^{252}Cf Plasma Desorption-Ionization with a Fourier Transform Mass Spectrometer: Analysis of Thermolabile and Non-volatile Biomolecules**

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Abstract: First and promising results obtained by the use of a combination of a ^{252}Cf plasma desorption-ionization (PDI) source and a Fourier transform mass spectrometer (FTMS) for the analysis of thermolabile and non-volatile biomolecules are reported.

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Various desorption methods have been investigated for studying the structures of compounds by mass spectrometry (MS)[1]. Recent reviews[2, 3] summarized new aspects and developments of the analysis of involatile high molecular weight biomolecules. Already attractive structural approaches have been developed with associate different desorption techniques to the MS/MS under high resolution conditions by using FTMS, secondary ions (SIMS)[4], or laser impact (LD)[5].

It is known that biomolecules characterized by very high molecular weights are desorbed by using ^{252}Cf plasma desorption (PDI)[6]. We have been interested by this technique because it is compatible with the high resolution measurements of FTMS, since the required low pressure is essentially maintained ($< 10^{-8}$ Torr) with only a minor residual background. Consequently, a double cell[7] or external source[7, 8] are not necessary. Thus ^{252}Cf-PDI/FTMS appears to be a very promising technique for analytical applications.

Our first measurements were recorded on a Spectrospin CMS 47 instrument equipped with a 3T supra-conducting magnet. The ^{252}Cf pastil and the mylar film with the disposed sample were confined in an aluminium cylinder (diameter 15 mm,

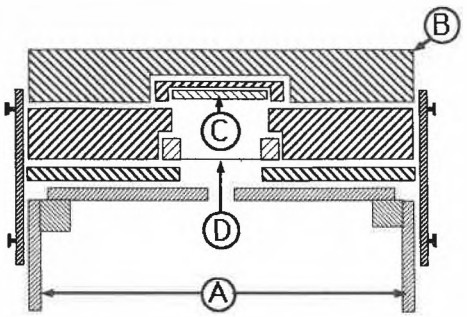

Fig. 1. Cross section of the trapping plate region of the ion source. A: original source; B: backing plate; C: ^{252}Cf source; D: mylar film with substance (sample).

height 12 mm), mounted in front of the trapping plate of the ICR cell, as shown in Fig. 1. The ^{252}Cf source (10 μCi) is furnished from the C.E.A. France. The 3 μg of underivated leucine enkephalin (Tyr-Gly-Gly-Phe-Leu, M_r = 555) used as a target have been purified by high performance liquid chromatography (HPLC) and are disposed by electrospray on mylar film. The support and the sample have the same potential as the trapping plates. The distance between the sample and the cell is about 4 mm and the hole through which the ions and neutrals may reach the cell has a diameter of 4 mm.

The analyses were performed in rapid-scan mode[9]. Ions formed and desorbed by radioactive decay are trapped within the ion source by the magnetic field. A compromise has to be found in order to get sufficient ions (ca. 10^3) without having to correct for ion-molecule reactions. A trapping time of 50 ms was chosed. The irradiation of the sample with α-particles of ^{252}Cf desorbs mainly neutral fragments. We were able to measure these neutrals by ionizing them with the standard electron beam (70 eV) of 40 ms duration before the detection cycle.

Leucine enkephalin is a polypeptide that is often used to investigate different desorption/ionization modes (LD[5, 10], SI[11], or PD[12]); we have chosen it in order to test the feasibility of the ^{252}Cf-PDI mode associated with FTMS. In Fig. 2a the spectrum of the ions due to ^{252}Cf-PDI (electron beam turned off) is displayed. The main ion is the molecular ion associated with a potassium atom. Only a few other ions can be seen. This is partly due to the very limited dynamic range of the rapid-scan mode. The molecular weight can conveniently be determined. The spectrum changes completely when the electron beam is turned on as is shown in Fig. 2b. Among the large number of ions, m/z 221, 260, 279, and 393 are diagnostic peaks of the leucine enkephalin which can usually be detected under PDI conditions. However, it should not be forgotten that some of the ions are due to the ionization and fragmentation of neutral radiolytical fragments of the parent molecule and could be potentially interesting for a structural analysis. The resolution was relatively low in these experiments because the measurements are made after the opening of the mass spectrometer to introduce the ^{252}Cf source and the sample. However, an addition of a solid state inlet system should allow high resolution spectra of an increased quality to be obtained.

