Protein Identification and imaging on FFPE and frozen tissues with MALDI-Ion mobility imaging

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MALDI imaging mass spectrometry (MALDI-IMS) has become a powerful tool for the detection and localization of drugs, proteins, and lipids on-tissue. Nevertheless, this approach can only perform identification of low mass molecules as lipids, pharmaceuticals, and peptides. In this article, a combination of approaches for the detection and imaging of proteins and their identification directly on-tissue is described after tryptic digestion. Enzymatic digestion protocols for different kinds of tissues—formalin fixed paraffin embedded (FFPE) and frozen tissues—are combined with MALDI-ion mobility mass spectrometry (IM-MS). This combination enables localization and identification of proteins via their related digested peptides. In a number of cases, ion mobility separates isobaric ions that cannot be identified by conventional MALDI time-of-flight (TOF) mass spectrometry. The amount of detected peaks per measurement increases (versus conventional MALDI-TOF), which enables mass and time selected ion images and the identification of separated ions. These experiments demonstrate the feasibility of direct proteins identification by ion-mobility-TOF IMS from tissue. The tissue digestion combined with MALDI-IM-TOF-IMS approach allows a proteomics “bottom-up” strategy with different kinds of tissue samples, especially FFPE tissues conserved for a long time in hospital sample banks. The combination of IM with IMS marks the development of IMS approaches as real proteomic tools, which brings new perspectives to biological studies.

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