# SpiralTOF-TOF

## Comparison of the JMS-S3000 SpiralTOF-TOF and a 4-Sector Tandem Double-Focusing Mass Spectrometer

**Introduction**

The JMS-3000 SpiralTOF™ has an optional TOF-TOF mode that features monoisotopic precursor ion selectivity, elimination of post source decay (PSD) ions, and high energy collision induced dissociation (CID). The JMS-700T MStation four-sector tandem double focusing mass spectrometer, although featuring a different analyzer and ionization techniques, has similar capabilities that have been previously used for a wide variety of applications including the structural analysis of complex biological molecules.

In this work, we compare the SpiralTOF-TOF with the MStation four sector tandem double focusing mass spectrometer using the same sample for MS/MS analysis.

**Experimental**

The sample analyzed by both systems was renin substrate tetradecapeptide (porcine), a peptide having an amino-acid sequence of DRVYIHPFHLLVYS. Table 1 shows the measurement conditions and sample sizes used for both systems.

| | JMS-S3000 | JMS-700T |
|---|---|---|
| Ionization method | MALDI | FAB (Xe 6 kV) |
| Sample quantity | 2.5 pmol | 1 nmol |
| Precusor ion | mono isotopic | mono isotopic |
| Target gas | He | Ar |
| Matrix | CHCA | Glycerin, NBA |
| Collision energy | 20000 eV | 5000 eV |

Table 1. Experimental conditions and specifications.

**Results and Discussion**

The SpiralTOF ion optics with the TOF-TOF option are shown in Fig. 1a. This design allows for the acquisition of high-energy CID product ion spectra for monoisotopically selected precursor ions. This precursor selection is made possible by the fact that the distance to the ion gate is 15 m. Additionally, the second TOF incorporates a re-acceleration mechanism into an offset parabolic reflectron (OPR) which enables the seamless observation of product ions ranging from very low *m/z* up to that of the precursor ion.

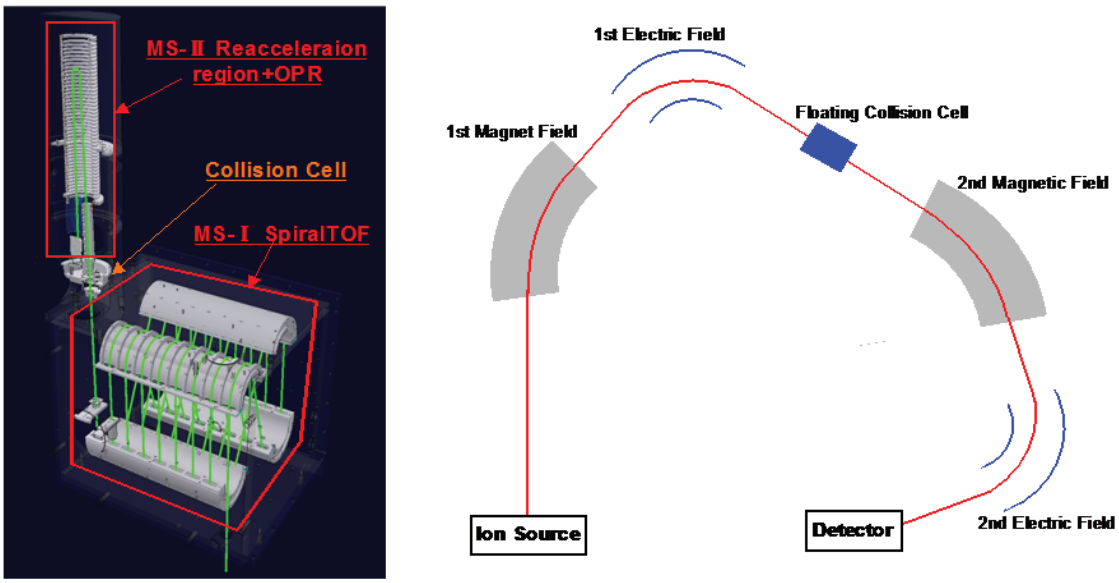


Figure 1. Ion trajectory - Left: JMS-S3000 SpiralTOF , Right: JMS-700T tandem MStation.



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The MStation tandem has the ion trajectory shown in Fig. 1b, which also allows the selection of ions that have a specific *m/z* but in this case using the first magnetic and electric fields as the MS1 analyzer. The selected ions then pass into the collision chamber which is floated at a given voltage level to reduce their overall speed before colliding with the collision gas. Subsequently, the resulting product ions are re-accelerated to give them sufficient kinetic energy to be analyzed efficiently by the second magnetic and electric fields.

