

INTERNAL HOMOLOGY IN THE α CHAIN OF BOVINE LUTEINIZING HORMONE

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1. Introduction

Recently, "internal homology" was demonstrated in the primary structure of human growth hormone, placental lactogen and ovine prolactin [1]. In order to know if the notion of internal homology could be extended to the structure of glycoprotein hormones, we have examined the primary structure of bovine luteinizing hormone α chain. The amino-terminal sequence of the chain was indeed strikingly similar with the amino-terminal sequence of the carboxy-terminal, cyanogen bromide fragment of the molecule.

2. Material and methods

Two preparations of bovine LH α chain, corresponding to homogeneous electrophoretic components, were used for the sequence studies. Their carboxymethylated derivatives were split by cyanogen bromide as described [2] and the sequence of the resulting peptides were determined according to Gray [3]. A performic acid oxidized bovine LH α preparation was also submitted to Edman degradation in an automatic sequenator designated and built by the Czechoslovak Academy of Science.

Table 1

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
|--|-----|-----|-----|-------|-----|-----|-----|------------|-----|-----|------------|------------|-----|-----|
| Amino-terminal sequences of bovine LH α chain | Phe | Pro | Asp | Gly | Glu | Phe | Thr | Met | Gln | Gly | Cys | Pro Thr | Glu | Cys |
| | | | | * Asp | Gly | Glu | Phe | | | | | | | |
| Amino-terminal sequence of the carboxy-terminal cyanogen bromide fragment. | | | | Gly | Asx | Val | Arg | Val Glx | Glx | Asx | His Ser | Thr | Glx | Cys |

As illustrated by Niall et al. [1], identical residues are enclosed in rectangles; residues related through highly favored codon substitutions are enclosed in circles. It should be noted that the number of identical residues could be increased by determination of the amide or acid form of the glutamyl residues.

* Sequence of a minor peptide population, lacking Phe-Pro, at the amino-terminus.

3. Results and discussion

The amino-terminal sequence of the entire bovine LH α chain was successfully performed for 14 steps with the automatic sequenator (see table 1). The sequence determination was complicated by an amino-terminal heterogeneity, a minor peptide population lacking the amino-terminal Phe-Pro. The heterogeneity of the amino-terminal end of bovine LH α chain and thyroid-stimulating hormone α chain was already described by Pierce et al. [4]. Ambiguity was noted at position 12, where part of the peptide population had Thr instead of Pro.

The sequence details of the carboxy-terminal cyanogen bromide fragment were described previously [5].

Comparison of both sequences (see table 1) is compatible with an internal homology within the polypeptide chain of bovine LH α . In most of the positions, the amino acids are either identical or

closely related through highly favored codon substitutions, as in the case of growth hormone, placental lactogen and prolactin [1].

It appears thus that, as for holopeptide hormones like growth hormone and prolactin, the structure of the pituitary glycoprotein hormones may partly evolve through a gene duplication phenomenon.

References

- [1] H.D. Niall, M.C. Hogan, R. Sauer, I.Y. Rosenblum and F.C. Greenwood, *Proc. Natl. Acad. Sci. U.S.* 68 (1971) 866.
- [2] G. Hennen, Z. Prusik and G. Maghuin-Rogister, *European J. Biochem.* 18 (1971) 376.
- [3] W.R. Gray, in: *Methods in Enzymology*, ed. C.W. Hirs (Academic Press, New York, 1967) p. 469.
- [4] J.G. Pierce, T.H. Liao, R.B. Carlsen and T. Reimo, *J. Biol. Chem.* 246 (1971) 866.
- [5] G. Maghuin-Rogister, J. Closset and G. Hennen, *FEBS Letters* 13 (1971) 301.