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강연제목: High-throughput and multiplexed single-EV/single-cell analysis technologies to unveil biological heterogeneity

Abstract:

While significant advancements have been made in single-cell analysis, such as single-cell RNA sequencing and single-cell proteomics for personalized medicine, analyzing subcellular organelles like extracellular vesicles (EVs) and mitochondria remains challenging due to their small size and hierarchical structure. In this talk, I will introduce platform technologies designed to analyze mitochondrial DNA (mtDNA) mutations at the single-cell level and molecular cargos of single EVs using a hydrogel-based rolling circle amplification (RCA) technique. For mtDNA mutation analysis, large-scale deletions were examined at both the single-cell and single-mtDNA levels. For single EV analysis, immune-related and cancer markers were analyzed at the single-molecule level. Multiplexed molecular information is encoded into RCA products, which are trapped in hydrogel beads and labeled with multiparametric fluorescence detection probes. These beads can be processed in a high-throughput manner using conventional laboratory equipment and analyzed with high-throughput flow cytometry. The proposed platform technologies provide new opportunities for personalized medicine by revealing biological heterogeneity at the subcellular level.

Brief Biosketch

Prof. Juhwan Park received his B.S., M.S., and Ph.D. in Bio and Brain Engineering from KAIST in 2014, 2016, and 2020, respectively. He then worked as a postdoctoral researcher at the Brain Science Institute of KIST (2021–2022) and the Department of Bioengineering at the University of Pennsylvania (2022–2024). In September 2024, he joined the Department of Bio and Fermentation Convergence Technology at Kookmin University. His research focuses on single-cell and extracellular vesicle (EV) analysis, lab-on-a-chip technology, microfluidics, and biosensing. He is a member of the Korea BioChip Society.