For comparison, the renin substrate tetradecapeptide (porcine) was analyzed using both systems. Fig. 2 shows the product ion spectra acquired for each system using the $[M+H]^+$ (*m/z* 1758.93) as the precursor ion. Because of the difference between the FAB (Fast Atom Bombardment) and MALDI (Matrix Assisted Laser Desorption/Ionization) ionization techniques, the SpiralTOF-TOF acquired the product ion spectrum using 1/100 less volume than was used to get a comparable spectrum for the MStation. The resulting spectra show the immonium ions and the same pattern of a- and d- series ions which are the characteristic product ions produced by high energy CID. For the product ion spectrum acquired with the MStation in Fig. 2, the floating voltage was set to a slightly high level of 5000 V in order to observe low mass ions efficiently. However, this actually reduced the resolution and transmission rate of the high mass ions. In contrast, the SpiralTOF was able to analyze the full mass range efficiently, as a result of the second accelerator and the OPR not requiring the process of voltage selection for the target mass range.

**Conclusions**

These results clearly demonstrate that the SpiralTOF-TOF produced the same structural information as a traditional four sector tandem double focusing mass spectrometer. Additionally, the SpiralTOF-TOF required a smaller sample volume and a simpler analysis procedure to produce comparable product ion spectra.

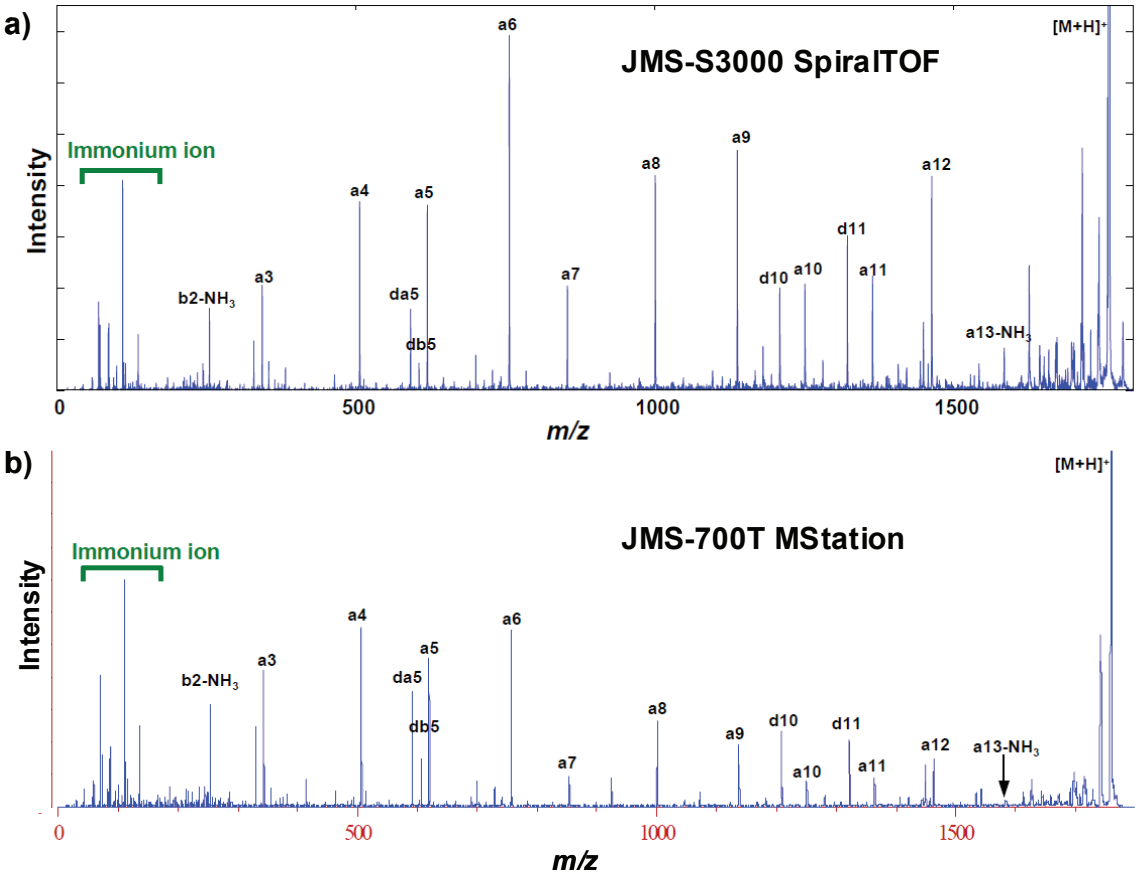


Figure 2. Product ion spectra of Renin-substrate tetradecapeptide by a) JMS-S3000 SpiralTOF-TOF and b) JMS-700T tandem MStation.



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