

PEPTIDES. PART XX.<sup>1</sup> HIGH RESOLUTION MASS  
 SPECTROMETRY OF CYCLIC PEPTIDES

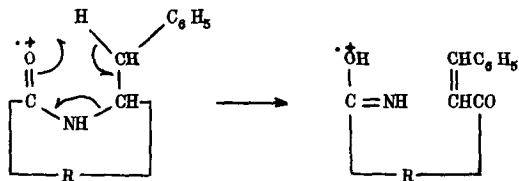
B. J. Millard

Robert Robinson Laboratories, University of Liverpool

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Mass spectra of cyclic depsipeptides have been reported,<sup>2,3</sup> but only one cyclic peptide, namely cyclo (Gly-L-Ala-D-Phe-Gly-D-Ala-L-Phe),<sup>4</sup> has apparently been examined.<sup>5</sup> This communication goes further by determinations of accurate masses of all the main fragments produced by electron impact on the same cyclic peptide and four others, namely cyclo (Gly-L-Leu-Gly-L-Leu-Gly),<sup>6</sup> cyclo (Gly-L-Leu-D-Leu-Gly-Gly),<sup>7</sup> cyclo (Gly-L-Leu-Gly-Gly-L-Leu-Gly)<sup>6</sup> and cyclo (Gly-L-Phe-L-Leu-Gly-L-Phe-L-Leu).<sup>8</sup> Sequences in cyclic peptides, which are not susceptible to all the usual methods of structural determination, can be deduced from their mass spectra.

Ring opening, with subsequent multiple fragmentation, occurs by several processes. For example, at a phenylalanine residue a transfer of hydrogen occurs which leads to an open-chain ion:



R = remainder of chain

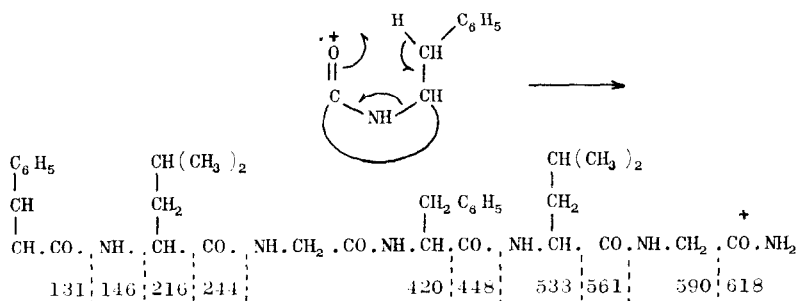
This ion undergoes further fragmentations as shown in the example



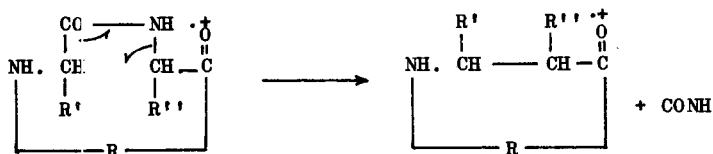
(ii) Phenylalanine

	CH(CH <sub>3</sub> ) <sub>2</sub>							CH(CH <sub>3</sub> ) <sub>2</sub>							
	CH <sub>2</sub>							CH <sub>2</sub> C <sub>6</sub> H <sub>5</sub>							
CO.	NH.	CH.	CO.	NH.	CH <sub>2</sub> .	CO.	NH.	CH.	CO.	NH.	CH.	CO.	NH.	CH <sub>2</sub> .	C≡O <sup>+</sup>
515	487	472	402	374	359	345	317	302	.....	.....	.....	.....	.....	.....	Type A
516	488	.....	403	375	360	346	318	303	.....	.....	.....	.....	.....	.....	Type B
514	486	.....	401	373	.....	344	316	301	.....	.....	.....	.....	.....	.....	Type C

(iii) opening by phenylalanine hydrogen transfer:

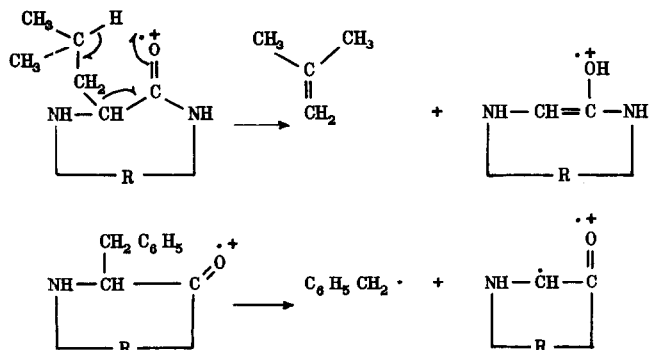


The identities of all ions shown were confirmed by accurate mass measurements, the measured mass to charge ratios being within 5 p.p.m. of the calculated ratios. Similar schemes may be written for the other four cyclic peptides; the compositions of the relevant prominent ions in the mass spectra of these peptides are shown in Table 1. All five cyclic peptides give a prominent ion at M-13 which is due to the loss of a molecule of HNCO. Furthermore, although the spectra are rich in metastable peaks, none of these correspond to the further fragmentation of the M-13 ion, whereas the open chain ions previously described undergo numerous fragmentations. This strongly suggests that the M-13 ion has a cyclic structure resulting from loss of HNCO in a cyclic process:

