THE USE OF ION MOBILITY SPECTROSCOPY (IMS) COUPLED WITH TIME-OF-FLIGHT MASS SPECTROMETRY FOR THE STUDY OF PHASE PROTEIN CONFORMATION

INTRODUCTION

The transfer of high molecular weight ions and non-covalently associated protein complexes from solution to the gas phase generally results in the formation of ions which possess relatively few charges. Therefore, these ions often appear on an orthogonal acceleration time-of-flight mass spectrometer.

We have recently described a novel quadrupole/TOF/MWMS/oa-ToF mass spectrometer, operated with an electrospray ion source that provides for the separation of ions based upon their mobility and subsequently their m/z [4].

The TWMS is a stacked-rings ion guide, operated at elevated pressure, with opposite phases of an rf voltage applied to adjacent plates to provide radial ion confinement. A continual sequence of dci pulses is superimposed on the continuing rf to provide ‘waves’ which propel ions through the gas. Protein species were ionised and the resulting ions separated based upon their ion mobility, or collision cross section, through the TWMS device and subsequently mass analysed using the oa-ToF analyser.

We have investigated the use of the hybrid ion mobility/time-of-flight system for the analysis of intact proteins. We have looked at proteins of different molecular masses and examined the IMS/MS data for the information that we can obtain. Here we discuss this work with examples of how IMS coupled with time-of-flight MS can be used for the systematic analysis of protein structure shown.

EXPERIMENTAL

All data were acquired on a Waters Synapt HDMS system.

RESULTS

The ToF MS spectrum of a native lysozyme infusion, displaying the expected charge state distribution from 6+ to 9+ is shown in Figure 3. The rectangles will be used to identify these ions on the corresponding DriftScope data plot in Figure 4 below.

Figure 1

Figure 1: Schematic diagram of the Waters Synapt HDMS instrument used in this study.

Figure 2

Figure 2: Schematic diagram of the Waters Tri-Wave device used in the Waters Synapt HDMS system.

Samples were introduced into the source at a flow rate of 1 µL min−1. The sample used in the study was a standard protein solution.

REFERENCES

5. K. Gilis, S. Fregile, K. Wurthung and R. Bateman “Traveling Wave Ion Propagation in Collisions –” Presented at the 3rd IASMS Conference, Montreal, Canada 2003. The traveling wave device described here is similar to that.

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