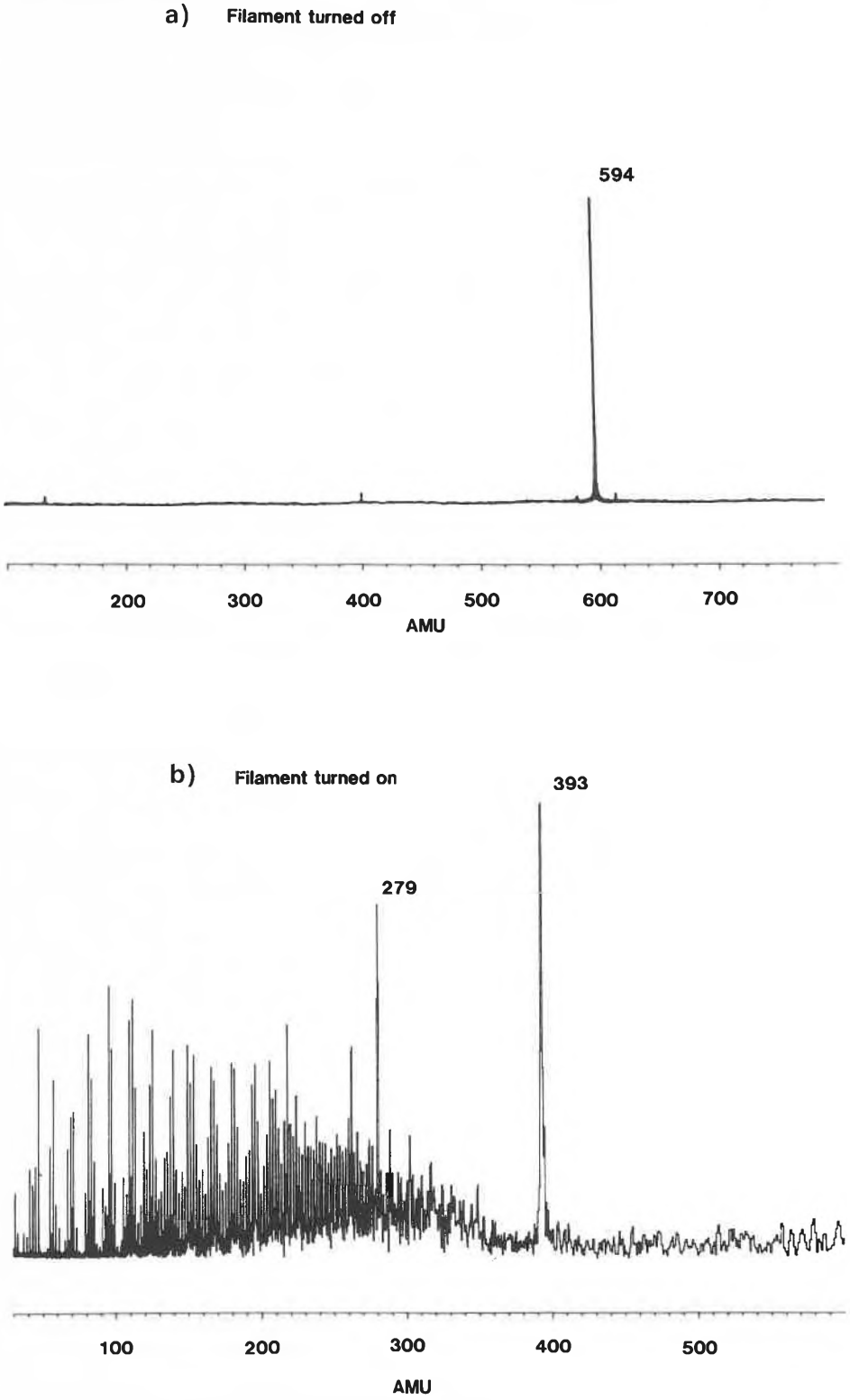

Fig. 2. Mass spectrum of leucine enkephalin: a) ions due to α-particles only; b) electron impact spectrum of neutrals.

These first results obtained by ^{252}Cf-PDI/FTMS are very promising for the analysis of peptides and generally of large biomolecules. This DI method leading to a high yield of cationized molecules can be very useful if MS/MS analysis is used. Furthermore, this mode is suitable for high resolution measurement without the use of a dual-cell or external ionization source.

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