COUPLING MALDI MS WITH HIGH-EFFICIENCY ION MOBILITY SPECTROMETRY FOR TISSUE IMAGING OF LOW MASS ENDOGENOUS COMPOUNDS

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Figure 1. Schematic of the MALDI Synapt HDMS system, showing the TripleD TOF MALDI Separation device.

Figure 2. MALDI Imaging Pattern Creator is used to select the area(s) to be automatically imaged using MALDI SYNAPT HDMS.

Figure 3. 2D ion maps of m/z 402.019 with IMS (2.7 ms – 3.3 ms) and m/z 402.079, respectively, where 2.7 ms – 3.3 ms and 3.3 ms – 4.1 ms, respectively, gives complete separation.

Figure 4. MS/MIS spectra of m/z 758.57 and 742.54. The ions show an enrichment of the n-m region as a consequence of the separation.

Figure 5. mapped spectrum obtained directly from kidney tissue. Lipids with m/z ≥ 1000 are of high interest in terms of their biological relevance and potential as disease markers.

Figure 6. 3D ion intensity maps for (a) the ion of m/z 401.075 and (b) the ion of m/z 403.024 of PC (16:0, 16:0) and (c) the ion of m/z 404.023 of PC (18:2, 16:0).

Figure 7. Partially overlapping peaks observed in an imaging experiment. This is a common occurrence when using IMS.

Figure 8. Two-dimensional incorporation of m/z 758.57, with fatty acid chain loss mass fragments.

CONCLUSION

- Performing the orthogonal acceleration MALDI (OAMS) mass spectrometry in a MALDI SYNAPT HDMS system, rapid high mass resolution MS and MS/MS data were obtained directly from tissue.
- The phospholipid fraction was characterized directly from tissue, using exact mass MS/MS data acquired with a precursor ion selection at m/z 402.019.
- The combination of high efficiency ion mobility spectrometry and orthogonal acceleration provided a further enhancement in mass spectrometric information.
- IMS can be used to produce images without interference from background ions of similar mass.
- This approach has been demonstrated to be a powerful tool for high throughput screening of complex biological samples.

REFERENCES

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