Tetrahedron Letters,Vol.24,No.21,pp 2163-2164,1983 0040-4039/83/212163-02$03.00/0
Printed in Great Britain

ON THE MASS SPECTROMETRIC STRUCTURE DETERMINATION OF THE CYCLIC TETRAPEPTIDE TENTOXIN

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Abstract: Contrary to a recent report, the electron impact mass spectrum of the title compound does show an abundant molecular ion, as well as appropriate fragment ions which make it about as suitable for sequence determination as is the fast atom bombardment spectrum.

Aubagnac, Devienne, and Combarieu [2] recently reported use of low-resolution fast-atom bombardment (FAB) mass spectrometry for structure determination of the phytotoxic cyclotetrapeptide tentoxin, which for several years has been known to be cyclo-(-Leu-(Z)-MeΔPhe-Gly-MeAla-). [3,4] They suggested that this FAB spectrum is superior to the electron impact (EI) spectrum for structure determination of this molecule, at least in part because no molecular ion appears in the EI spectrum. This statement is surprising, for at least in the four different low- and high-resolution spectrometers with which we have obtained EI spectra of tentoxin [3] (at Arkansas, Purdue, Florida State, and Illinois) the molecular ion is quite abundant, ranging from 30% of base peak intensity [4] to being itself the base peak [5] depending upon the spectrometer.

The published FAB spectrum [2] apparently has an advantage over EI spectra in that it readily shows all four of the ions corresponding to loss of only one amino acid residue from the molecular ion (M - Gly, M - MeAla, M - Leu, and M - MeΔPhe) and also all four ions from loss of two complete residues. Of these, only M - Leu, M - Leu-MeΔPhe, and M - MeAla-Leu are significantly abundant in the EI spectrum. On the other hand, the EI spectrum [3,6] seems to have an advantage in that it shows many significant fragments which either contain or have lost only part of two adjacent residues, such as $C_6H_9NO_2^+$ ($CH_2CONMeCHMeCO^+$, m/z 127.0636) and $C_{16}H_{19}NO_2^+$ ($CHBuCONMeC(=CHPh)CO^+$, m/z 257.1414). FAB fragmentation of this molecule seems to emphasize the former type of cleavage to the near exclusion of the latter, and it is the latter which are especially needed in the case of cyclic peptides to distinguish, for example, the sequence cyclo(-Leu-MeΔPhe-Gly-MeAla-) from cyclo(-Leu-MeAla-Gly-MeΔPhe). [3] The ions discussed in ref. [2] do not differentiate those structures. Of course, such problems would be avoided by using both EI and FAB spectra, or by using FAB ionization in conjunction with MS/MS techniques as has been applied in sequencing other cyclic peptides.[7]

References and Notes

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(Received in Germany 28 February 1983)