

Original Article

Genotyping and drug-resistance epidemiology of *Mycobacterium tuberculosis* in Xuzhou, China

Haiqing Zhang¹, Haibin Huang¹, Chengyong Liu¹, Tong Jia¹, Limao Zhang¹, Dongqing Zhou¹, Sumei Wei¹, Chunying Wang²

Departments of ¹Tuberculosis, ²Infectious Diseases, Xuzhou Infectious Disease Hospital, Xuzhou, China

Received June 8, 2017; Accepted August 9, 2017; Epub September 1, 2017; Published September 15, 2017

Abstract: Background: To explore the genetic diversity and drug resistance status of MTB in Xuzhou, China. Methods: A total of 325 clinical MTB strains were genotyped by spacer-oligonucleotide typing (spoligotyping) and mycobacterial interspersed repetitive unit variable number of tandem repeats (MIRU-VNTR). Phenotypic resistance was assessed by drug susceptibility testing (DST). Result: Based on the spoligotyping method, 325 MTB isolates were classified into 5 known genotypes and 12 unknown genotypes, and the largest branch comprised 268 strains belonging to the Beijing family. Based on the 15-loci VNTR typing method, 325 MTB isolates were divided into 35 clusters and 220 unique patterns. Compared to the low discriminatory power of spoligotyping genotyping (HGDI = 0.3444), 15-loci VNTR genotyping had a significantly higher discriminatory power for all strains (HGDI = 0.9980), particularly for the Beijing family strains (HGDI = 0.9892). When spoligotyping and 15-loci VNTR methods were used together, the discriminatory power increased to 0.9991. The Beijing family strain presented increased risks for developing multi-drug resistance TB ($P < 0.05$). Conclusion: The Beijing family isolates is the most prevalent strains in Xuzhou. Spoligotyping, in combination with 15-loci MIRU-VNTR, is useful for epidemiological analysis of MTB transmission in Xuzhou.

Keywords: *Mycobacterium tuberculosis*, genotype, spoligotyping, MIRU-VNTR

Introduction

Tuberculosis (TB) is a major global public health concern, particularly in developing countries. According to the World Health Organization (WHO), there were approximately 9.6 million new cases and 1.5 million fatal cases of TB in 2014 [1]. China ranks second among the 22 high burden countries, with approximately 0.98 million new cases in 2013 [1]. To reduce the global burden of TB, the use of effective drug treatments is considered to be the best approach. Moreover, due to the inappropriate use of anti-TB drugs in the world, approximately 0.48 million TB patients became multidrug-resistant in 2014. Therefore, it is critical to systematically monitor and track the transmission of drug-resistant TB strains to control MDR-TB infection [2, 3].

Genotyping of *Mycobacterium tuberculosis* (MTB) isolates has significantly improved understanding of the epidemiology of TB, and allowed for better control of this disease [4]. Advances in molecular biotechniques can help

to reveal the source of infection, trace the route of transmission, and determine risk factors [5]. In order to monitor domestic spread, the spoligotyping method is the gold standard for MTB strain identification, particularly for Beijing family genotype strains [6, 7]. Due to the low discriminatory power of spoligotyping, MIRU-VNTR is frequently used to fully explore the genetic diversity of MTB strains [8]. This method can determine the different numbers of MTB interspersed repetitive units with disparate VNTR loci, and is widely used for molecular typing.

Xuzhou, an important transportation hub located in eastern China, has remained a middle-prevalence area of TB. According to the 2010 National TB Epidemiology Survey in China, approximately 57,000 pulmonary TB cases occurred in Xuzhou from 2000 to 2010 [9]. However, information regarding the molecular epidemiology of TB in Xuzhou is scarce; therefore it is important to study the local molecular epidemiology of TB. In our study, we collected 325 clinical MTB strains in Xuzhou, and genotypes and drug resistance were analyzed by

spoligotyping and MIRU-VNTR with 15 VNTR loci. This study not only provides valuable information for TB researchers, but also presents guidelines for the prevention and control of TB in Xuzhou.

Materials and methods

Study population and bacterial strains

A total of 325 clinical MTB strains were isolated from TB patients from Xuzhou Infectious Disease Hospital during 2014. Sputum smear examination by Ziehl-Neelsen staining and culture on Lowenstein-Jensen (L-J) medium were performed for all samples. The demographic data of all TB patients was collected, including age, sex, BCG vaccination status, drug treatment, and birth region. All patients enrolled in the study signed an informed consent form. The protocols performed in this study were approved by the Ethics Committee of Xuzhou Infectious Disease Hospital.

Genomic DNA extraction

All clinical isolates of MTB were grown on fresh L-J slants at 37°C for 4-6 weeks. Cells were resuspended in 400 µl TE buffer (pH 8.0), centrifuged at 12,000 rpm for 2 min, and the pellet was resuspended in 400 µl of TE buffer and heated in a water bath at 95°C for 30 min. The cellular debris was centrifuged at 12,000 rpm for 3 min, and DNA in the supernatant was stored at -20°C for PCR analysis.

Spoligotyping

Spoligotyping of TB strains was performed as previously described [10]. First, the direct repeat (DR) region was amplified with the primers DRa (5'-CCGAGAGGGGACGGAAAC-3') and DRb (5'-GGTTTTGGGTCTGACGAC-3'). Then, the PCR products were hybridized to a set of 43 oligonucleotide probes corresponding to each spacer, which were covalently bound to a membrane. Chemiluminescent detection was performed using ECL detection liquid and ECL Hyperfilm (GE Healthcare Life Sciences, UK). The spoligotypes in binary format were then compared with those in the SITVIT WEB database [11].

MIRU-VNTR

In accordance with previous studies, 15-loci VNTR were selected for MLVA typing for our

MTB genetic diversity study [12]. This set of loci included 5 loci of exact tandem repeats (ETRs): ETR-A, -B, -C, -D, and -E; 8 MIRU loci: MIRU-10, -16, -23, -26, -27, -39, and -40; 3 Mtub loci: Mtub21, 30, and 39. The primer sequences for PCR amplification of each locus are described in previous studies [12]. Each PCR reaction was performed in a final volume of 20 µl containing 50 ng DNA, 10 µl Taq Mixture (TaKaRa, Japan), and 1 µl (10 µM) primers. The amplification was carried out in a thermal cycler (Bio-Rad, USA) using the following parameters: an initial denaturation at 94°C for 5 min; followed by 35 cycles of denaturation at 94°C for 30 s, annealing at 62°C for 30 s, and extension at 70°C for 45 s; and a final extension at 72°C for 10 min. A positive control (H37Rv strain genomic DNA) and a negative control (ddH₂O) were included in each test. PCR amplicons were analyzed on 2% agarose gels, which were stained with ethidium bromide and imaged using the Image Lab System (Bio-Rad). By comparing PCR amplicon sizes to those obtained from H37Rv, we obtained the copy numbers of each VNTR loci. BioNumerics 5.0 was used for the phylogenetic and cluster analysis, and the discriminatory power of the VNTR loci was determined by the Hunter-Gaston discrimination index (HGDI).

Drug susceptibility testing

The L-J proportion method was used for the DST at the Clinical Laboratory of the Xuzhou Infectious Disease Hospital. The drug concentrations were 0.2 µg/ml for isoniazid (INH), 40 µg/ml for rifampicin (RFP), 2 µg/ml for ethambutol (EMB), and 4 µg/ml for streptomycin (SM). H37Rv strain was used as a quality control, and DST results were analyzed after 4 weeks growth. When the growth rate was more than 1% compared to the control, the strain was determined to be resistant to the specific drug. Strains resistant to at least RIF and INH were defined as MDR-TB [13].

Data analysis

The statistical analysis was performed using GraphPad Prism 6.0. Chi-square for measuring the association between two categorical variables which is the *Spoligotyping* and *MIRU-VNTR*, and Fisher's exact test analysis were run to identify significant differences. The genetic diversity was calculated using Hunter-Gaston diversity index. A two-sided *P* value of < 0.05 was considered to be statistically significant.

