ESI-MS detection of mAb tryptic digest standard with a small-footprint ion trap mass spectrometer.

Overview

○ The MT Explorer 30 (MTE 30) is a compact ion trap tandem mass spectrometer suitable for both lab-based workflows and field deployment. It enables rapid, sensitive, and accurate identification of biomolecules.

○ This application note illustrates the use of the MTE 30 for the detection of tryptic digests of a monoclonal antibody with electrospray ionization mass spectrometry (ESI-MS).

○ The MTE 30 is an easy-to-use tool for antibody characterization in bioanalytical processes and workflows, including field applications.

Introduction

○ A tryptic digest of an antibody cleaves at lysine and arginine, producing peptide fragments that readily protonate during ionization. Peptide detection typically relies on electrospray ionization (ESI) coupled with a high-end mass spectrometer, but these systems are costly, require expertise, and are not fieldable.

○ A miniature mass spectrometer with ESI capabilities provides an accessible alternative, enabling onsite peptide analysis with reduced resource requirements without sacrificing performance. Here, ESI-MS analysis of an mAb Tryptic Digest standard demonstrates effective peptide detection.

Methods

Sample Preparation:

mAb Tryptic Digest standard (Waters, USA) stock was diluted in a water and acetonitrile solution with 0.1% Formic Acid 10x for a concentration of 40µg/mL. Direct infusion with ESI-MS analysis was performed on MTE 30 in positive ion mode with 0.8 µL/min.

DSAP-ESI Source and MT Explorer 30 Mass Spectrometer

Results and Discussion

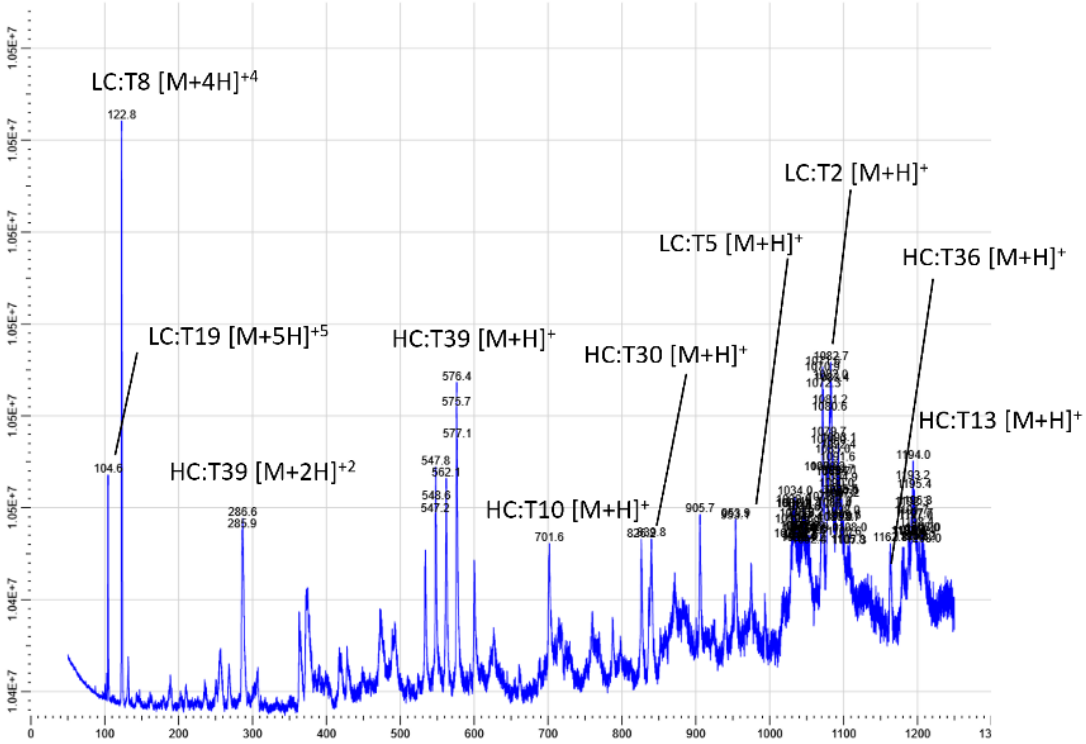

Fig. 2 ChromExplorer ESI-MS raw spectrum with peak annotations (full range 35-1250) NIST mAb Trypsin Digest.

a.
DIQMTQSPSTLSASVGDRVTITCSASSRVGYMHWY
QQKPGKAPKLLIYDTSKLASGVPSRFSGSGSGTEFT
LTISSLQPDDFATYYCFQGSGYPFTFGGGTKVEIKRT
VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV
QWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

b.
pQVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMS
VGWIRQPPGKALEWLADIWWDDKKHYNPSLKDRLTI
SKDTSKNQVVLKVTNMDPADTATYYCARDMIFNFYF
DVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPG

Fig.3 Visual representation of sequence detection by the MT Explorer 30. Blue shading represents the peptide sequences detected. a. Light Chain (LC) Sequence Coverage (singly, doubly, triply charged peptides – 65.7%) b. Heavy Chain (HC) Sequence Coverage - (singly, doubly, triply charged peptides – 42.3%)

- The MT Explorer 30 successfully detected ~50% of the total antibody sequence with minimal sample preparation or instrument optimization. This breakthrough provides a promising avenue for accessible, point-of-care and field proteomics.

- Further optimization and development of sample preparation methods, coupled with advancements in instrumentation, hold promise for expanding the applications of the MTE 30 in protein analysis and biopharmaceutical research.