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Editorial

Whole-genome sequencing as the new framework of clinical microbiology and highlights in this issue

Hae-Sun Chung
Department of Laboratory Medicine, Ewha Womans University College of Medicine, Seoul, Korea

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Correspondence to
Hae-Sun Chung
E-mail: sunny0521.chung@ewha.ac.kr

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The expanding role of whole-genome sequencing in clinical microbiology: A specially invited review

Infectious diseases remain a leading cause of morbidity and mortality worldwide, and antimicrobial resistance (AMR) continues to erode the effectiveness of standard treatment pathways. Against this backdrop, whole-genome sequencing (WGS) has shifted from being a specialized research capability to a practical engine for clinical decision support, outbreak investigation, and pathogen surveillance. The review by the distinguished Japanese scholar Professor Takashi Takahashi [1], "*Whole-genome sequencing applications for evolution of clinical microbiology*," arrives at a timely moment, capturing not only what WGS can do today but also how rapidly its laboratory and analytic ecosystems are evolving.

The major strength of the review is its clear laboratory-facing structure. It systematically walks readers through major next-generation sequencing (NGS) platforms, workflows for generating genomes, comparative genomics, RNA-seq, genome-based typing, genome-based AMR detection, and identification of integrative and conjugative elements that mobilize resistance, supported by four figures and three tables that anchor key concepts in practice. Such arrangement makes the review useful both as an introduction for newcomers and as a reference for established laboratories refining their pipelines.

The review is particularly meaningful because it is written from the perspective of a researcher who has repeatedly implemented whole-genome and transcriptome methods in real laboratory workflows and not merely summarized them. Throughout the review, the methodological discussion is anchored in first-hand bench-to-bioinformatics experience, from generating pathogen genomes using short-read sequencing and hybrid long/short-read assembly to applying pan-genome and comparative genomics to clinically relevant questions, as well as extending these approaches to transcriptomic analyses of host-entry environments. The same practical lens shapes the treatment of mobile genetic elements and the spread of AMR, drawing on recent characterizations of integrative and conjugative elements carrying resistance determinants in streptococci. Overall, the review reads as guidance distilled from hands-on experience in conducting, troubleshooting, and interpreting results in clinical and "One Health" contexts.

The review is an invited comprehensive lecture, and we express our sincere gratitude for Professor Takahashi's generous contribution. We also thank Professor Sunjoo Kim for arranging and facilitating this invitation. The friendship and sustained academic exchanges between the two professors are truly exemplary, and they offer a model that younger scholars should respect, emulate, and carry forward. Looking ahead, *Annals of Clinical Microbiology* (ACM) will continue to promote and expand activities that strengthen international academic collaboration, encourage meaningful cross-border dialogue, and build enduring research partnerships across disciplines and institutions.

Continuing special issue: Advances in diagnostics and drug susceptibility testing for mycobacterial diseases in Korea

Following the launch of the special issue "*Current Trends in Laboratory Diagnosis and Public Health of Mycobacterial Diseases in Korea*" in the previous issue, the current issue continues this planned series with three additional articles. A review article [2] addresses drug susceptibility testing (DST) for tuberculosis (TB). This review describes the current phenotypic and molecular DST methods, along with emerging NGS-based approaches, and explains how their appropriate interpretation can guide the effective management of multidrug-resistant and rifampicin-resistant TB. Two original studies are also included: one investigating the impact of nontuberculous mycobacteria (NTM) on the performance of Xpert MTB/RIF and Xpert MTB/RIF Ultra for detecting TB and rifampin resistance [3] and the other evaluating the SLOMYCO test system for DST of the *Mycobacterium avium* complex (MAC) [4]. The original study on NTM interference using Xpert MTB/RIF and Xpert MTB/RIF Ultra [3] showed that high-burden NTM did not compromise *Mycobacterium tuberculosis* (MTB) detection or rifampin-resistance determination, supporting the robustness of both assays in NTM-prevalent settings. The method-evaluation study on MAC DST using the SLOMYCO test system [4] reported high agreement with reference broth microdilutions for clarithromycin and amikacin in a susceptible population, while indicating that variability for moxifloxacin and linezolid warrants refined breakpoints and further validation with resistant isolates.

Together, these contributions capture recent advances and clinical implications for both TB and NTM. This continuing special issue initiative was designed to place Korea's epidemiological situation alongside rapid progress in diagnostic methods for MTB and NTM to underscore the public health and clinical importance of latent infection and active disease and to convey the central role of laboratories in prompt diagnosis, surveillance, and evidence-based interventions.

Other articles in this issue

Alongside the invited review by Professor Takahashi [1] and the special issue on "*Current Trends in Laboratory Diagnosis and Public Health of Mycobacterial Diseases in Korea*," this issue also includes three original research articles. A nationwide retrospective cohort analysis based on National Health Insurance Big Data (2020–2022) [5] examined the patterns of microbiological test utilization in pulmonary TB and major bacterial infections, showing that test requests vary with demographic characteristics, comorbidity burden, socioeconomic and regional factors, disability status, disease severity, selected clinical exposures (including chemotherapy and steroid use), and type of medical institution. Another original study [6] characterizes β-lactam resistance in non-typeable *Haemophilus influenzae* isolates in Korea, reporting high resistance to ampicillin and identifying *blaTEM*-mediated β-lactamase production together with multiple penicillin-binding protein 3 (*ftsI*) mutations as principal mechanisms, thereby supporting the need for continued AMR monitoring. A third study [7] evaluated the GenBody hMPV Ag Rapid Test against reverse transcription–quantitative polymerase chain reaction in a retrospective single-center series and demonstrated high overall agreement with no false-positive results, while noting reduced detection in higher-Ct specimens, highlighting the importance of cautious interpretation in low-viral-load samples and the value of further prospective validation.

Closing remarks and acknowledgements

In 2025, ACM has published four quarterly issues, each featuring a balanced mix of review and original research articles. Throughout the year, the published work consistently aligned with ACM's aims and scope and demonstrated strong scholarly quality in the core areas of clinical microbiology. This year's achievements were further strengthened by the public support made available through Korea's Lottery Fund (Ministry of Strategy and Finance) and the Science and Technology Promotion Fund (Ministry of Science and ICT). This support helped ACM advance efforts aimed at delivering social value, while contributing to the continued development of national science and technology.

Finally, sincere appreciation is given to everyone who made these publications possible. The authors have provided a scientific foundation through careful study design and meaningful results, while the reviewers have offered rigorous and constructive assessments that have helped to refine the manuscripts and safeguarded their quality. Gratitude is also owed to the editorial board for steady guidance and to our publishing partner for the dependable production support. Above all, thanks go to our readers, whose sustained interest and engagement keep ACM's work relevant and impactful, and whose confidence encourages our continued commitment to advancing medicine and human health.

Ethics statement

This was not a human population study; therefore, institutional review board approval 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. There are no other potential conflicts of interest relevant to this article.

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Data availability

None.

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