Experimental

The ion mobility flow into the electrospray source at 540 mV. The source conditions were tuned for each sample to give optimal signals. The high field and low field regions were repeated for up to six times to ensure reproducible mobility data. The helium cell conditions were optimized with a neutral-gas flow of 110 mL/min (proximity not measured directly). Approximately twice the main gas flow is used. The standard Synapt was operated with 0–60 sL/m in the helium cell and the Synapt G2 with 2–60 sL/m. Three settings were used for each experiment.

Bradykinin Multimers

The formation of multimeric charged multimeric species of the form (M+H)n has been demonstrated for various peptides including Bradykinin. The first basis of these species to the same m/z value but can be separated by their differences in mobility. The mass accuracy of the nominal m/z 636.1663 ion species of Bradykinin using the standard mobility cell and the new, high pressure cell.

RESULTS AND DISCUSSION

Inverse Sequence Peptides

The inverse sequence peptides GRGDS and GDSGR (m/z 490) have been studied previously and were used to determine the molecular ion species of each at m/z 246 were determined to have a difference in collision cross section (ΔΩ) of 5.2%, in an 0.5 mbar N2 drift tube as an atmospheric pressure. In Figure 3, the mobility arrival time spectrum is shown. The inverse sequence peptides at m/z 246.

Figure 6

The arrival time distributions of the inverse peptide (a) KG_ADC_01 37 (0.806) and (b) KG_ADC_02.raw : 1 226.9514 430.9147. With the new, higher pressure mobility cell, the mobility reso- lution (ΔΩ) has increased by approximately a factor of three over the standard mobility cell. In addition, these data show the mobility arrival time peaks for single m/z species are well resolved. The doubly charged precursor ion of glu-fibrin peptide B at m/z 785.6 was selected using the quadrupole mass filter and transmitted into the travelling wave (inset are the data for the peptides run individually) with ~0.5 mbar of N2 in the IMS cell and the Synapt G2 with 2.5 mbar N2, 40 V wave. The high pressure cell is shown for a mixture of the two peptides.

Figure 7

The mobility chromatogram and m/z vs arrival time for sodium formate (a) with mobility separation (b) with mobility separation.

conclusion

A new high resolution travelling wave IMS operating in the presence of ~200 mbar high pressure N2 drift entry cell has been described. Mobility resolution increases of 3-4x are achieved over a standard Synapt G2, with a high pressure mobility cell.

The high pressure cell is shown for a mixture of the two peptides.

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