

Genotypic diversity of *Mycobacterium tuberculosis* strains in Myanmar

Thanda Tun, Khin Saw Aye, Wint Wint Nyunt, John A. Crump, Chie Nakajima, Yasuhiko Suzuki, Kyi Kyi Thinn, Gregory M. Cook & Htin Lin Aung

To cite this article: Thanda Tun, Khin Saw Aye, Wint Wint Nyunt, John A. Crump, Chie Nakajima, Yasuhiko Suzuki, Kyi Kyi Thinn, Gregory M. Cook & Htin Lin Aung (2016): Genotypic diversity of *Mycobacterium tuberculosis* strains in Myanmar, *Infectious Diseases*, DOI: [10.1080/23744235.2016.1231419](https://doi.org/10.1080/23744235.2016.1231419)

To link to this article: <http://dx.doi.org/10.1080/23744235.2016.1231419>



Published online: 19 Sep 2016.



Submit your article to this journal [↗](#)



View related articles [↗](#)



View Crossmark data [↗](#)

LETTER TO THE EDITOR

Genotypic diversity of *Mycobacterium tuberculosis* strains in Myanmar

Sir,

The Beijing lineage of *Mycobacterium tuberculosis* (*MTB*) comprises a family of strains with common genetic characteristics and is the most prominent lineage of *MTB* in East Asia. In line with that, it was recently reported in the present journal that the Beijing family strains accounted for 81% and 57% in Jiangsu Province [1] and Xinjiang Province [2] of China, respectively. In the latter study, the *MTB* isolates were genetically diverse with minimal clustering and the authors hypothesized that a majority of TB cases in Xinjiang may be explained by non-recent transmission and endogenous reactivation.

Myanmar is one of 22 high tuberculosis (TB) burden countries with a high prevalence of drug-resistant *MTB*. [3] Myanmar's common borders with two high TB burden countries, China and India, which together account for one-third of the world's TB cases. [3] Myanmar is administratively divided into 14 states and regions. Despite several reports on the distribution of *MTB* genotypes in neighbouring countries, data on the genotypic diversity of *MTB* in Myanmar are only available from Yangon, the country's largest city in Yangon Region. [4]

Here, we report the genotypic diversity of *MTB* strains more widely in Myanmar. We collected sputum samples with acid-fast bacilli (AFB) grading 2+ or 3+ from 72 patients from 10 out of 14 administrative states/regions that were referred to the National Tuberculosis Reference Laboratory (NTRL), Yangon, between October 2012 and August 2013. Spoligotyping was performed, and the results were compared as described previously [4,5] with the Spoligo-International Types (SIT) numbers and the sublineages described in the SpolDB4

database. [6] A total of 16 SITs were identified among the 72 isolates as shown in Table 1. Among these, 55 (76.4%) strains corresponded to Beijing family (SIT1), 7 (9.8%) to EAI family (EAI6_BGD1, EAI3_IND, EA15), 4 (5.6%) to CAS family (CAS, CAS1-DELHI), 2 (2.8%) to Beijing-like family, one (1.4%) to LAM family (LAM9), one (1.4%) to KILI family, while two strains (2.8%) were of undefined (U) origin. We further validated 14/72 (19.4%) of spoligotyping results using whole-genome sequencing (WGS). [7] The SIT1 of Beijing lineage was the most prevalent SIT among the isolates in this study.

Beijing lineage strains are common in East Asia, particularly in China and the Southeast Asian countries of Thailand and Vietnam. Similarly, the EAI6_BGD1 and EAI3_IND, CAS1-DELHI sublineages are mostly found in Bangladesh and India. The presence of strains prevalent in neighbouring countries in Myanmar could be attributed to migration, trans-border trading and tourism.

Isolates were tested for drug resistance with phenotypic drug susceptibility testing of the first-line anti-TB drugs; isoniazid (INH), rifampicin (RIF), ethambutol (EMB) and streptomycin (STR). Of 72 isolates, 58 (80.6%) were resistant to INH and RIF. Of 58 multidrug-resistant tuberculosis (MDR-TB) strains, 49 (84.5%) belonged to the SIT1 Beijing family. Of Beijing strains, 49 (89%) of 55 were MDR whereas of non-Beijing strains, 9 (53%) of 17 were MDR (p value $< .001$).