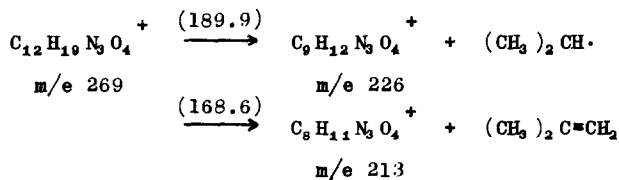


The loss of neutral fragments from the centre of chains of atoms without disruption of the chains is not unusual.<sup>9</sup> The loss of a molecule of HNCO is not therefore analogous to the loss of CO<sub>2</sub> with ring opening<sup>2</sup> which occurs in cyclic depsi-peptides.

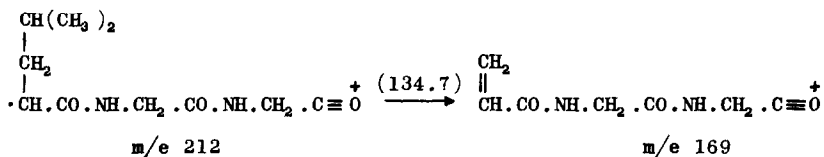
In addition to those fragmentations just described, the cyclic peptides lose side-chains by the normal processes well recognised for open-chain peptides:



A few subsidiary fragmentations occur in some ions produced from the leucine peptides. The ion of  $m/e$  269 produced in all three cases by type A fragmentation can lose both a C<sub>4</sub>H<sub>8</sub> and C<sub>3</sub>H<sub>7</sub> fragment from the side-chain, as shown by the appearance of metastable peaks (values shown in brackets).



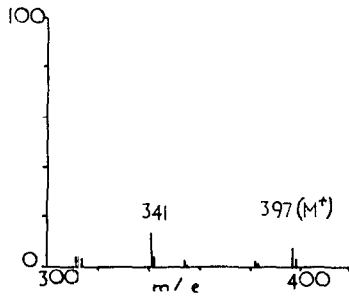
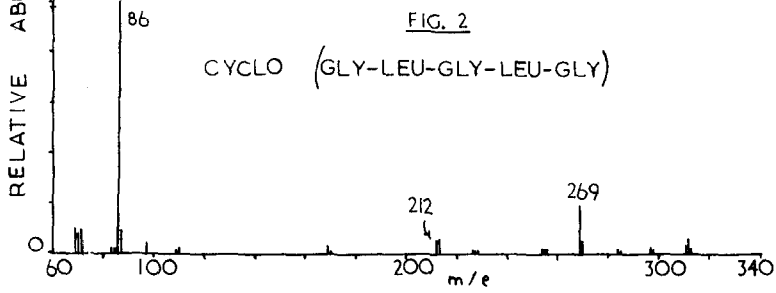
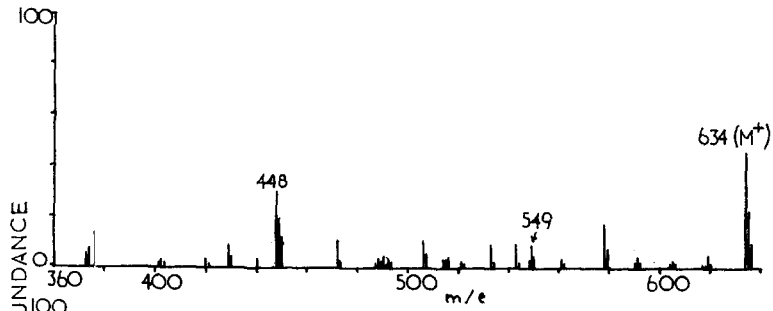
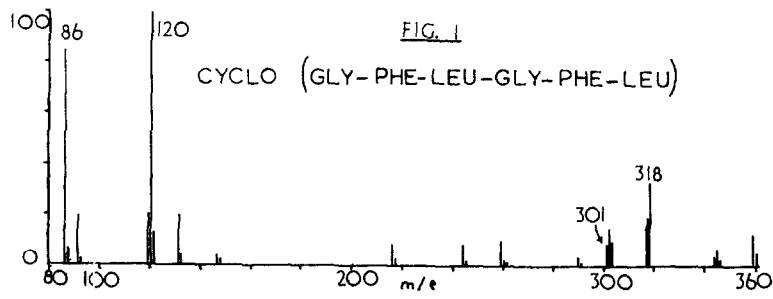
Where an ion of m/e 212 is produced, loss of a C<sub>3</sub>H<sub>7</sub> fragment occurs:



Figures 1 and 2 show respectively the mass spectra of cyclo (Gly-L-Phe-L-Leu-Gly-L-Phe-L-Leu) and cyclo (Gly-L-Leu-Gly-L-Leu-Gly). All spectra and accurate mass measurements were obtained on an A.E.I. M.S.9 mass spectrometer using a direct inlet system and source temperature of 250°.

#### Acknowledgements

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