Tissue-Based Molecular Workup

Tae-Jung Kim

Organization The Catholic University of Korea, Yeouido St. Mary's Hospital, Hospital Pathology Department
Current Position Professor

Educational background

2015-2016 Research Scholar, Dana Farber Cancer Institute
2015-2016 Research Scholar, Broad Institute of MIT and Harvard
2004-2009 Ph.D., Hospital Pathology, The Catholic University of Korea
1997-2003 B.A., College of Medicine, The Catholic University of Korea

Professional experience

2023-Present Professor, The Catholic University of Korea, Yeouido St. Mary's Hospital, Department of Hospital Pathology
2009-2023 Instructor-Associate Professor, The Catholic University of Korea, Yeouido St. Mary's Hospital, Department of Hospital Pathology

Molecular profiling has revolutionized the clinical management of non-small-cell lung cancers (NSCLCs), enabling the effective application of tyrosine kinase inhibitors (TKIs). Oncogenic alterations such as EGFR and KRAS mutations, as well as translocations or fusions involving ALK, ROS1, and RET, can render tumor cells sensitive to specific TKIs and lead to significant clinical benefit. To detect such genomic drivers, a range of molecular diagnostic platforms—including PCR-based assays, DNA sequencing, and fluorescence in situ hybridization (FISH)—are routinely employed in pathology practice. These single-gene techniques remain essential, especially when rapid turnaround is required for urgent therapeutic decisions. Parallel to these advances, TKIs directed against additional actionable alterations are under investigation, reflecting the expanding spectrum of targetable oncogenic drivers. High-throughput sequencing platforms, particularly next-generation sequencing (NGS), have emerged as powerful tools that not only inform targeted therapy selection but also enable the discovery of novel genetic alterations. Multiplex NGS panels improve efficiency and cost-effectiveness; however, inconclusive or borderline findings may still necessitate confirmation by ancillary single-gene assays. Thus, strategic integration of broad sequencing with targeted methods is crucial to ensure accuracy, reliability, and timely clinical reporting.
Recently, whole genome sequencing (WGS) and targeted WGS approaches have gained attention as potential complements to panel-based NGS. These platforms offer the advantage of capturing rare or unexpected variants, structural rearrangements, and mutational signatures that may otherwise be overlooked. Although technical and cost-related challenges remain, ongoing translational efforts suggest that WGS and targeted WGS could become clinically applicable in the near future.
In summary, an optimized tissue-based molecular workup relies on the thoughtful combination of multiplex sequencing technologies and rapid single-gene assays. Such approaches ensure precision, timeliness, and comprehensiveness in guiding the use of targeted therapies for patients with NSCLC.