Relative quantification using TMT11plex on a modified Q Exactive HF mass spectrometer

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ABSTRACT

Relative quantification by isobaric tandem mass tags (TMT) is a highly multiplexed, quantitative proteomic technique that affords a comprehensive assessment of protein expression differences. The TMT 11-plex approach has been adapted for use on the Thermo Scientific Q Exactive HF mass spectrometer to explore the utility of this system for relative quantification. The results demonstrate that the Q Exactive HF is capable of achieving high multi-plexed quantification, with particular advantages for analyses requiring high dynamic range measurements. The performance of the instrument was evaluated using a number of simulated workflows, including a representative TMT approach for high dynamic range multiplexed quantification. The results demonstrate that the Q Exactive HF offers excellent performance for TMT-based relative quantification, with particular advantages for analyses requiring high dynamic range measurements.

INTRODUCTION

To achieve a better understanding of cellular pathways relevant to health and disease with the use of a single organism, tissue, or cell line, it is essential to have a robust and reliable quantitative proteomics platform. Various techniques have been developed for quantitative proteomics, including label-free proteomics, isobaric tagging mass spectrometry (TMT), and stable isotope labeling. In recent years, TMT has emerged as a highly sensitive and specific method for relative quantification of protein expression differences. TMT is based on the labeling of proteins with isobaric reporter ions, which are then separated by mass spectrometry and detected by mass spectrometry with high sensitivity. TMT has been widely adopted in proteomics studies due to its high accuracy, specificity, and sensitivity. However, the application of TMT has been limited by the availability of high-performance instruments with adequate sensitivity and dynamic range. The Q Exactive HF is a high-performance mass spectrometer with a high dynamic range and excellent sensitivity, making it an ideal instrument for TMT-based relative quantification. In this study, we evaluated the performance of the Q Exactive HF in TMT-based relative quantification using a simulated workflow.

MATERIALS AND METHODS

Sample preparation

The sample preparation was performed using the TMT11plex approach. The samples were prepared using the TMT11plex reagents (Thermo Fisher Scientific) as described in the manufacturer’s instructions. The samples were then analyzed using the Q Exactive HF mass spectrometer.

RESULTS

The results demonstrated that the Q Exactive HF is capable of achieving high multi-plexed quantification, with particular advantages for analyses requiring high dynamic range measurements. The performance of the instrument was evaluated using a number of simulated workflows, including a representative TMT approach for high dynamic range multiplexed quantification. The results demonstrate that the Q Exactive HF offers excellent performance for TMT-based relative quantification, with particular advantages for analyses requiring high dynamic range measurements.

CONCLUSIONS

The Q Exactive HF is capable of achieving high multi-plexed quantification, with particular advantages for analyses requiring high dynamic range measurements. The performance of the instrument was evaluated using a number of simulated workflows, including a representative TMT approach for high dynamic range multiplexed quantification. The results demonstrate that the Q Exactive HF offers excellent performance for TMT-based relative quantification, with particular advantages for analyses requiring high dynamic range measurements.

REFERENCES


TRADEMARKS/LICENSING

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