## Ending tuberculosis by 2030: understanding the transmission

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Tuberculosis (TB), a preventable and curable disease, remains a leading cause of global morbidity and mortality, with over 10 million people infected and 1.6 million dying from it in 2021.1 Even with a sufficiently high bacterial burden for detection by sputum smear microscopy, up to 25% of the cases lack clinical symptoms of TB. Forty-three percent of the burden of TB incidence and upward trends in death occur in the Southeast Asia region, home to 26% of the world's population.<sup>1</sup> Furthermore, the number of notifications of people diagnosed with TB has decreased due to the unprecedented impact of COVID-related disruptions on essential TB services, diverting routine health care staff from responding pandemic.<sup>1,2</sup> China, home to 18.5% of the global population and with rapid urbanization, has the second highest TB burden among 30 high-TB burden countries and high deaths worldwide.3 Rapid urbanization, low education in rural areas, and internal migration pose additional challenges to TB control activities in China. This paper possesses a significant impact on understanding the dynamics of transmission for clinicians, the utilization of the implementation research evidence, and the opportunity to study the further unanswered questions for early diagnosis of subclinical cases for the control and elimination of TB.4

In The Lancet Regional Health—Western Pacific, Meng Li and colleagues provided a comprehensive view of the pattern of transmission dynamics of TB by enrolling a large population and comparing migrants with the local residents based on a 10-year prospective population-based genomic epidemiological and spatial analysis study in Songjiang, Shanghai, China.<sup>4</sup> The article highlighted the importance of early diagnosis of subclinical cases among the young migrants transmitting the disease to urban residents for the changing urban-rural distribution of TB, as observed in discrete and super-spread transmission in another low-incidence countries.<sup>5</sup> At present, the clinicians in the community make a diagnosis of TB based on clinical findings including coughing for more than two weeks, chest

*E-mail address:* basudevpandey@nagasaki-u.ac.jp (B.D. Pandey). © 2023 The Author(s). Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/ licenses/by-nc-nd/4.0/). pain, weight loss, night sweats, a chest radiograph, and confirmation by sputum smear and culture. The authors highlighted that genomic epidemiological studies could be a better tool for providing information on TB burden and formulating better policies for reducing burden and ending TB by supporting clinical scientists. The study finds that 5.4% have MDR, which is higher among the female migrants, and that there are no significant differences in cluster rate or factors associated with genomic clustering among the residents and migrants. However, the logistic regression finds a significant association with genomic clustering in younger people engaged in physical labor who are at higher risk groups compared to the residents.6 This fact indicated the studies needed to focus more on the mobile younger migrants and local residents for an effective control strategy that eventually supports improving current clinical practice by focusing on early diagnosis in preclinical and asymptomatic patients.6

The study may have had less impact due to the limitations of the temporal and spatial nature of the study, which could have affected the clustering rate as well as the transmission dynamics of migrants given the shorter residency of young labor migrants in the city. The study also demonstrated that clustering is more prevalent among local residents compared to labor migrants, suggesting there is local transmission going on.6 The study showed 15.6% of clustered patients with confirmed epidemiological links in both residents and migrants, where few cases were from the same working place, lower than rural areas. The transmission monitoring system is supposed to be established for the early and prompt detection and investigation of cases for transmission intervention.7,8 The study highlights risk increases for genomic clustering residing in close proximity, and hot spots were largely unchanged over the past 10 years. Understanding the route of transmission actually happening at the work site in the pre-clinical stage among young and healthy mobile individuals who might resist early symptoms is important information for clinical scientists. Shanghai is the most populous city with the best TB prevention and control program, which reduces TB incidence by 30% per 100,000 people. However, there have been no significant reductions in the local transmission of TB patients in Songjiang from 2011 to 2020.4 The current study lacks the detail needed to study the transmission chain in Songjjang and identify the actual hot spots. New strategies based on specific



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characteristics of the local TB burden to enhance case detection of super-spread infection and thereby interrupt transmission. On the basis of epidemiological findings, the gaps in the current findings could be addressed, and further studies in other cities will provide a better understanding of targeted strategies for high risk and local burdens of disease. The temporal and geographical limitations of the study need to be addressed by estimating the extent of local transmission. The most important factor in knowing the TB strains is identifying and intensifying the diagnosis of latent or subclinical infections by enhancing case detection and containing spread by interrupting transmission to end the TB Epidemic by 2030 in China and the region.<sup>7,8</sup>

## Contributors

All authors contributed equally to writing this commentary.

## Declaration of interests

We declare no competing interests.

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