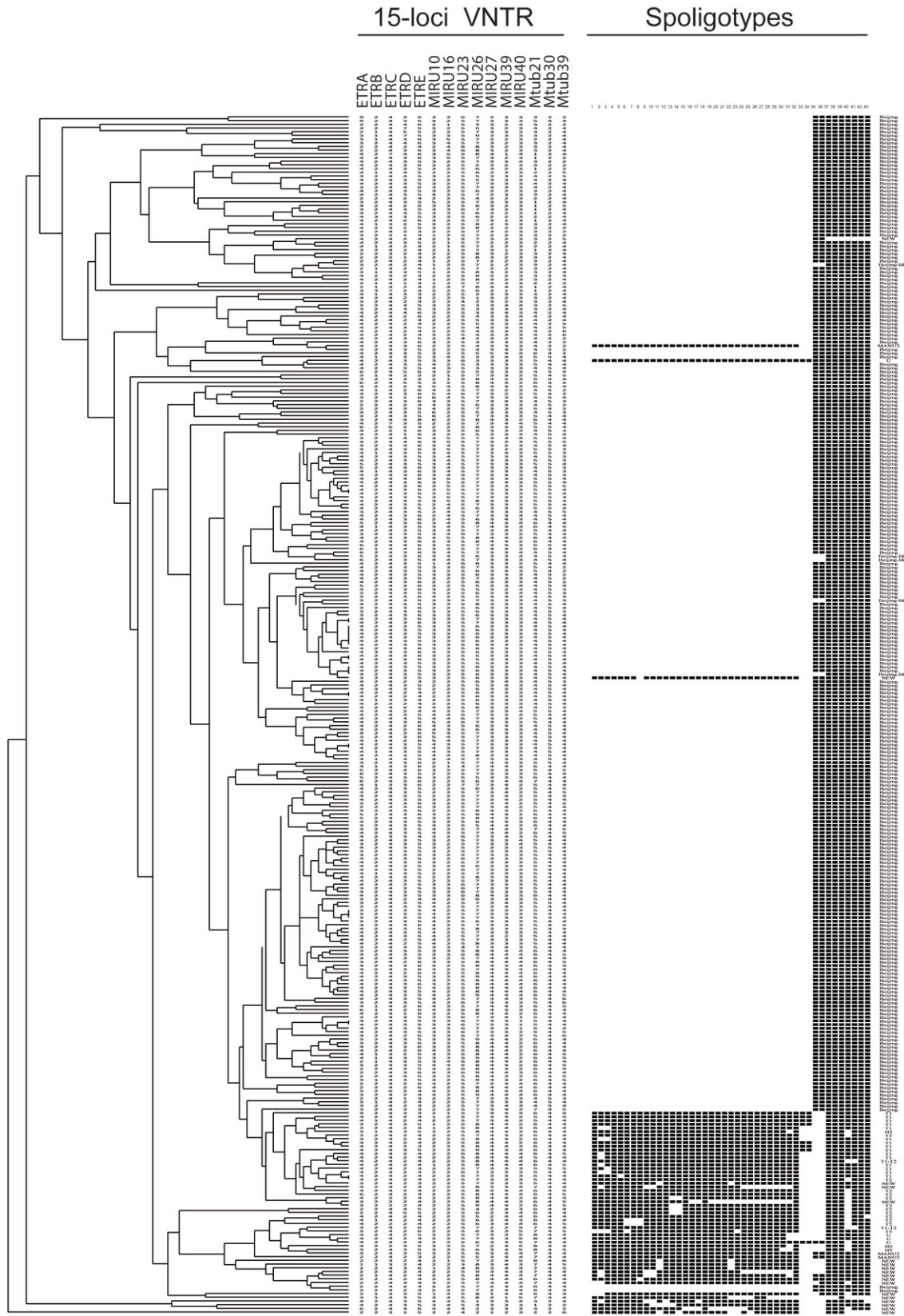


Figure 2. Genotyping with spoligotyping and 15-loci MIRU-VNTR.

Table 1. The repeat number of 15-loci VNTR for 325 MTB strains

VNTR loci	HGDI score	No. of repeats in H37Rv	Repeat Numbers of VNTR-loci in the Isolates									
			1	2	3	4	5	6	7	8	9	
ETRA	0.585	3	1	35	73	193	9	12				2
ETRB	0.229	3	38	283	4							
ETRC	0.163	4		9	14	297		2	3			
ETRD	0.553	3	9	94	195	21	4		2			
ETRE	0.665	3		2	16	63	152	91			1	
MIRU10	0.679	3	14	102	143	55	7	4				
MIRU16	0.591	2	11	193	61	45	15					
MIRU23	0.242	6			1	7	281	34	2			
MIRU26	0.726	3	2	4	11	8	21	53	143	72	11	
MIRU27	0.471	3	2	30	225	67	1					
MIRU39	0.598	2	5	42	172	106						
MIRU40	0.577	1	4	49	202	61	9					
Mtub21	0.785	2	12	8	32	85	93	75	15	5		
Mtub30	0.622	2			67	163	95					
Mtub39	0.477	5		27	19	229	43	7				

Table 2. Different discriminatory power of different typing methods used for 325 MTB strains

Method	No. of clustered strains	No. of clusters	Cluster size	Clustering rate (%)	HGDI score		
					All strains	Beijing family	Other strains
Spoligotyping	310	16	2-263	90.46	0.3444	0.0375	0.9655
15-loci VNTR	105	35	2-6	21.54	0.9980	0.9892	0.9963
Spoligotyping and VNTR	87	26	2-5	18.77	0.9991	0.9932	0.9989

patterns, by the MLVA with 15-loci VNTR (**Figure 2** and **Table S1**). The number of clustered isolates was 105 and the clustering rate was 21.54%. To verify the discriminatory power of each locus and the cumulative discriminatory power of all 15 loci, we calculated the discriminatory power of each locus to obtain the HGDI discriminatory power (**Table 1**). Each of the 15 loci showed different discriminatory powers, which consisted of 5 high (> 0.6) discriminatory loci (Mtub21, MIRU26, MIRU10, ETRE, Mtub30), 7 moderate (0.3 to 0.6) discriminatory loci (MIRU39, MIRU16, ETRA, MIRU40, ETRD, Mtub39, MIRU27), and 3 poor (< 0.3) discriminatory loci (MIRU23, ETRB, ETRC), based on the HGDI values.

Comparison of spoligotyping and VNTR genotyping

Comparing the genotyping results of 325 isolates with spoligotyping and 15-loci VNTR indicated the discriminatory power of these two genotyping methods (**Table 2**). Compared to

15-loci VNTR, spoligotyping had a low discriminatory power (HGDI = 0.344), particularly when applied to Beijing family strains (HGDI = 0.0375). Moreover, among the 31 different types, spoligotyping identified 15 unique strains and 16 clusters grouped containing 310 strains, with a clustering rate of 90.46%. The 15-loci VNTR identified 220 unique strains and 35 clusters grouped containing 105 strains, with a clustering rate of 21.54%. Moreover, 15-loci VNTR genotyping had a significantly higher discriminatory power for all strains (HGDI = 0.9980), particularly for Beijing family strain genotyping (HGDI = 0.9892). When spoligotyping and 15-loci VNTR methods were combined, the discriminatory power increased to 0.9991, and the clustering rate was reduced to 18.77%.

