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Editorial

Introduction to the special issue on current trends in laboratory diagnosis and public health of mycobacterial diseases in Korea and highlights in this issue

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Tuberculosis (TB) and other mycobacterial diseases are major public health concerns. Globally, *Mycobacterium tuberculosis* (MTB) causes > 10 million new TB cases and ~1.5 million deaths each year; the incidence of TB has declined by 8.7% from 2015 to 2022, yet the burden remains high [1]. In Korea, incidence of TB has fallen steadily, on average by 7.2% annually since 2011, reflecting sustained control efforts [2]. In addition to active TB, latent TB infection—along with its intermediate stages, such as incipient and subclinical TB—forms a critical reservoir that fuels future diseases, underscoring the need for targeted screening and prevention [3]. Meanwhile, nontuberculous mycobacterial (NTM) disease is gaining prominence, with global incidence rising by approximately 4% annually [4] and a growing number of cases reported in Korea since the first pulmonary NTM infections were identified in 1981 [5].

Clinical microbiology laboratories are central to strategies for controlling TB. The field has moved beyond time-consuming phenotypic and biochemical methods to rapid and accurate tools, such as immunochromatographic assays, polymerase chain reaction (PCR), matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), targeted sequencing, and next-generation approaches such as whole-genome sequencing (WGS), which accelerate species identification, enable strain-level genotyping, and support resistance surveillance and outbreak investigation.

This special issue, "*Current Trends in Laboratory Diagnosis and Public Health of Mycobacterial Diseases in Korea*," synthesizes these developments. Our aim is to integrate epidemiological trends in Korea with advances in diagnostic methodology for MTB and NTM, highlight the clinical and public health importance of latent and active TB, and articulate the pivotal role of laboratories in timely diagnosis, surveillance, and evidence-based interventions. This special issue features three outstanding review articles and one original article that provide an in-depth overview of the current trends in laboratory diagnosis and public health of mycobacterial diseases in Korea.

This special issue begins with a review of the current status of mycobacterial identification in clinical laboratories in Korea [6]. This review charts the transition from conventional microscopy, culture, and biochemical testing to rapid, highly accurate platforms for identifying *M. tuberculosis* complex (MTBC) and NTM. In routine Korean practice, MPT64 (*M. tuberculosis* protein 64)-targeted immunochromatographic assays and real-time PCR enable swift MTBC confirmation from cultures, whereas species-level NTM identification is based on mycolic acid analysis, MALDI-TOF MS, PCR-restriction fragment length polymorphism, line probe assays, and sequencing of targets such as 16S rRNA and *rpoB*. It further positions next-generation sequencing as an emerging integrative solution capable of concurrent species identification and drug resistance profiling, which will reshape diagnostics and surveillance.

Another review examines challenges and advances in molecular typing of mycobacteria, covering both MTB and NTM [7]. The review contrasts the differing aims—outbreak investigation and resistance prediction for MTB versus species-level resolution and relapse-versus-reinfection discrimination for NTM—and compares traditional techniques (e.g. spoligotyping, mycobacterial interspersed repetitive unit-variable number tandem repeat) with higher-resolution approaches (e.g. multilocus sequence typing, WGS). It highlights opportunities in portable sequencing, artificial intelligence (AI)-assisted analytics, and curated genomic databases, while underscoring the need to standardize NTM pipelines and embed genotypic data into global surveillance.

The final review focuses on latent TB, outlining the principles and clinical applications of interferon-gamma release assays (IGRAs) relative to the tuberculin skin test [8]. It emphasizes the higher specificity of IGRAs and their lack of cross-reactivity with BCG vaccination, discusses factors influencing performance, the challenge of indeterminate results in immunocompromised patients, and notes the preventive effect of isoniazid–rifampicin regimens, while calling for longer follow-up to improve interpretation.

The original research article is a retrospective cohort study using Korea's national reimbursement data (2018–2021) to assess TB care before and during the coronavirus disease 2019 (COVID-19) pandemic [9]. Despite the downward trend in treatment discontinuation, mortality increased during the pandemic, particularly among patients with malnutrition or diabetes. The study highlights disruptions in access to TB services and calls for pandemic-resilient policies to safeguard TB care.

Together, these articles connect Korea's laboratory realities with cutting-edge molecular and immunological tools, emphasizing the rising importance of NTM alongside MTB and the public health imperative of latent TB diagnosis and prevention. They collectively articulate the central role of clinical microbiology laboratories in enabling rapid identification, high-resolution genotyping, and evidence-based interventions that strengthen patient management and national surveillance. Complementing the three reviews, the retrospective cohort study using national reimbursement data quantifies the impact of the COVID-19 pandemic on TB management in Korea, underscoring the need for pandemic-resilient TB services and policies.

In addition to the mycobacteria-focused special issue articles, this issue includes three outstanding and impactful original research articles that add substantial value to the field.

A diagnostic study examines five years of application of a glutamate dehydrogenase (GDH)/toxin-based algorithm for *Clostridioides difficile* infection (CDI) at a single Korean center [10]. Across 8,685 tests, the combined GDH/toxin enzyme immunoassay achieved 82.6% sensitivity and 96.9% negative predictive value compared to toxin B PCR, supporting cost-effective first-line screening, diagnostic stewardship, and the development of national guidelines. Beyond metrics, the study offers real-world evidence to standardize CDI workflows and optimize resource use in Korean hospitals.

A genomic study characterized the complete genomes of representative methicillin-resistant *Staphylococcus aureus* clinical strains prevalent in Korea (2014–2017) using WGS with short- and longread sequencing [11]. Whole-genome analysis was used to define genome metrics, virulence and resistance profiles, and epidemiological markers linked to the staphylococcal cassette chromosome *mec* (SCC*mec*) and *spa* types. These gap-free references contribute to strengthening molecular epidemiology, surveillance, and evolutionary analyses.

A diagnostic accuracy study evaluated two clinical identification platforms for *Haemophilus* spp. [12]. The VITEK MS system (bioMérieux) correctly identified all 115 *H. influenzae* and three *H. parainfluenzae* isolates (100% sensitivity and specificity), whereas the VITEK 2 system (bioMérieux) showed lower concordance with frequent low discrimination. These findings support MALDI-TOF MS-based workflows for biochemical panels in Korean laboratories.

The special issue "*Current Trends in Laboratory Diagnosis and Public Health of Mycobacterial Diseases in Korea*" will continue in our next issue, and we warmly invite your continued interest. We also welcome high-quality and impactful submissions aligned with the aims and scope of *Annals of Clinical Microbiology* (ACM, https://www.acm.or.kr/about/aims-and-scope/).

We extend our deepest gratitude to the authors whose rigor and creativity drive this issue; to the reviewers, whose thoughtful, often unseen evaluations elevate its quality; to the editorial board for expert stewardship; and to our publishing partner for professional support in bringing this work to the community. We thank the readers for their trust, curiosity, and continued engagement. Your collective contributions sustain ACM's mission to advance medicine and human health.

Ethics statement

This was not a human population study; therefore, approval by the institutional review board and informed consent were not required.

Conflicts of interest

Hae-Sun Chung has been the editor-in-chief of *Annals of Clinical Microbiology* since January 2022. However, she was not involved in the review process of this article. No other potential conflict of interest relevant to this article was reported.

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Data availability

None.

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