Advantages of new high pressure MALDI FTMS design

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The previously reported design of an HP-MALDI FTMS system1,2 in which desorption of ions occurs under high-pressure, assisted by a ~5 mbar gas pulse, has a number of advantages over commercial systems. Fourier transform ion cyclotron resonance mass spectrometry provides excellent mass accuracy (~2 ppm), resolving power (~100 K), dynamic range (~1000) and throughput (thousand/day if automated) and coupled with the stabilizing high pressure MALDI, appears to be the preferred instrument for protein analysis. The multi-shot accumulation procedure provides sufficient sensitivity for biological samples. The ultimate goal of this design is an automated system for high throughput protein analyses including robotic sample preparation, data acquisition, and MSn on peaks that are not assigned from the database prediction.

The conventional MALDI system was redesigned for the high-pressure ion source to allow desorption of ions directly from TLC plates, or other surface techniques such as surface plasmon resonance or peptide/protein array chips. Ions are desorbed using a dual UV/IR laser from Biopic Lasersysteme® (Berlin, Germany) at elevated pressure (~3 mbar) for collisional cooling of the internal vibrational motion3. The optics focus the laser beam between the hexapole rods, desorbing ions, cooling them, and accumulating them in the hexapole prior to sending them as a package to the ICR cell.

Another major improvement in this design is the use of a large area XY stage that can handle multiple samples. These plates are controlled with homemade software and accept Bruker® sample plates, which can be prepared directly using a commercial robotic system. The dual laser allows use of the 355 nm laser Nd:YAG tripled wavelength as well as the Er:YAG 2.94 µm wavelength; the latter improves sensitivity and shot-to-shot stability of the signal.

Use of a gas pulse to assist trapping and collisional cooling of the ions before transfer to the analyzer cell improves sensitivity and allows study of weak interactions as are involved in modified proteins, protein-peptide or peptide-peptide complexes. The data for the Hepatitis viral capsid phosphoprotein digest, Trichomonas vaginalis protein digest, and ganglioside molecules shows the potential for this type of proteomic study.

The spectra obtained from various polypeptides (such as substance P, Angiotensinogen, Renin Substrate, Melittin, RRREEE(pS)EEAA phosphopeptide and etc.) shows the potential for production of multiply charged ions in MALDI. The key parameter for generation of these ions is the pressure at the surface of ion desorption and the geometry of the RF-only accumulation hexapole in the MALDI source.

The use of non-conducting MALDI surfaces was not found to be a crucial parameter for multiply charged ion production. Multiply charged ions were fragmented using SORI CAD. Experimental data shows a clear difference in fragmentation pattern between singly and doubly charged ions.

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Figure 1. HP MALDI: Isolation of phosphopeptide 2+ by SWIFT 75 V in the ICR cell.

Figure 2. HP MALDI: Renin Substrate 2+ SWIFT by 75 V and SORI CAD 905 m/z, 7V

1) Peter B. O’Connor and Catherine E. Costello Application of Multishot Acquisition in Fourier Transform Mass Spectrometer, Anal. Chem. 2000, 72, 5125-5130
5) Baykut G., Jertz R., Witt M., Matrix-assisted Laser Desorption/ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry With Pulsed In-source Collision Gas And In-source Ion Accumulation