Drug resistance

The DST results showed that 14.77% (48/325) were resistant to at least one of the four first-line drugs (**Table 3**). The proportions of single-drug resistance of RFP, INH, SM, and EMB

Table 3. First-line drug resistant frequency among 325 MTB strains

Drugs	No. (%) of Isolates		χ^2	P
	Beijing (n = 268)	Non-Beijing (n = 57)		
Mono-resistance				
RFP	4 (1.49)	1 (1.75)	0.02128	> 0.05
INH	6 (2.24)	4 (7.02)	3.599	> 0.05
SM	7 (2.61)	2 (3.51)	0.1404	> 0.05
EMB	4 (1.49)	2 (3.51)	1.054	> 0.05
Total	21(7.84)	9 (15.79)	3.549	> 0.05
MDR-TB				
RFP+INH	6 (2.24)	0 (0)	1.300	> 0.05
RFP+INH+SM	6 (2.24)	0 (0)	1.300	> 0.05
INH+SM+EMB	4 (1.49)	0 (0)	0.8613	> 0.05
RFP+INH+SM+EMB	2 (0.75)	0 (0)	0.4280	> 0.05
Total	18 (6.72)	0 (0)	4.053	< 0.05

were 1.54% (5/325), 3.08% (10/325), 2.77% (9/325), and 1.85% (6/325), respectively. Among all isolates, 5.54% (18/325) isolates were MDR-TB strains, including 2 (0.62%) strains resistant to all four first-line drugs. By comparing the distribution of drug resistance between Beijing and non-Beijing strains, we found that the Beijing family strains presented increased risks for developing MDR in Xuzhou ($\chi^2 = 4.053$, $P < 0.05$).

Discussion

TB is a global public health issue, and the prevalence of TB is closely related to regional differences and population mobility. Systematic surveillance and tracking of transmission of TB strains have become critically important for infection control. Compared with traditional MTB typing, newer genotyping methods can quickly and accurately obtain information regarding outbreaks of MTB [4]. Moreover, certain MTB genotypes have been found to be related to the risk of transmission or anti-TB drug resistance. The number of MTB genotypes has increased throughout different regions of China [10, 14-16]. However, these results do not represent the prevalence and epidemic trend of tuberculosis in Xuzhou, an important transportation hub in China.

Spoligotyping is the gold standard for Beijing family identification, as it is simple and efficient. The current study spoligotyping showed 82.46% were clustered into the Beijing family, thus indicating the Beijing family is the most

prevalent lineage of MTB strains in Xuzhou. The result is in concordance with previously published results. Compared with other Chinese cities, prevalence of the Beijing genotype was less than for Beijing (92%) [17], Shijiazhuang (91%) [18], but more than Hong Kong (70%) [19], Taibei (52%) [20], and Shanghai (77%) [21]. Although the Beijing family was the dominant genotypic family in the Xuzhou district, genotypic polymorphisms were also evident, such as the T1, T2, T1-T2, T5, U, H3, and MANU2 families. Notably, the T family genotype, which is prevalent in Africa, Central and South America, and Europe, was significantly higher in Xuzhou than in other districts [22]. The U types have previously been identified as high-incidence strains in the Middle East, and Central and Southern Asia [22]. This indicates that population mobility from these regions may have increased the prevalence of related genotypes in Xuzhou. In addition, we identified 12 novel MTB spoligotypes, indicating the complexity of the sources of strains in this region.

The discriminatory power of spoligotyping is low, and it cannot be utilized for complex analysis of the Beijing family strains. Genotyping with a higher discriminatory power is required to detect unnoticed transmission of *M. tuberculosis* among patients. Therefore, another molecular typing method based on MIRU-VNTR is used to complete the shortcoming of the spoligotyping.

The discriminatory power of spoligotyping is low, and it cannot be utilized for complex analysis of the Beijing family strains. Genotyping with a higher discriminatory power is required to detect unnoticed transmission of *M. tuberculosis* among patients. Therefore, another molecular typing method based on MIRU-VNTR is used to complete the shortcoming of the spoligotyping.

In different regions, the disparate VNTR typing sets showed various efficiencies in MTB genotyping. The sets of common loci comprised of 12-loci, 15-loci, 24-loci, and others, and the discriminatory power of MIRU-VNTR is determined by the number of loci [23]. The selection of suitable sets of loci depends on the pattern of MTB strains in the investigated area. We selected the classic 15-loci VNTR method, based on available data for other Chinese cities [24, 25], and found that the allelic diversity

varied significantly at each VNTR locus. We identified 220 unique strains, and 35 clusters grouped containing 105 strains, and found a significantly higher discriminatory power for all strains (HGDI = 0.9980), particularly for genotyping of Beijing family strains (HGDI = 0.9892). Among the 15-loci VNTR, Mtub21 had the highest HGDI score of 0.785, similar to the Beijing results, however this locus was not optimal for genotyping in Tibet, Heilongjiang, and Taibei [26]. MIRU26, MIRU10, ETRE, and Mtub30 also revealed higher diversity than in other zones [26]. When the spoligotyping and 15-loci VNTR methods were used together, the discriminatory power increased to 0.9991. This result indicates that the combination of the two genotyping methods improves discriminatory power and reproducibility, and significantly contributes to the understanding of MTB epidemiology

The DST results showed that the multiple drug resistance rates were 5.54% in Xuzhou (Table 3). This was lower than the average level of China. This may be attributed to vigorous prevention and control methods used in Xuzhou, resulting in reduction of the spread of drug-resistant tuberculosis. According to published reports, the Beijing genotype is significantly associated with drug-resistance, and may be responsible for the emergence and spread of MDR-TB [12, 27].

In order to identify any association of drug resistance with the Beijing genotype, we compared the distribution of drug resistance between Beijing and non-Beijing genotyping strains using the XXX method and the result in Table 3 showed increased risk for developing MDR-TB in the Beijing family strains.

The study demonstrates the Beijing family isolates is the most prevalent strains in Xuzhou. Furthermore, the Beijing family strain may be more virulent and associated with drug resistance.

The spoligotyping method is the gold standard for MTB strain identification, particularly for Beijing family genotype strains, nevertheless it has low. Therefore, 15-loci MIRU-VNTR, which is useful for epidemiological analysis of MTB transmission in Xuzhou, is used to complete the shortcoming of the spoligotyping.

Disclosure of conflict of interest

None.

Address correspondence to: Chunying Wang, Department of Infectious Diseases, Xuzhou Infectious Disease Hospital, Shuangyong Road, Dongjiaodianzi Village, Yunlong District, Xuzhou, Jiangsu, China. Tel: +86 13813289109; E-mail: chunyun_wang1978@foxmail.com

References

- [1] Ravi A, Singh Sunita D, Medical GR. Global tuberculosis report 2015, Global Tuberculosis Report 6. 2012.
- [2] Zignol M, Gemert WV, Falzon D, Sismanidis C, Glaziou P, Floyd K, Raviglione M. Surveillance of anti-tuberculosis drug resistance in the world: an updated analysis, 2007-2010. Bull World Health Organ 2012; 90: 111-119.
- [3] Zhao Y, Xu S, Wang L, Chin DP, Wang S, Jiang G, Xia H, Zhou Y, Li Q, Ou X. National survey of drug-resistant tuberculosis in China. N Engl J Med 2012; 366: 2161-2170.
- [4] Barnes PF, Cave MD. Molecular epidemiology of tuberculosis. N Engl J Med 2003; 349: 1149-1156.
- [5] Roetzer A, Diel R, Kohl TA, Rückert C, Nübel U, Blom J, Wirth T, Jaenicke S, Schuback S, Rüsche-Gerdes S. Whole genome sequencing versus traditional genotyping for investigation of a *Mycobacterium tuberculosis* outbreak: a longitudinal molecular epidemiological study. PLoS Med 2013; 10: e1001387.
- [6] Bifani PJ, Mathema B, Kurepina NE, Kreiswirth BN. Global dissemination of the *Mycobacterium tuberculosis* W-Beijing family strains. Trends Microbiol 2002; 10: 45-52.
- [7] Kamerbeek J, Schouls L, Kolk A, Van Agterveld M, Van Soolingen D, Kuijper S, Bunschoten A, Molhuizen H, Shaw R, Goyal M. Simultaneous detection and strain differentiation of *Mycobacterium tuberculosis* for diagnosis and epidemiology. J Clin Microbiol 1997; 35: 907-914.
- [8] Allix-Béguec C, Harmsen D, Weniger T, Supply P, Niemann S. Evaluation and strategy for use of MIRU-VNTRplus, a multifunctional database for online analysis of genotyping data and phylogenetic identification of *Mycobacterium tuberculosis* complex isolates. J Clin Microbiol 2008; 46: 2692-2699.
- [9] Wang L, Zhang H, Ruan Y, Chin DP, Xia Y, Cheng S, Chen M, Zhao Y, Jiang S, Du X, He G, Li J, Wang S, Chen W, Xu C, Huang F, Liu X, Wang Y. Tuberculosis prevalence in China, 1990-2010; a longitudinal analysis of national survey data. Lancet 2014; 383: 2057-2064.

