Tissue and subnuclear neighborhoods uncovered by high-resolution, multiplexed protein imaging

Xavier Rovira-Clavé¹

¹ Institute for Bioengineering of Catalonia (IBEC), Barcelona Institute of Science and Technology (BIST), Barcelona, 08028, Spain; xrovirac@ibecbarcelona.eu

A set of imaging technologies that profile tens to hundreds of antibodies at subcellular resolution have recently emerged to characterize single cells in their native tissue environment. One of such technologies, Multiplex Ion Beam Imaging (MIBI), harnesses a high energy ion beam to eject the atomic components of samples and a time-of-flight mass spectrometer to reconstruct their spatial positions. In this presentation, I will delve into our latest innovations for MIBI: 1) epitope barcoding for in situ tracking of cell lineages and phenotypes in tumor models [1], 2) computational tools for spatial analysis of cell lineages, 3) a comparison with a cyclic, fluorescence-base spatial proteomics technology in a cohort of clinical samples, 4) the use of a high-resolution cesium ion beam to visualize biomolecules and small molecules at the nanometer scale within cancer cells [2], and 5) its coupling to expansion microscopy, which expands tissues while preserving protein staining, allowing high-plex imaging for detailed analysis of subcellular features in archival clinical tissue samples [3]. By highlighting novel tools and applications for these technical advancements, our work exemplifies how high-resolution, multiplexed protein imaging is transforming our understanding of tissue and cell biology.

References

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^{*}Co-first authors

[†] Co-last authors