MDR SIT1 Beijing family strains are common and widespread in Myanmar. Rapid diagnosis and effective treatment, as described previously, [7] is needed to control further expansion of this clone in the country.

Acknowledgements

We thank the staff from the National TB Reference Laboratory in Yangon, Myanmar for technical support. Ethical approval (12/11041) for this study was given by the Research and Ethical Committee of the University of Medicine 1, Yangon, Myanmar.

Disclosure statement

The authors declared no conflicts of interest.

Funding

This work was supported in part by the Japan Initiative for Global Research Network on Infectious Diseases (J-GRID) from Japan Agency for Medical Research and development, AMED, in part by a special research grant from the Japan Agency for Medical Research and Development (AMED), Grant Number 16fk0108302h0003, and in part by the grant from MEXT for the Joint Research Program of the Research Center for Zoonosis Control, Hokkaido University. TT received funding for travel and accommodation from the University of Otago Development Office to perform data analysis at the University of Otago, Dunedin, New Zealand. HLA was supported by the e-ASIA (East Asia) Joint Research Programme Grant from the New Zealand Health Research Council [grant number 15/648].

ORCID

John A. Crump  <http://orcid.org/0000-0002-4529-102X>
HtinLin Aung  <http://orcid.org/0000-0002-0465-6256>


References

- [1] Lu W, Lu B, Liu Q, et al. Genotypes of *Mycobacterium tuberculosis* isolates in rural China: using MIRU-VNTR and spoligotyping methods. *Scand J Infect Dis*. 2014;46:98–106.
- [2] Yuan L, Mi L, Li Y, et al. Genotypic characteristics of *Mycobacterium tuberculosis* circulating in Xinjiang, China. *Infect Dis (Lond)*. 2016;48:108–115.
- [3] World Health Organization [Internet]. WHO Global Tuberculosis Report 2015; 2015. Available from: http://www.who.int/tb/publications/global_report/en/
- [4] Phyu S, Stavrum R, Lwin T, et al. Predominance of *Mycobacterium tuberculosis* EAI and Beijing lineages in Yangon, Myanmar. *J Clin Microbiol*. 2009;47:335–344.
- [5] Hang'ombe MB, Munyeme M, Nakajima C, et al. *Mycobacterium bovis* infection at the interface between domestic and wild animals in Zambia. *BMC Vet Res*. 2012;8:221.
- [6] Brudey K, Driscoll JR, Rigouts L, et al. *Mycobacterium tuberculosis* complex genetic diversity: mining the fourth international spoligotyping database (SpolDB4) for classification, population genetics and epidemiology. *BMC Microbiol*. 2006;6:23.
- [7] Aung HL, Tun T, Moradigaravand D, et al. Whole-genome sequencing of multidrug-resistant *Mycobacterium tuberculosis* isolates from Myanmar. *J Glob Antimicrob Resist*. 2016;6:113–117.

Thanda Tun
National Health Laboratory, Ministry of Health and Sports,
Yangon, Myanmar



Khin Saw Aye
Department of Medical Research, Ministry of Health and
Sports, Yangon, Myanmar

Wint Wint Nyunt
National Tuberculosis Reference Laboratory, Ministry of
Health and Sports, Yangon, Myanmar

John A. Crump 
Centre for International Health, Dunedin School of
Medicine, University of Otago, Dunedin, New Zealand

Chie Nakajima and Yasuhiko Suzuki
Hokkaido University Research
Centre for Zoonosis Control, Sapporo, Japan
Global Institution for Collaborative Research and Education
(GI-CoRE), Hokkaido University, Sapporo, Japan

Kyi Kyi Thinn
Department of Microbiology
University of Medicine 1, Yangon, Myanmar

Gregory M. Cook and Htin Lin Aung 
Department of Microbiology and Immunology, Otago
School of Medical Sciences, University of Otago
Dunedin, New Zealand
 htin.aung@otago.ac.nz

Received 16 August 2016; revised 21 August 2016;
accepted 24 August 2016