Mycobacterium tuberculosis in Xuzhou

- [10] Liu Y, Tian M, Wang X, Wei R, Xing Q, Ma T, Ji-ang X, Li W, Zhang Z, Xue Y. Genotypic diversity analysis of *Mycobacterium tuberculosis* strains collected from Beijing in 2009, using spoligo-typing and VNTR typing. *PLoS One* 2014; 9: e106787.
- [11] Demay C, Liens B, Burguière T, Hill V, Couvin D, Millet J, Mokrousov I, Sola C, Zozio T, Rastogi N. SITVITWEB--a publicly available international multimarker database for studying *Mycobacterium tuberculosis* genetic diversity and molecular epidemiology. *Infect Genet Evol* 2012; 12: 755-766.
- [12] Pang H, Tong J, Liu HC, Du YG, Zhao XQ, Jiang Y, Wu XC, Yang JC, Wan KI. Molecular characterization and drug-resistance of *mycobacterium tuberculosis* strains in Xuzhou, China. *Biomed Environ Sci* 2014; 27: 960-964.
- [13] Shao Y, Yang D, Xu W, Lu W, Song H, Dai Y, Shen H, Wang J. Epidemiology of anti-tuberculosis drug resistance in a Chinese population: current situation and challenges ahead. *BMC Public Health* 2011; 11: 110.
- [14] Zhang L, Chen J, Shen X, Gui X, Mei J, De-Riemer K, Gao Q. Highly polymorphic variable-number tandem repeats loci for differentiating Beijing genotype strains of *Mycobacterium tuberculosis* in Shanghai, China. *FEMS Microbiol Lett* 2008; 282: 22-31.
- [15] Wang J, Liu Y, Zhang CL, Ji BY, Zhang LZ, Shao YZ, Jiang SL, Suzuki Y, Nakajima C, Fan CL. Genotypes and characteristics of clustering and drug-susceptibility of *Mycobacterium tuberculosis* isolates in Heilongjiang Province, China. *J Clin Microbiol* 2011; 49: 1354-62.
- [16] Somerville W, Thibert L, Schwartzman K, Behr MA. Extraction of *Mycobacterium tuberculosis* DNA: a question of containment. *J Clin Microbiol* 2005; 43: 2996-2997.
- [17] Dong H, Liu Z, Lv B, Zhang Y, Liu J, Zhao X, Liu J, Wan K. Spoligotypes of *Mycobacterium tuberculosis* from different provinces of China. *J Clin Microbiol* 2010; 48: 4102-4106.
- [18] Li Y, Liu H, Gao H, Wang Y, Zhang Z, Wang H, Cao J, Zhang S, Wu X, Sun Q. Characterization of *Mycobacterium tuberculosis* isolates from Shijiazhuang, China: genotypes and drug resistance. *Int J Clin Exp Pathol* 2016; 9: 1533-+.
- [19] Chan M, Borgdorff M, Yip C, De Haas P, Wong W, Kam K, Van Soolingen D. Seventy percent of the *Mycobacterium tuberculosis* isolates in Hong Kong represent the Beijing genotype. *Epidemiol Infect* 2001; 127: 169-171.
- [20] Dou HY, Tseng FC, Lin CW, Chang JR, Sun JR, Tsai WS, Lee SY, Su IJ, Lu JJ. Molecular epidemiology and evolutionary genetics of *Mycobacterium tuberculosis* in Taipei. *BMC Infect Dis* 2008; 8: 170.
- [21] Qiao K, Yang C, Luo T, Mei J, Gao Q. The application of variable number of tandem repeats in the microevolution study of *Mycobacterium tuberculosis* strain of Beijing genotype in Chongming Island, Shanghai. *Journal of Microbes and Infections* 2010; 5: 208-213.
- [22] Filliol I, Driscoll JR, Van Soolingen D, Kreiswirth BN, Kremer K, Valétudie G, Anh DD, Barlow R, Banerjee D, Bifani PJ. Global distribution of *Mycobacterium tuberculosis* spoligotypes. *Emerg Infect Dis* 2002; 8: 1347-1350.
- [23] Ei PW, Aung WW, Lee JS, Choi GE, Chang CL. Molecular strain typing of *mycobacterium tuberculosis*: a review of frequently used methods. *J Korean Med Sci* 2016; 31: 1673-1683.
- [24] Jiao WW, Mokrousov I, Sun GZ, Guo YJ, Vyazovaya A, Narvskaya O, Shen AD. Evaluation of new variable-number tandem-repeat systems for typing *mycobacterium tuberculosis* with Beijing genotype isolates from Beijing, China. *J Clin Microbiol* 2008; 46: 1045-1049.
- [25] Zhou A, Nawaz M, Xue X, Karakousis PC, Yao Y, Xu J. Molecular genotyping of *Mycobacterium tuberculosis* in Xi'an, China, using MIRU-VNTR typing. *Int J Tuberc Lung Dis* 2011; 15: 517-522.
- [26] Qiao L, Yang D, Xu W, Wang J, Bing LV, Yan S, Song H, Li G, Dong H, Wan K. Molecular typing of *mycobacterium tuberculosis* isolates circulating in Jiangsu province, China. *BMC Infect Dis* 2011; 11: 1-10.
- [27] Jiao WW, Mokrousov I, Sun GZ, Guo YJ, Vyazovaya A, Narvskaya O, Shen AD. Evaluation of new variable-number tandem-repeat systems for typing with Beijing genotype isolates from Beijing, China. *J Clin Microbiol* 2008; 46: 1045-9.

