Two Dimensional Mass Spectrometry (2DMS): How Far Can We Go in Protoemics?

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Introduction

- Liquid chromatography (LC) is an essential tool for proteomics
- Suffers from:
  1. Bias of the chromatography columns
  2. Incompatibility with certain separation conditions

- 2DMS provides an extra separation dimension in the ICR cell[1]
- Applications for: bottom-up and top-down of standard protein;[2] small molecules;[3] polymers[4]

- Herein, we demonstrate the use of 2DMS for proteomics samples and compare the 2DMS results to LC tandem MS data

Experimental Section

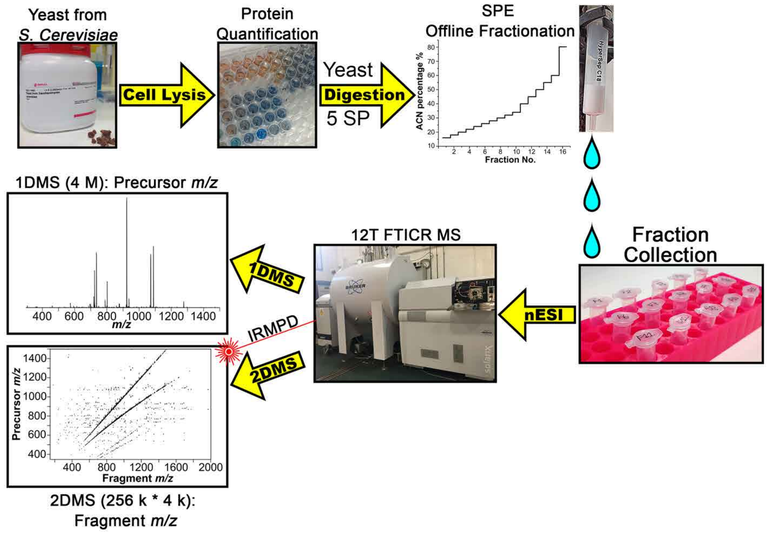

Fig 1. A summarised workflow of the sample preparation and 2DMS data acquisition of the offline fractionated yeast as well as 5 standard proteins (SP)

Result - 5 Standard Proteins

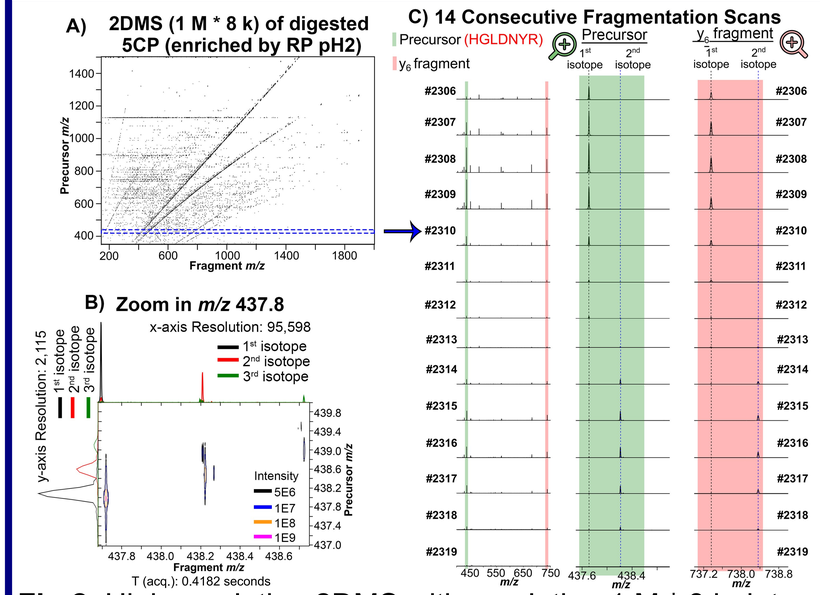

Fig 2. High resolution 2DMS with resolution 1 M * 8 k data-points of trytic digested 5SP

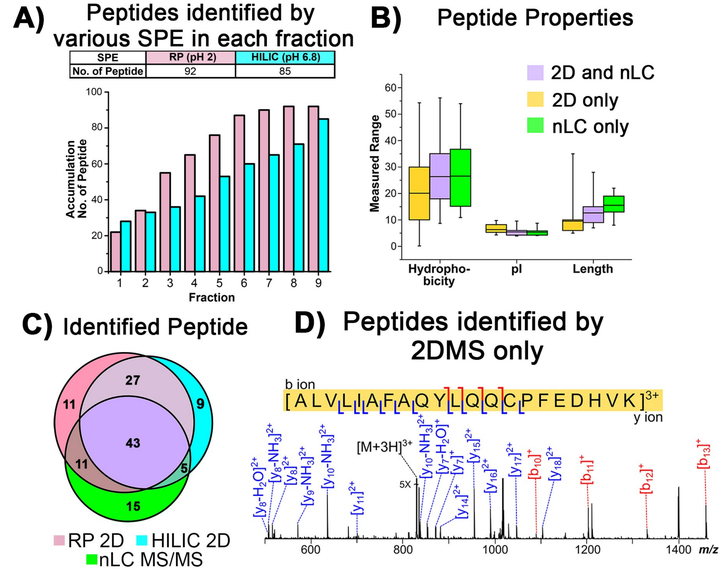

Fig 3. Proteomic results of tryptic digested 5SP using 2DMS with SPE fractionation and nLC MS/MS

Result - Yeast Proteome

Fig 4. Summarised results of digested yeast using 2DMS and nLC MS/MS

Conclusion

- 2DMS is a viable alternative technique for proteomic studies
- Complementary peptide and protein assignments between 2DMS and nLC-MS/MS allows deeper proteome coverage
- 2DMS has a higher efficiency in observing hydrophilic, basic, or short peptides, which may be beneficial for assignment of hydrophilic PTMs, i.e. phosphopeptides and glycopeptides

Acknowledgment

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References

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