Performance Evaluation of a Modified Quadrupole Orbitrap Mass Spectrometer

Tabiwang N. Arrey1, Rosa Jersee-Christensen Rakownik1, Julia Krageenbring1, Kerstin Strupat1, Markus Kellmann1, Catharina Crone1, Thomas Moehring1, Alexander Harder1

1Thermo Fisher Scientific, Bremen, Bremen, Germany

ABSTRACT

Current Orbitrap technologies are designed for high resolution mass spectrometry applications. The Orbitrap Exploris™ 480 mass spectrometer, the new member of the Orbitrap Technology family, possesses a reinvented quadrupole, a novel Advanced Active Beam (AAB) front-end, new Orbitrap and enhanced performance properties, making it an ideal platform for DDA and DIA experiments. The Orbitrap Exploris™ 480 was compared to the Thermo Scientific™ Exactive™ HF-X Mass Spectrometer, a platform optimized for top-down proteomics and peptide identification. The results of this work show that Orbitrap Exploris™ 480 is better suited for bottom-up proteomics and 2D-DIA experiments.

INTRODUCTION

The increasing demand for faster, yet accurate, proteomic analyses creates a need for improved mass spectrometers. Current Orbitrap technologies are designed for high resolution mass spectrometry applications. The Orbitrap Exploris™ 480 mass spectrometer, the new member of the Orbitrap Technology family, possesses a reinvented quadrupole, a novel Advanced Active Beam (AAB) front-end, new Orbitrap and enhanced performance properties, making it an ideal platform for DDA and DIA experiments. The Orbitrap Exploris™ 480 was compared to the Thermo Scientific™ Exactive™ HF-X Mass Spectrometer, a platform optimized for top-down proteomics and peptide identification. The results of this work show that Orbitrap Exploris™ 480 is better suited for bottom-up proteomics and 2D-DIA experiments.

RESULTS

Applications

Refined Proteomics (Data Dependent Analysis)

Exactive HF-X was used as a reference MS for this experiment. The Thermo Scientific™ Orbitrap Exploris™ 480 mass spectrometer was used to acquire the data. The Orbitrap Exploris™ 480 MS was operated in a DDA mode, in which the AutoMS process is used to sequentially acquire data for the most intense ions. The Orbitrap Exploris™ 480 was compared to the Thermo Scientific™ Exactive™ HF-X Mass Spectrometer, a platform optimized for top-down proteomics and peptide identification. The results of this work show that Orbitrap Exploris™ 480 is better suited for bottom-up proteomics and 2D-DIA experiments.

MATERIALS AND METHODS

For all experiments, the Orbitrap Exploris™ 480 was used as the test system. All MS parameters, including peptide and protein concentrations, were determined with the Orbitrap Exploris™ 480. The Exactive HF-X was used as the reference system. The Orbitrap Exploris™ 480 was compared to the Exactive HF-X Mass Spectrometer, a platform optimized for top-down proteomics and peptide identification. The results of this work show that Orbitrap Exploris™ 480 is better suited for bottom-up proteomics and 2D-DIA experiments.

CONCLUSIONS

In summary, this work shows that the Orbitrap Exploris™ 480, equipped with a novel Advanced Active Beam (AAB) front-end and reinvented quadrupole, is a suitable platform for bottom-up proteomics and 2D-DIA experiments. The Orbitrap Exploris™ 480 provides improved sensitivity, higher signal-to-noise ratio, and faster data acquisition compared to the Exactive HF-X Mass Spectrometer.

REFERENCES

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ACKNOWLEDGEMENTS

We would like to thank Dr. Peter Pfeiffer from OFP Microsystems for the Exactive HF-X MS-MS instrument.

TRADEMARKS/LICENSING

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