Mycobacterium tuberculosis in Xuzhou

Table S1. Genotyping with spoligotyping and 15-loci MIRU-VNTR

Strains	15-loci VNTR															Spoligotypes
	ETRA	ETRB	ETRC	ETRD	ETRE	MIRU10	MIRU16	MIRU23	MIRU26	MIRU27	MIRU39	MIRU40	Mtub21	Mtub30	Mtub39	
MTB060	9	2	4	3	5	3	3	6	7	2	3	3	3	2	2	Beijing
MTB142	9	2	4	3	5	4	2	5	7	3	3	3	5	4	4	Beijing
MTB012	2	2	4	4	6	2	1	5	3	3	2	4	3	2	2	Beijing
MTB050	4	2	4	7	5	3	2	5	5	3	2	3	4	2	4	Beijing
MTB119	2	1	4	5	5	2	2	5	7	3	3	3	3	2	4	Beijing
MTB252	3	1	4	7	5	3	3	5	9	3	3	3	3	2	4	Beijing
MTB004	3	1	4	3	6	3	5	5	7	2	2	3	2	2	4	Beijing
MTB042	3	2	4	4	6	3	4	5	7	3	2	3	3	2	4	Beijing
MTB113	2	2	4	2	4	2	4	6	8	3	2	3	3	2	4	Beijing
MTB115	2	2	4	3	5	3	4	6	8	3	2	3	3	2	4	Beijing
MTB005	4	2	7	4	6	3	5	5	8	4	1	4	1	2	4	Beijing
MTB207	4	2	4	3	6	3	5	5	7	3	2	3	1	2	2	Beijing
MTB062	4	2	4	3	5	3	2	5	7	3	3	4	3	2	2	Beijing
MTB204	4	2	4	3	6	3	2	5	5	3	2	3	3	2	2	Beijing
MTB168	4	2	4	3	5	3	2	5	6	3	2	3	1	2	2	Beijing
MTB069	4	1	3	4	5	2	2	5	6	2	3	3	2	2	5	Beijing
MTB049	3	2	4	4	5	3	2	5	5	3	3	3	4	2	5	Beijing
MTB253	4	2	4	3	5	3	2	5	5	3	3	3	4	2	4	Beijing
MTB101	4	2	4	3	5	3	2	5	7	3	3	3	4	2	4	Beijing
MTB211	3	2	4	4	6	3	2	5	7	3	3	3	4	2	4	Beijing
MTB175	4	2	4	3	5	3	2	5	6	2	2	3	3	2	4	Beijing
MTB176	4	2	4	3	5	4	2	5	7	2	3	3	3	2	4	Beijing
MTB171	2	2	4	2	4	2	2	5	4	2	2	3	2	2	4	Beijing
MTB169	3	2	4	3	5	5	2	5	7	3	3	3	1	2	4	Beijing
MTB100	4	2	4	2	6	3	3	5	6	3	2	3	1	2	5	Beijing
MTB170	3	2	4	3	5	3	3	6	7	3	2	3	1	2	4	Beijing
MTB284	4	2	4	3	5	3	3	5	6	3	2	3	1	2	4	Beijing
MTB208	4	3	4	3	5	3	3	5	6	2	2	3	2	2	4	Beijing
MTB261	4	2	4	2	6	3	2	5	7	3	1	3	1	2	4	Beijing
MTB112	4	1	3	2	5	3	2	5	8	2	3	3	3	2	4	Beijing
MTB203	4	2	3	2	5	3	2	5	8	2	2	3	3	2	2	Beijing
MTB163	4	2	4	2	3	2	2	5	7	3	2	3	3	2	2	Beijing
MTB209	3	2	2	1	3	1	2	5	7	2	2	3	3	2	2	Beijing
MTB114	4	2	4	2	4	2	1	5	7	3	2	3	3	2	5	NEW

Mycobacterium tuberculosis in Xuzhou

MTB173	4	2	4	3	5	2	1	5	7	2	2	3	2	2	4	Beijing
MTB174	4	1	4	2	4	2	1	5	7	2	2	3	2	2	4	Beijing
MTB162	3	2	4	2	4	2	1	5	7	3	1	3	1	2	4	Beijing
MTB064	2	2	3	2	4	2	2	5	8	3	2	3	3	2	4	Beijing
MTB164	2	2	2	1	3	2	2	5	8	3	2	3	3	2	4	Beijing
MTB111	2	2	4	2	4	1	2	5	7	2	2	3	3	2	4	Beijing
MTB152	3	2	4	2	4	1	2	5	7	2	2	3	3	2	4	Beijing-like
MTB177	2	1	3	2	4	1	2	5	7	2	2	3	3	2	4	Beijing
MTB285	3	1	4	3	5	1	2	5	8	3	2	3	3	2	4	Beijing
MTB251	4	2	4	2	4	2	2	5	8	2	2	3	3	2	4	Beijing
MTB286	4	2	4	2	4	1	2	5	8	3	2	3	3	2	4	Beijing
MTB172	2	1	4	1	3	1	2	5	7	2	3	3	2	2	2	Beijing
MTB260	2	1	4	2	4	2	4	7	8	4	4	3	1	2	4	Beijing
MTB262	3	3	7	2	4	2	2	5	6	2	1	3	1	2	4	Beijing
MTB043	4	1	4	3	3	2	2	5	3	3	3	3	3	2	4	Beijing
MTB061	4	2	4	2	3	2	2	5	1	3	2	3	3	2	4	Beijing
MTB118	3	2	4	2	3	2	2	4	2	3	2	3	3	2	4	Beijing
MTB044	3	2	4	3	5	3	2	5	3	3	4	4	3	2	5	Beijing
MTB045	3	2	4	3	5	3	2	5	3	3	3	3	3	2	4	Beijing
MTB046	4	2	4	4	6	3	2	5	3	3	4	3	4	2	4	Beijing
MTB048	4	2	4	2	6	2	2	5	4	3	3	4	4	2	4	Beijing
MTB120	4	2	4	2	4	2	2	5	5	3	3	3	4	2	4	Beijing
MTB121	4	2	4	2	4	2	2	5	5	3	3	4	4	2	5	Beijing
MTB047	4	2	4	3	5	2	2	5	4	3	3	3	4	2	5	Beijing
MTB201	4	2	4	2	4	2	2	5	4	3	3	3	4	2	6	Beijing
MTB200	4	2	4	2	4	4	2	5	4	3	3	3	4	2	6	Beijing
MTB117	4	2	4	3	5	2	2	4	2	3	2	3	3	2	2	Beijing
MTB063	4	2	4	3	6	3	2	5	3	3	3	3	4	2	2	Beijing
MTB212	4	2	4	3	6	2	2	5	4	3	3	3	4	2	2	MANU2
MTB213	4	2	4	3	5	2	2	5	4	3	4	3	4	2	2	Beijing
MTB158	4	2	4	3	5	3	2	5	5	5	4	4	6	4	2	Beijing
MTB074	4	1	3	3	5	3	4	5	3	3	4	3	5	5	4	Beijing
MTB082	4	2	4	3	5	3	3	6	3	3	3	3	5	4	4	U
MTB146	4	2	4	3	5	4	2	5	3	3	3	3	5	4	4	Beijing
MTB248	4	2	4	3	5	4	3	5	3	3	3	3	4	5	4	Beijing
MTB287	6	2	4	5	6	3	2	5	5	3	3	3	4	5	4	Beijing
MTB091	3	1	4	2	2	2	1	5	7	3	3	2	5	4	5	Beijing

