, Naumann L, Kroppenstedt RM, et al. (2000) Novel diagnostic algorithm for identification of mycobacteria using genus-specific amplification of the 16S-23S rRNA gene spacer and restriction endonucleases. J Clin Microbiol 38:1094–1104.
11. Rusch-Gerdes S, Domeld G, Nardi G, Gimondo MR, Welsch H-M, et al. (1999) Multicenter evaluation of the Mycobacterium Growth Indicator Tube for testing susceptibility of Mycobacterium tuberculosis to first-line drugs. J Clin Microbiol 37:1084–1090.
12. Rusch-Gerdes S, Pfiffner GE, Casal M, Chadbwick M, Siddiqui S (2006) Multicenter laboratory validation of the BACTEC MGIT 960 technique for testing suitability of Mycobacterium tuberculosis to classical second-line drugs and newer antimicrobials. J Clin Microbiol 44:693–696.
13. van Ingen J, Simons S, de Zwaan R, van der Loos T, Kamst-van Agterveld M, et al. (2010) Comparative study on genotypic and phenotypic second-line drug resistance testing of Mycobacterium tuberculosis complex isolates. J Clin Microbiol 48:2749–2753.
14. Supp L, Allg C, Lejean S, Cardoso-Oelemann M, Rusch-Gerdes S, et al. (2006) Proposal for standardization of optimized mycobacterial interpersed repetitive unit-variable-number tandem repeat typing of Mycobacterium tuberculosis. J Clin Microbiol 44:4490–4501.
15. Homolka S, Post E, Oberhauser B, George AG, Westman L, et al. (2008) High genetic diversity among Mycobacterium tuberculosis complex strains from Sierra Leone. BMC Microbiol 8:103.
16. Noeske J, Voela N, Fon E, Abena Foe JL (2012) Early results of systematic drug susceptibility testing in pulmonary tuberculosis retreatment cases in Cameroon. BMC Res Notes 5:160.
17. Ramanawmy S, Maser JM (1998) Molecular genetic basis of antimicrobial agent resistance in Mycobacterium tuberculosis: update. Tuberc Lung Dis 79:3–39.
18. Campbell PJ, Mordock GP, Sikes RD, Dalton TL, Methock B, et al. (2011) Molecular detection of mutations associated with first- and second-line drug resistance compared with conventional drug susceptibility testing of Mycobacterium tuberculosis. Antimicrob Agents Chemother 55:2032–2041.
19. Van Deun A, Barrera L, Bastian I, Fattorini L, Hoffmann H, et al. (2009) Mycobacterium tuberculosis strains with highly discordant rifampin susceptibility test results. J Clin Microbiol 47:3501–3506.
20. Maturi F, Sterling TR, Kaiga AW, Blackman A, van der Heijden YF, et al. (2012) A systematic review of gyrase mutations associated with fluoroquinolone-resistant Mycobacterium tuberculosis and a proposed gyrase numbering system. J Antimicrob Chemother 67:819–831.
21. Pantol A, Petrella S, Maturi S, Bonfier B, Bastian S, et al. (2011) DNA gyrA and gyrB mutations in Mycobacterium tuberculosis are necessary to demonstrate fluoroquinolone resistance secondary to gyr mutations in Mycobacterium tuberculosis. Antimicrob Agents Chemother 55:4524–4529.
22. Umubeyi AN, Rigous L, Shamputa IC, Fissette K, Elkriz Y, et al. (2007) Limited fluoroquinolone resistance among Mycobacterium tuberculosis isolates from Rwanda: results of a national survey. J Antimicrob Chemother 59:1031–1033.
23. Mitarai S, Ksarababolula M, Terumasa H, Luabasi D, Kasolo FC, et al. (2005) Mycobacterium tuberculosis and gcf variation in Zambia. Trop Med and Health 33:91–94.
24. Mpagama SG, Houp E, Stroup S, Kumburu H, Gratz J, et al. (2013) Application of quantitative second-line drug susceptibility testing at a multidrug-resistant tuberculosis hospital in Tanzania. BMC Infect Dis 13:432.
25. Lee J, Armstrong DT, Sengsoba W, Park JA, Yu Y, et al. (2014) Sensitivity MYCOTB MIC plate for testing Mycobacterium tuberculosis susceptibility to first- and second-line drugs. Antimicrob Agents Chemother 58:11–8.
26. Hall L, Judge KP, Clark SL, Dionne K, Merson R, et al. (2012) Evaluation of the Sensitivity MycoTB plate for susceptibility testing of the Mycobacterium tuberculosis complex against first- and second-line agents. J Clin Microbiol 50:3732–3734.
27. Godreuil S, Torreia G, Terrea D, Chevenet F, Daigboua S, et al. (2007) First molecular epidemiology study of Mycobacterium tuberculosis in Burkina Faso. J Clin Microbiol 45:921–927.
28. Groolthe R, Ghebremichael S, Svennum J, Rabna P, Colombati R, et al. (2011) The Guinea-Bissau family of Mycobacterium tuberculosis complex revisited. PLoS One 6:e18601.
29. Aguero TB, Valsay AN, Blackman RJ, Shiklett KR, Reves R, et al. (1999) Spread of strain W, a highly drug-resistant strain of Mycobacterium tuberculosis, across the United States. Clin Infect Dis 28:93–92.
30. Dong H, Liu Z, Lv B, Zhang Y, Liu J, et al. (2010) Spoligotypes of Mycobacterium tuberculosis from different Provinces of China. J Clin Microbiol 48:4102–4106.

doi:10.1371/journal.pone.0095083.t003

PLOS ONE | www.plosone.org 5 April 2014 | Volume 9 | Issue 4 | e95083
31. Drobniewski F, Balabanova Y, Nikolayevsky V, Ruddy M, Kuznetsov S, et al. (2005) Drug-resistant tuberculosis, clinical virulence, and the dominance of the Beijing strain family in Russia. JAMA 293:2726–2731.

32. Van Soolingen D, Qian L, de Haas PE, Douglas JT, Traore H, et al. (1995) Predominance of a single genotype of Mycobacterium tuberculosis in countries of East Asia. J Clin Microbiol 33:3234–3238.