



Deep Visual Proteomics: Single cell mass spectrometry for molecular cartography of human cancer tissue

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The need for single-cell approaches in understanding cell function has been recognized for decades. This is especially important for the understanding of intratumoral heterogeneity in tumors to improve the diagnosis and treatment of specific cancer subtypes. While single-cell RNA sequencing has revealed novel molecular regulators associated with tumor growth, metastasis and drug resistance, this has not yet been extended to the protein level, the closest proxy for biological function or dysfunction. Single-cell variations are particularly challenging to study due to limited sensitivity and robustness of current proteomics technology.

Here we combine artificial intelligence (AI)-powered image-based analysis of cellular phenotypes with ultra-high sensitivity (single-cell) mass spectrometry (MS)-based proteomics. This concept, called Deep Visual Proteomics (DVP), ties together the visual information defining cellular identity and heterogeneity with cellular neighborhoods and the underlying proteomic signatures in an unbiased and systems-wide way. Applied to biobank tissue samples of melanoma, DVP captured the spatial proteome during disease progression from normal melanocytes, via pre-cancerous in-situ lesions to fully invasive melanoma. We described how key pathways of cancer progression – such as metabolic ones and RNA splicing switch in a spatial manner. This highlights the ability of DVP to retain the spatial information of proteome variation in the tissue context and how this can shed light on understanding cancer cell evolution, development, and pathogenesis.

Biography:

Andreas is an associate professor in the clinical proteomics group of Professor Matthias Mann at the Novo Nordisk Foundation Center for Protein Research, University of Copenhagen. He has a dual education profile with a degree in Biotechnology Engineering and a PhD in protein research from the

Anhalt University of Applied Sciences and the University of Hamburg respectively. He is not only excited about natural and technical science research and how it contributes to advances in biomedicine, but also about the idea that collaborative and interdisciplinary research is key to ground-breaking discoveries. For this reason, his research focuses on the development and application of a novel interdisciplinary concept called `Deep Visual Proteomics`, which combines advanced imaging, artificial intelligence, and single-cell mass spectrometry-based proteomics to understand mechanisms of health and disease.