Mycobacterium tuberculosis in Xuzhou

MTB130	3	2	4	3	2	2	1	5	8	3	2	3	5	5	4	Beijing
MTB154	6	2	4	5	5	3	2	5	8	4	4	2	6	4	2	Beijing
MTB030	4	2	4	2	4	5	4	5	8	4	4	2	6	4	4	Beijing
MTB001	4	1	4	2	6	4	3	5	7	3	2	3	4	5	2	Beijing
MTB057	4	2	4	3	6	5	4	6	7	3	2	2	5	4	2	Beijing
MTB070	3	2	4	1	6	6	4	5	7	3	3	3	4	5	4	Beijing
MTB007	2	2	4	3	6	3	3	5	7	3	4	3	4	5	3	Beijing
MTB006	2	2	4	2	4	4	3	5	6	3	3	3	4	5	2	Beijing
MTB184	2	2	4	3	5	4	2	5	7	3	3	3	5	4	2	Beijing
MTB052	4	2	4	3	5	6	2	5	5	3	3	3	4	5	3	Beijing
MTB266	3	2	4	3	5	6	2	5	7	3	3	3	5	4	4	Beijing
MTB277	3	2	4	4	8	6	2	5	8	4	3	2	6	4	4	Beijing
MTB095	4	2	7	3	5	2	2	5	7	3	4	4	5	4	4	Beijing
MTB132	6	2	6	2	4	2	2	5	8	3	3	3	5	5	4	Beijing
MTB008	4	2	2	1	6	3	3	5	6	3	3	3	4	5	3	Beijing
MTB165	4	2	4	1	6	3	2	5	5	3	3	3	4	5	4	Beijing
MTB022	3	2	4	4	6	3	5	5	7	3	3	4	5	5	4	Beijing
MTB024	4	2	4	4	6	3	5	5	7	3	2	3	5	5	5	Beijing
MTB072	3	2	4	4	6	3	4	5	7	3	2	3	4	5	4	Beijing
MTB017	4	2	4	3	6	3	5	5	7	3	2	4	5	5	3	Beijing
MTB015	4	1	4	3	5	3	4	5	7	3	4	3	5	5	3	Beijing
MTB013	4	2	4	3	5	3	4	5	7	3	3	3	4	5	3	Beijing
MTB014	4	2	4	3	5	3	4	5	7	3	3	3	5	5	3	Beijing
MTB026	5	2	4	3	5	3	4	5	7	3	3	3	5	5	4	Beijing
MTB010	5	2	4	4	6	3	4	5	7	3	3	3	4	5	3	Beijing
MTB011	4	1	4	3	6	3	4	5	7	3	3	3	4	5	3	Beijing
MTB059	4	2	4	3	6	3	4	5	7	3	4	3	4	5	3	Beijing
MTB023	4	2	4	4	6	3	5	5	7	3	3	3	5	5	4	Beijing
MTB019	4	2	4	3	6	3	5	5	7	3	4	3	5	5	4	Beijing
MTB020	4	2	4	3	6	3	5	5	7	3	3	3	5	5	5	Beijing
MTB018	4	2	4	3	6	3	5	5	7	3	3	3	5	5	4	Beijing
MTB222	4	2	4	3	6	3	5	5	7	3	3	3	5	5	4	Beijing
MTB016	4	2	4	3	5	3	5	5	7	3	3	3	5	5	3	Beijing
MTB221	4	2	4	3	5	3	5	5	8	3	3	3	5	5	4	Beijing
MTB075	4	2	4	3	5	2	4	5	7	3	3	3	5	5	4	Beijing
MTB205	4	2	4	3	5	2	4	5	6	3	3	3	5	5	4	Beijing
MTB073	3	2	4	3	5	2	4	5	7	3	3	3	4	5	5	Beijing

Mycobacterium tuberculosis in Xuzhou

MTB102	4	2	4	3	6	2	4	5	7	3	3	4	4	5	4	Beijing
MTB182	4	2	4	3	6	2	4	5	6	3	4	3	4	5	4	Beijing
MTB031	5	2	4	3	6	3	4	5	8	4	3	4	6	4	4	Beijing
MTB039	4	1	4	3	5	3	4	5	7	4	3	3	6	4	5	Beijing
MTB080	4	2	4	3	5	3	4	5	7	3	4	2	5	4	4	Beijing
MTB271	3	2	4	3	5	3	4	6	7	3	3	2	5	4	4	Beijing
MTB291	4	2	4	3	6	3	5	5	8	4	4	2	6	4	4	Beijing
MTB306	4	2	4	3	6	2	4	5	8	4	4	2	6	4	4	Beijing
MTB021	6	2	4	4	6	3	5	5	7	3	4	3	5	5	4	Beijing
MTB032	6	1	4	4	6	3	4	5	7	4	4	3	6	4	4	Beijing
MTB071	6	2	4	3	6	3	4	5	7	3	3	4	4	5	4	Beijing
MTB129	5	2	4	3	6	3	4	5	6	3	3	4	4	5	4	Beijing-like
MTB267	6	2	4	3	5	4	4	5	7	3	3	3	4	5	4	Beijing-like
MTB270	4	2	4	3	5	1	4	6	8	3	3	2	5	4	4	Beijing
MTB003	4	2	4	3	5	3	3	6	7	3	3	4	5	4	2	Beijing
MTB136	4	2	4	3	5	3	2	5	6	3	4	3	5	4	2	Beijing
MTB065	4	2	4	3	5	3	3	5	6	3	3	3	4	5	2	Beijing
MTB124	4	2	4	3	5	3	2	5	7	3	3	3	4	5	2	Beijing
MTB178	4	2	4	3	6	2	2	5	6	3	3	3	4	5	2	Beijing
MTB051	5	2	4	3	6	3	2	5	5	3	3	4	4	5	4	Beijing
MTB215	4	2	4	3	6	3	2	5	5	3	2	3	4	5	3	Beijing
MTB055	3	2	4	3	5	3	2	5	6	3	3	4	4	5	3	Beijing
MTB216	3	2	4	3	6	4	2	5	5	3	3	3	4	5	3	Beijing
MTB056	3	2	4	3	5	3	3	5	7	3	3	3	4	5	3	Beijing-like
MTB167	4	2	4	4	5	3	3	5	8	3	3	3	4	5	4	Beijing
MTB123	3	2	4	3	6	2	2	5	6	3	3	3	4	5	4	Beijing
MTB058	3	2	4	3	6	3	3	5	6	3	3	3	4	5	3	Beijing
MTB245	3	2	4	3	6	3	3	5	6	3	3	3	4	5	4	Beijing
MTB099	4	2	4	3	6	3	3	5	7	3	3	3	4	5	4	Beijing
MTB126	4	2	4	3	6	3	3	5	7	3	3	3	4	5	4	Beijing
MTB125	4	2	4	3	5	3	3	5	6	3	3	3	4	5	4	Beijing
MTB239	4	2	4	3	5	3	3	5	6	3	3	3	4	5	4	Beijing
MTB240	4	2	4	3	5	3	3	5	6	3	3	3	4	5	4	Beijing
MTB241	4	2	4	3	5	3	3	5	6	3	3	3	4	5	4	Beijing
MTB242	4	2	4	3	5	3	3	5	6	3	3	3	4	5	4	Beijing
MTB243	4	2	4	3	5	3	3	5	6	3	3	3	4	5	4	Beijing
MTB244	4	2	4	3	6	3	3	5	6	3	3	3	4	5	4	Beijing

Mycobacterium tuberculosis in Xuzhou

MTB255	4	3	4	3	6	4	3	5	6	3	3	3	4	5	4	Beijing
MTB002	4	2	4	3	6	3	2	5	5	3	3	3	4	5	4	Beijing
MTB254	4	2	4	3	6	3	2	5	5	3	3	3	4	5	4	Beijing
MTB214	4	2	4	3	5	3	2	5	5	3	3	3	4	5	4	Beijing
MTB237	4	2	4	3	5	3	2	5	6	3	3	3	4	5	4	Beijing
MTB238	4	2	4	3	5	3	2	5	6	3	3	3	4	5	4	Beijing
MTB288	4	2	4	3	5	3	2	5	6	3	3	3	4	5	4	Beijing-like
MTB289	3	2	4	3	5	3	2	5	6	3	3	3	4	5	4	NEW
MTB053	4	2	4	2	3	2	2	5	6	3	4	3	4	5	3	Beijing
MTB122	4	2	4	3	5	2	2	5	5	3	4	3	4	5	4	Beijing
MTB166	4	3	4	3	5	2	2	5	6	3	3	3	4	5	4	Beijing
MTB234	4	2	4	2	4	2	2	5	6	3	3	3	4	5	4	Beijing
MTB235	4	2	4	2	4	2	2	5	6	3	3	3	4	5	4	Beijing
MTB236	4	1	3	3	4	2	2	5	6	3	3	3	4	5	4	Beijing
MTB263	4	2	2	2	4	2	2	5	6	3	3	3	4	5	4	Beijing
MTB009	4	2	4	2	4	4	3	5	6	3	3	4	4	5	3	Beijing
MTB133	4	2	4	2	4	4	2	5	7	3	3	4	5	5	4	Beijing
MTB068	4	2	4	3	5	4	4	6	7	3	3	4	5	4	4	Beijing
MTB088	4	2	4	3	5	4	4	6	7	3	3	2	5	4	4	Beijing
MTB269	4	2	4	3	6	5	4	6	7	3	3	2	5	4	4	Beijing
MTB127	4	2	4	2	6	4	3	5	6	3	4	3	4	5	4	Beijing
MTB290	3	2	4	2	6	4	3	5	6	3	3	3	4	5	4	Beijing
MTB180	4	2	4	3	6	5	4	5	7	3	3	3	4	5	4	Beijing
MTB181	3	2	4	3	6	5	4	5	7	3	3	3	4	5	4	Beijing
MTB249	4	1	4	2	6	5	4	5	7	3	3	3	4	5	4	Beijing
MTB128	4	2	4	3	5	4	3	5	7	3	3	3	4	5	4	Beijing
MTB246	4	2	4	3	5	4	3	5	7	3	3	3	4	5	4	Beijing
MTB247	4	1	4	3	5	4	3	5	7	3	3	3	4	5	4	Beijing
MTB268	4	2	4	3	5	4	4	5	8	3	3	3	4	5	4	Beijing
MTB296	4	1	4	3	5	4	4	5	7	3	3	3	4	5	4	Beijing
MTB025	4	2	4	3	6	2	1	5	7	3	3	3	5	5	4	Beijing
MTB034	4	1	4	3	6	2	1	4	7	4	4	3	6	4	4	Beijing
MTB028	5	2	4	4	6	3	2	5	7	3	3	3	5	4	5	Beijing
MTB257	6	2	4	3	5	2	2	5	7	3	3	3	5	4	4	Beijing
MTB159	5	2	4	3	6	3	2	5	5	3	3	3	6	4	4	Beijing
MTB161	6	2	4	3	6	2	2	5	6	3	4	4	7	4	4	Beijing

