

LETTER TO EDITOR

Tuberculosis screening and AMR gene profiling in Malaysia's migrant worker communities

Hui-min NEOH^{1*}, Fariha Adriana FADZIL¹, Nurul Amirah MOHAMAD FAROOK¹, Muhammad Azreen MAT HUSIN¹, Adrian Anthony PEREIRA², Siti Roszilawati RAMLI³ and Kiaticchai FAKSRI⁴

¹UKM Medical Molecular Biology Institute (UMBI), Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; ²North South Initiative (NSI), Selangor, Malaysia; ³Bacteriology Unit, Infectious Disease Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health, Malaysia; ⁴Department of Microbiology, Faculty of Medicine, Khon Kaen University, Khon Kaen, Thailand

Dear Editor,

Recent reports have shown an increase in tuberculosis cases in Malaysia, with cases exceeding 3,000 in the first and second quarters of 2026. As many as 500 cases were reported in a single week in February 2026.¹ Tuberculosis is not new to Malaysia; cases of the disease were first reported in the early years of the 20th century.² Pulmonary tuberculosis spreads mainly in crowded and poorly ventilated areas, leaving marginalised communities (such as economic migrants living in overcrowded dormitories with poor hygiene standards) exposed to a higher risk of the disease.³

We carried out a cross-sectional study to determine the silent carriage of *Mycobacterium tuberculosis* in the sputum samples of 258 economic migrants (159 Indonesians, 51 Bangladeshis, and 48 Nepalis) working in Klang Valley, Malaysia, from December 2023 to May 2024. Informed consent was obtained from all study subjects who participated in the investigation via liaison with the North-South Initiative, a Malaysia-based non-profit organisation that works to promote sustainable development in Malaysia and other developing countries.

Obtained samples were cultured onto Löwenstein-Jensen (LJ) medium. Colonies obtained from positive cultures were subjected to acid-fast bacilli staining and PCR confirmation of *M. tuberculosis*. In addition, DNA was extracted from the sputum samples for 16S rRNA next-generation sequencing (16S-NGS) on the Illumina NovaSeq 6000 platform. Extracted DNA was also subjected to PCR amplification for the detection of five antimicrobial resistance (AMR) genes (*mecA*, *ermB*, *mefA*, *blaZ*, and *tetK*) associated with drug-resistant bacteria.⁴ These genes code for resistance to antibiotics commonly prescribed in primary clinics in Malaysia.

Both LJ culture and 16SNGS results were negative for *M. tuberculosis* across all samples. 16SNGS results showed an abundance of oropharyngeal flora (*Rothia* and *Streptococcus spp.*) commonly reported in healthy individuals. Unexpectedly, a high prevalence of the macrolide resistance gene *mefA* was detected (>90% in Indonesian and Bangladeshi participants), while *ermB* (>50% in Nepalese participants) and *blaZ* (>17% in Indonesian participants) showed moderate prevalence. *ermB* and *blaZ* are associated with resistance to macrolides and penicillin, respectively. These antibiotics are commonly prescribed in primary clinics for upper respiratory tract infections.

The issue of antibiotic overprescription in primary clinics has been highlighted before; it is estimated that bacterial infections requiring antibiotic treatment account for less than 5% of patients presenting with upper respiratory tract infections.⁵ Visits to these clinics are often one-off; therefore, antibiotics are mostly prescribed prior to the confirmation of bacterial or viral infections. This may lead to increased antibiotic selection pressure in the community and could be inadvertently linked to the findings of high macrolide resistance genes in our study samples. While it remains to be determined whether individuals harbouring AMR genes in their sputum samples will experience treatment failure with the associated antibiotic(s), the high prevalence of these genes in community samples is a matter of concern and should be further investigated.

*Address for correspondence: Hui-min Neoh, UKM Medical Molecular Biology Institute (UMBI), Universiti Kebangsaan Malaysia, 56000, Cheras, Kuala Lumpur, Malaysia. +60391456321 (HMN); Email: hui-min@hctm.ukm.edu.my

In summary, no evidence of asymptomatic carriage of *Mycobacterium tuberculosis* was detected in this preliminary study of economic migrants in the Klang Valley. However, the high prevalence of macrolide resistance genes in sputum samples from the community warrants further investigation.

Keywords: tuberculosis screening, macrolide resistance, migrant communities

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