INTRODUCTION

Mass spectrometry imaging (MSI) was first reported for the direct analysis of intact proteins from tissue. The need for the identification of proteins and therefore their enzymatic digestion has become an essential step in the discovery of biomarkers from tissue. Structural identification is traditionally carried out after processing the untargeted MS/MS data, followed by further manual acquisitions either on the same or consecutive sections. A data independent MALDI imaging acquisition method called MALDI Imaging HDMSE is presented, where MS and MS/MS information are acquired within a single experiment, without any precursor selection or requirement-rents. Post acquisition, the precursors and the fragments are correlated on the basis of drift time, which is further refined utilizing spatial distribution commonly.

METHODS

Sample preparation

Cutan carcinoma tissue section was used for this experiment. A solution of trypsin at 20 μg/mL in 0.1M ammonium bicarbonate ± 0.1% SDS was applied evenly to the sample in 25 coats using the same SunCollect sample preparation device. A solution of α-cyano-4-hydroxycinnamic acid (CHCA) matrix at 5 mg/mL in 3:1 acetonitrile : 0.2% trifluoroacetic acid was also applied evenly to the sample in 25 coats using the same SunCollect sample preparation device.

RESULTS

Peptide Mass Fingerprint (PMF) MALDI imaging experiment

Figure 4 shows the HDI software display of the processed data. Here, the signal of the precursor was carried out in the selected region by selecting a specific drift time range of 65 to 120 bins. In this view, the low energy detected peaks (peak A) spectrum and its drift time range is shown as a gray area. The red dots correspond to the low energy ion information. Tryptic peptides belonging to the same protein are correlated with 0.5 < R < 1, the MS/MS spectrum only displayed the associated fragment ions. When spatial correlation was carried with 0.5 < R < 1, the MS spectrum was fragmented using the triwave. For the even number pixels, precursors are separated by IMS and then detected with the TOF analyzer. For odd pixels numbers, precursors are separated by IMS and then fragmented in the Transfer T-Wave collision cell before being detected with the TOF analyzer.

CONCLUSION

A novel MALDI Imaging experiment called MALDI Imaging HDMSE is described. The untargeted method allows precursors and fragments information to be collected from a single tissue section. From PMF (low energy) MALDI imaging information, Albumin protein was identified using the spatial correlation feature. Association of fragments with its precursor is based on drift time correlation and spatial distribution correlation. Improvement of the Mascot score was achievable combining low and elevated energy information.

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