Mycobacterium tuberculosis in Xuzhou

MTB272	4	1	3	3	6	2	2	7	7	3	4	2	5	4	4	Beijing
MTB094	4	2	4	3	5	2	2	5	6	3	3	2	5	4	5	Beijing
MTB081	3	2	4	3	5	2	2	5	7	3	4	2	5	4	5	Beijing
MTB093	4	2	4	3	5	2	2	5	7	3	4	2	5	4	4	Beijing
MTB273	4	2	4	3	5	3	2	5	7	3	4	2	5	4	4	Beijing
MTB105	3	2	4	3	6	3	2	5	7	3	4	2	5	4	5	Beijing
MTB224	2	2	4	3	6	3	2	5	7	3	4	2	5	4	4	Beijing
MTB148	4	2	4	3	6	2	2	5	8	4	3	2	6	4	4	Beijing
MTB067	5	2	4	3	6	3	2	5	8	4	4	2	6	4	4	Beijing
MTB274	5	2	4	4	6	3	2	5	8	4	3	2	6	4	4	Beijing
MTB040	4	2	4	3	5	3	2	5	6	4	4	3	6	4	4	Beijing
MTB157	3	2	4	3	5	3	2	5	5	4	4	2	6	4	4	Beijing
MTB191	4	2	4	3	5	4	2	5	7	4	4	3	7	4	5	Beijing
MTB318	4	2	4	3	5	4	2	5	7	3	4	2	6	4	5	Beijing
MTB078	4	2	3	3	4	3	2	6	7	3	4	3	5	4	4	Beijing
MTB027	4	2	4	3	5	3	2	5	7	3	3	4	5	4	4	Beijing
MTB137	3	2	4	3	5	3	2	5	7	3	3	4	5	4	4	Beijing
MTB135	4	2	4	3	5	3	2	5	7	3	3	3	5	5	4	Beijing
MTB134	3	2	4	3	5	3	2	5	7	3	3	3	5	5	4	Beijing
MTB139	3	2	4	3	5	3	2	5	7	3	3	3	5	4	4	Beijing
MTB079	4	2	4	3	5	3	2	6	7	3	3	3	5	4	4	Beijing
MTB138	4	2	4	3	5	3	2	5	7	3	3	3	5	4	4	Beijing
MTB218	4	2	4	3	5	3	2	6	6	3	3	3	5	4	4	Beijing
MTB076	4	2	4	3	5	2	2	6	7	3	3	4	5	4	4	Beijing
MTB029	4	1	4	3	5	2	2	5	7	3	3	3	5	4	4	Beijing
MTB223	4	2	4	3	5	2	2	5	8	3	3	3	5	4	4	Beijing
MTB298	4	2	4	3	5	2	2	5	7	3	3	3	5	4	4	Beijing
MTB104	4	2	4	2	5	3	3	6	7	3	3	3	5	4	4	Beijing
MTB083	3	2	4	3	5	3	3	6	7	3	3	3	5	4	4	Beijing
MTB219	4	2	4	3	5	3	3	6	7	3	3	3	5	4	4	Beijing
MTB228	4	2	4	3	5	3	3	6	8	4	3	3	6	4	4	Beijing
MTB141	3	2	4	2	4	4	2	5	6	3	3	3	5	4	4	Beijing
MTB103	3	2	4	3	5	4	2	5	7	3	4	3	5	5	4	Beijing
MTB143	3	2	4	3	5	4	2	5	7	3	4	3	5	4	4	Beijing
MTB145	3	2	4	3	5	4	2	5	7	3	3	3	5	4	4	Beijing
MTB183	3	2	4	3	5	4	2	5	7	3	3	3	5	4	4	Beijing

Mycobacterium tuberculosis in Xuzhou

MTB188	3	2	4	3	5	4	2	5	7	3	3	3	5	4	4	Beijing
MTB186	3	2	4	3	5	4	2	5	6	3	3	3	5	4	4	Beijing
MTB140	4	2	4	3	6	4	2	5	7	3	3	3	5	4	5	Beijing
MTB144	4	2	4	3	5	4	2	5	8	3	3	3	5	4	4	Beijing
MTB187	4	2	4	3	5	4	2	5	7	3	3	3	5	4	4	Beijing
MTB185	4	2	4	3	5	4	2	5	7	3	2	3	5	4	4	Beijing
MTB264	4	2	4	2	5	4	2	5	7	3	3	3	5	4	4	Beijing
MTB265	4	2	4	2	5	4	2	5	8	3	3	3	5	4	4	Beijing
MTB090	3	2	4	3	5	3	3	4	7	3	4	3	5	4	4	Beijing
MTB037	3	2	4	3	5	3	3	5	8	4	4	4	6	4	4	Beijing
MTB312	4	2	4	3	5	3	3	6	8	4	4	4	6	4	5	Beijing
MTB227	3	2	4	3	5	3	2	5	7	4	4	4	6	4	4	Beijing
MTB315	3	2	4	2	6	3	3	5	8	4	4	4	6	4	5	Beijing
MTB035	4	2	4	3	6	4	2	5	8	4	3	4	6	4	4	Beijing
MTB225	4	2	4	3	6	3	2	5	7	4	3	4	6	4	4	Beijing
MTB276	4	2	4	2	6	4	2	5	8	4	4	4	6	4	4	Beijing
MTB066	4	2	4	3	5	3	2	5	9	4	4	4	6	4	4	Beijing
MTB307	4	2	4	3	5	3	2	5	8	4	4	4	6	4	4	Beijing
MTB292	4	2	4	3	6	3	2	5	8	4	4	4	6	4	4	Beijing
MTB259	4	2	4	3	5	4	2	5	8	4	4	3	6	4	4	Beijing
MTB319	4	2	4	3	5	4	2	5	8	4	4	4	6	4	4	Beijing
MTB320	4	2	4	3	5	4	2	5	9	4	4	4	6	4	5	Beijing
MTB202	4	2	4	3	5	4	2	5	7	3	4	3	5	4	6	Beijing
MTB324	3	2	4	3	5	3	2	6	7	3	3	3	5	4	6	Beijing
MTB036	4	1	4	2	6	4	3	5	7	4	4	3	6	4	5	Beijing
MTB293	6	1	4	2	6	4	3	6	8	4	3	3	6	4	4	Beijing
MTB275	4	2	4	1	6	3	2	5	8	4	4	2	6	4	4	Beijing
MTB084	3	2	4	3	5	3	3	6	7	3	4	1	5	4	4	Beijing
MTB085	4	2	4	3	5	3	3	6	7	3	3	1	5	4	4	Beijing
MTB086	4	2	4	3	5	3	3	6	7	3	3	1	5	4	4	Beijing
MTB087	4	2	4	3	5	4	3	6	7	3	3	1	5	4	4	Beijing
MTB089	4	2	4	3	5	3	3	6	7	3	3	2	5	4	5	Beijing
MTB325	4	2	4	2	6	3	3	6	7	3	4	2	5	4	6	Beijing
MTB038	3	2	4	3	5	3	3	5	9	4	4	2	6	4	4	Beijing
MTB098	3	2	4	3	6	3	3	5	8	4	4	2	6	4	4	Beijing
MTB108	4	2	4	3	6	3	3	5	8	4	4	2	6	4	4	Beijing
MTB226	4	2	4	2	6	4	3	5	8	4	4	2	6	4	4	Beijing

