Chemical Ionization Mass Spectrometry of Prostaglandins

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Summary Chemical ionization mass spectrometry has been used to elucidate the structure of prostaglandins.

BECAUSE prostaglandins[1–5] usually occur at the nanogram level in natural sources, highly sensitive analytical methods are needed to elucidate their structure. We have used electron impact (EI) and chemical ionization (CI) mass spectrometric techniques[6] to study the structure of prostaglandins.

Chemical ionization mass spectrometry employs a set of reagent ions produced by electron bombardment of a reagent gas at *ca.* 1 mm Hg pressure.[7] Methane gives predominantly CH_5^+, $C_2H_5^+$, and $C_3H_5^+$ ions. Protonated and adduct ions are then formed *via* ion–molecule reactions with the organic compound, present at a concentration of *ca.* 0·1%. Because the amount of energy transferred by this process is much less than the energy transferred by electron impact, the fragmentation of the "molecular ion" is less extensive.

The mass spectra were obtained on a Dupont 21–110B mass spectrometer modified for use in high pressure work.[8] Methane at 0·5 Torr was the reactant gas. 15 Nanomoles of

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material were introduced into the source with a direct introduction probe. The samples vapourized at 200—220 °C.

The Figure shows the CI mass spectrum of prostaglandin A_1, (PGA_1), other prostaglandins give similar spectra. However, in some cases, ions were not found in the molecular ion region, but were present corresponding to losses of molecules of water.

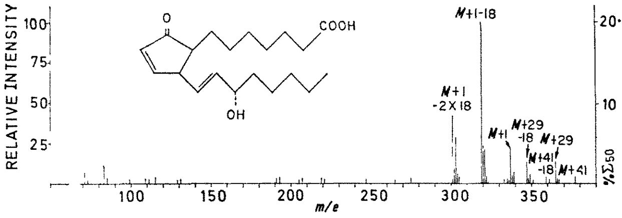

FIGURE. *Chemical ionization mass spectrum of prostaglandin* A_1, *molecular weight* **336**.

The CI mass spectrum of PGA_1, shows an "$M + 1$" ion at *m/e* 337, in addition to the loss of one and two molecules of water from this ion at *m/e* 319 and 301, respectively. The "adduct" ions are present at $M + 29$ and $M + 41$ in addition to the loss of one molecule of water from these ions at *m/e* 347 and 359, respectively. The presence of an "$M - 1$" ion at *m/e* 335, is a common feature in the chemical ionization mass spectra of hydrocarbons.[9]

The other carboxylic acids studied were trihydroxy ($PGF_{1\alpha}$, $PGF_{1\beta}$), dihydroxy-mono-one (PGE_1, PGE_2) and monohydroxy-mono-ones. In all cases, the number of molecules of water lost equalled the number of hydroxy-groups plus one. The loss of this additional molecule of water may be caused by the carboxy group (although this process requires an activation of a hydrogen atom on C-6, where C-1 is the carboxy carbon);[10] or it may involve the ketone group (although this water loss also occurs in the non-ketonic prostaglandins). Stable isotope labelling is necessary to resolve this interesting issue.

The rest of the CI mass spectrum has no prominent peaks. This is a characteristic of CI spectra, where abundant ions in the molecular ion region are produced and fragmentation is minimal.

Those prostaglandins that did not produce any $M + 1$ ions were *O*-methylated[11,12,13] using methyl iodide and the methylsulphinylmethide carbanion[14]. The derivative formed adds only **14** mass units per replaceable hydrogen to the compound and bulky groups are not lost by ionization or fragmentation processes helping to retain structural information in the molecular ion region.

Isotope labelling studies are required for the elucidation of various fragmentation pathways.

We thank the National Institutes of Health and the Robert A. Welch Foundation for financial support and Dr. John E. Pike of the Upjohn Company, Kalamazoo, Michigan for a gift of the prostaglandins.

(*Received, June* 21*st*, 1971; *Com.* 1014.)

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