Editorial

Refining Tuberculosis Control Strategies: From Precision Diagnosis to Life-course Management

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Tuberculosis (TB) remains one of the most persistent and formidable public health challenges globally. Despite the ambitious targets set by the World Health Organization End TB Strategy, the path to elimination is fraught with obstacles. According to the *Global Tuberculosis Report 2025*, while global incidence has been stabilization, the burden of multidrug-resistant tuberculosis (MDR-TB) and the long-term sequelae facing survivors continue to hinder progress[1]. As a high-burden country, China stands at the forefront of this battle, navigating a shifting epidemiological landscape that demands adaptive and innovative responses[2]. The traditional paradigm, which focuses predominantly on bacteriological cure, is no longer sufficient. To truly "End TB," control strategies must evolve into a comprehensive continuum of care that encompasses early precision diagnosis, targeted protection of vulnerable demographics, and life-course management of respiratory health[3].

The complexity of the modern TB epidemic is starkly illustrated by the rising threat of antimicrobial resistance (AMR) in younger populations. In this issue of *Biomedical and Environmental Sciences*, Wang et al. shed light on a critical but often overlooked demographic: adolescents and young adults[4]. Their study on drug-resistant pulmonary TB among patients aged 10–24 years reveals concerning statistics, with MDR-TB accounting for 3.18%–3.76% of new cases and over 11% of previously treated cases. The identification of high-frequency mutations, such as Ser315Thr in the *katG* gene and Ser450Leu in the *rpoB* gene, delineates the predominant molecular mechanisms of resistance in this group. These findings are alarming not only because of the clinical difficulty in treating MDR-TB but also due to the social dynamics of this age group. Adolescents, often congregating in schools and social venues, represent potential "super-spreaders" within the community. The stability of MDR-TB rates observed over the study period suggests that current interventions have not yet effectively disrupted transmission chains in this specific population. This study serves as a clarion call for age-disaggregated surveillance and suggests that school-based screening programs and targeted molecular epidemiology should be prioritized to prevent schools from becoming reservoirs of drug-resistant strains.

To effectively combat the spread of MDR-TB, rapid and accurate diagnosis is the cornerstone. Traditional phenotypic drug susceptibility testing (pDST), while the gold standard, suffers from long turnaround times that delay appropriate treatment. Addressing this technological gap, Zhang and Peng provide a timely review in this issue on the application of High-Throughput Sequencing (HTS) for TB diagnosis and AMR detection[5]. HTS technologies have revolutionized pathogen research by offering comprehensive genomic profiling that goes far beyond the limited targets of conventional molecular tests like GeneXpert. The authors lucidly discuss how HTS can bridge the gap between diagnosis and treatment, enabling a shift towards "precision TB medicine". By integrating HTS into clinical workflows, clinicians can tailor regimens based on specific mutation profiles—such as those identified by Wang et al.—thereby improving treatment success rates and preventing the amplification of resistance. While challenges regarding bioinformatics standardization and cost remain, the adoption of culture-free sequencing approaches represents the future of TB diagnostics, particularly for complex resistance patterns.

However, the definition of a "TB cure" must be expanded to include the preservation of long-term lung health. Evidence is mounting that pulmonary TB can leave permanent architectural damage, leading

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to chronic airflow obstruction even after microbiological success. Sheng et al. present a significant 5-year prospective cohort study in this issue that challenges the traditional endpoint of TB care[6]. They found that airflow obstruction in TB survivors progressed from 13.2% at baseline to 17.0% at the 5-year follow-up, characterized by a phenotype clinically distinct but functionally similar to chronic obstructive pulmonary disease (COPD). Notably, this progression occurred even in young, non-smoking individuals, challenging the assumption that such sequelae are limited to older patients or smokers. It suggests that the current "test and treat" strategy leaves a gap in post-treatment care. Pulmonary rehabilitation and routine spirometry monitoring should be integrated into national TB control programs, shifting the focus from a disease-centered model to a patient-centered life-course approach.

Furthermore, TB control cannot be viewed in isolation from the broader ecological context of antibiotic consumption. The ecological analysis by Zhao et al. in this issue illustrates the complex relationship between antibiotic use and resistance trends in China from 2016 to 2022[7]. While the study covers a spectrum of WHO-priority pathogens, its implications extend to TB control. The divergence observed—declining resistance in some pathogens (e.g., *Acinetobacter baumannii*) while it rises in others (e.g., *Klebsiella pneumoniae*)—highlights that antimicrobial stewardship is a dynamic ecosystem. The rigorous regulation of antibiotic classes impacting *Mycobacterium tuberculosis* and co-infecting pathogens is essential to maintaining the efficacy of our limited drug arsenal.

In conclusion, the research presented in this issue of *Biomedical and Environmental Sciences* paints a comprehensive picture of the challenges and opportunities in the modern TB landscape in China. Collectively, these studies call for a multi-pronged strategy: urgent protection of vulnerable young populations through enhanced active case finding, the acceleration of advanced genomic technologies for precision diagnosis, and the extension of care beyond microbiological cure to ensure long-term respiratory health. By synthesizing high-quality evidence from genomic surveillance, clinical cohorts, and ecological studies, we can refine our policies to not only cure the disease but also restore the full health and quality of life of the nation.

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