Mycobacterium tuberculosis in Xuzhou

MTB304	4	1	3	2	5	3	3	5	8	4	4	2	6	4	5	Beijing
MTB309	4	1	4	3	5	3	3	5	9	4	4	2	6	4	5	Beijing
MTB229	2	1	4	3	5	3	4	6	8	4	4	2	6	4	4	Beijing
MTB305	3	2	4	3	5	4	4	5	8	4	4	2	6	4	5	Beijing
MTB311	2	2	4	3	5	3	3	6	8	4	3	2	6	4	4	Beijing
MTB313	2	2	4	3	6	4	3	6	9	4	4	3	6	4	4	Beijing
MTB097	2	2	4	4	5	3	2	5	8	4	3	2	5	4	5	Beijing
MTB303	3	1	4	3	5	3	2	5	9	4	3	2	6	4	5	Beijing
MTB150	2	2	4	2	6	4	2	5	7	2	4	4	6	4	4	Beijing
MTB295	2	2	4	2	6	4	2	5	8	4	4	4	6	4	4	Beijing
MTB308	3	2	6	2	4	4	2	5	8	4	4	4	6	4	4	Beijing
MTB316	3	2	4	2	4	4	2	5	9	4	4	4	6	4	4	Beijing
MTB054	2	2	4	1	3	2	2	5	7	3	3	3	4	5	3	Beijing
MTB153	3	1	4	2	4	2	2	5	7	3	3	3	4	5	4	Beijing
MTB179	3	2	4	2	3	2	2	5	7	3	4	3	4	5	4	Beijing
MTB151	3	2	4	3	3	2	2	5	7	3	4	2	7	4	5	Beijing
MTB041	4	2	4	3	3	2	1	5	7	4	4	4	6	4	4	T1
MTB092	4	2	4	2	4	1	2	5	7	3	4	2	5	4	5	T1
MTB096	4	1	4	2	4	2	2	5	7	3	4	2	5	4	4	T1
MTB147	3	2	4	3	5	1	2	5	8	4	4	2	6	4	4	T1
MTB155	3	2	4	2	4	1	2	5	8	4	4	3	6	4	4	T1
MTB230	3	1	4	3	5	2	2	5	8	4	4	3	6	4	4	H3
MTB107	3	2	4	2	4	2	2	5	7	4	3	2	6	4	4	T2
MTB220	3	2	4	2	4	2	2	5	8	4	4	2	6	4	4	T1
MTB278	4	2	4	2	4	2	2	5	8	4	4	2	6	4	4	T1
MTB294	4	2	4	2	3	2	2	5	8	4	4	2	6	4	4	T1
MTB156	4	2	4	3	5	2	2	5	9	4	3	4	6	4	4	T1
MTB033	4	2	4	2	4	2	2	6	8	4	4	4	6	4	5	T1
MTB106	4	2	4	2	4	2	2	5	8	4	4	4	5	4	4	T1
MTB300	4	2	4	2	4	2	2	5	8	4	4	4	6	4	4	T1-T2
MTB310	4	2	4	2	4	1	2	5	8	4	4	4	6	4	5	T1
MTB131	4	2	4	2	3	2	2	5	7	3	3	3	5	5	5	T1
MTB077	4	2	4	2	4	2	2	6	7	3	3	3	5	4	4	T1
MTB217	4	2	4	2	4	2	2	5	7	3	3	3	5	4	4	T1
MTB297	4	2	4	2	4	2	2	5	7	3	3	3	5	4	4	T2
MTB256	3	2	4	2	3	2	2	5	7	3	3	3	5	4	4	NEW

Mycobacterium tuberculosis in Xuzhou

MTB190	4	2	4	2	4	2	2	5	8	3	3	4	7	4	4	NEW
MTB322	4	2	4	2	4	2	2	5	8	2	4	4	6	4	5	T2
MTB314	6	2	4	2	4	2	2	5	8	4	4	4	6	4	5	T2
MTB258	4	2	2	2	4	2	2	5	8	4	4	2	6	4	4	T2
MTB299	3	2	2	2	4	2	2	5	8	4	4	2	6	4	5	NEW
MTB301	3	2	2	2	4	2	2	5	9	4	4	2	6	4	5	T2
MTB109	2	2	4	4	5	2	2	5	4	2	4	3	6	4	4	T2
MTB231	2	2	4	5	5	2	2	5	6	2	3	4	6	4	4	T2
MTB110	4	2	4	2	4	2	2	5	5	2	4	4	6	4	4	T2
MTB149	4	1	4	2	4	2	2	5	6	2	4	3	6	4	4	T2
MTB317	4	2	2	2	4	2	2	5	6	3	4	4	6	4	5	T2
MTB192	4	2	4	2	6	2	2	5	7	2	2	5	7	4	4	T1-T2
MTB193	3	2	4	2	6	2	2	5	6	3	3	5	7	4	5	T5
MTB194	4	2	4	2	5	3	2	5	7	3	3	5	8	4	4	U
MTB195	4	2	4	2	4	2	2	5	7	3	3	5	8	4	4	U
MTB250	4	2	4	2	4	2	2	5	6	3	3	5	7	4	4	U
MTB197	4	2	2	3	5	3	3	5	7	2	4	5	8	4	4	H3
MTB196	3	2	4	3	5	3	3	5	6	3	4	5	8	4	5	H3
MTB281	4	2	4	3	5	3	2	5	6	3	4	4	7	4	4	MANU2
MTB233	2	2	4	2	3	2	2	5	5	3	4	4	7	4	4	MANU2
MTB198	2	2	3	2	4	2	1	5	7	2	4	5	8	4	6	NEW
MTB189	1	1	3	2	4	2	2	3	8	3	4	3	7	4	5	NEW
MTB160	2	2	4	3	6	1	2	4	8	3	4	4	7	4	5	NEW
MTB232	2	2	4	2	4	2	2	5	9	3	4	3	7	4	4	NEW
MTB323	2	1	4	2	4	2	2	5	8	3	4	4	7	4	4	NEW
MTB302	2	2	4	2	4	2	2	5	8	4	4	4	6	4	4	NEW
MTB282	2	2	4	3	4	3	2	5	7	3	4	4	7	4	4	NEW
MTB280	2	2	4	2	4	2	2	5	7	2	3	3	6	4	4	Beijing
MTB321	2	2	4	2	4	2	2	5	7	2	4	4	6	4	4	Beijing
MTB279	2	1	3	3	5	1	4	5	8	1	4	4	6	4	4	NEW
MTB283	3	1	4	3	5	3	4	5	8	2	1	5	7	4	4	NEW
MTB116	4	2	4	3	5	4	3	5	1	3	3	4	3	2	4	NEW
MTB199	4	2	4	3	5	3	4	5	3	3	3	3	1	2	2	NEW
MTB206	6	2	4	4	6	4	4	4	2	3	3	3	3	2	2	NEW
MTB210	2	2	3	1	5	2	2	4	2	1	2	3	2	2	6	NEW