CLEAVAGE OF γ -CARBOXYGLUTAMYL PEPTIDE BONDS BY CYANOGEN BROMIDE AND BY N-BROMOSUCCINIMIDE

Kouichi KATAYAMA* and Koiti TITANI

Department of Biochemistry, University of Washington, Seattle, WA 98195, USA

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1. Introduction

Factor IX is the zymogen of a serine protease involved in the middle phase of the intrinsic pathway of blood coagulation and, like four other coagulation factors, prothrombin, factor X, factor VII and protein C, requires vitamin K for its biosynthesis [1]. The vitamin K-dependent modification was recently shown to lead to a series of γ -carboxyglutamyl residues located in amino-terminal region of the molecule [2-5].

During the study of the amino acid sequence of the amino-terminal segment of bovine factor $IX_{a\alpha}$ (obtained by activation of factor IX by a protease from Russell's viper venom [6]), we observed that cyanogen bromide cleaved not only the single methionyl bond but also, in an unexpected manner, peptide bonds in a region which is rich in γ -carboxy-glutamyl residues.

The present communication identifies the sites of cleavage by cyanogen bromide and indicates that other bromine-containing reagents such as N-bromosuccinimide and BNPS-skatole (bromine adduct of 2-(2-nitrophenyl sulfenyl)-3-methyl indole) effect similar cleavage.

2. Materials and methods

Bovine factor $IX_{a\alpha}$ [6] was generously supplied by Dr Kazuo Fujikawa of this Department. The amino-

* Permanent address: Eisai Research Laboratories, Eisai Co. Ltd, Koishikawa 4, Bunkyo-ku, Tokyo, Japan terminal segment (residues 1-181) was isolated by chromatography on a column of SP-Sephadex C-25 in the presence of 7 M urea after reduction and pyridylethylation of active factor $IX_{a\alpha}$. A heptapeptide (residues 5-11) was prepared by successive digestion of fragment CB II (residues 1-61) with trypsin and subtilisin as described below. The sequence of this peptide has been determined in [7]; two residues in the sequence were subsequently identified in [5] as γ -carboxyglutamyl residues.

Cyanogen bromide was a product of Eastman (reagent grade) or Pierce. BNPS-skatole and N-bromosuccinimide were obtained from Pierce and Nutritional Biochemicals, respectively. DL-allo-Hydroxyglutamic acid was obtained from US Biochemical Co.

Cleavage with cyanogen bromide was carried out at room temperature [8] or 4°C [9] in 70% formic acid for various periods of time. The reaction mixture was diluted with water and lyophilized. Reaction with N-bromosuccinimide was carried out at room temperature in 70% acetic acid for 30 min and terminated by adding a small amount of 88% formic acid [10]. Reaction with BNPS-skatole was performed at room temperature in 80% acetic acid for various periods of time [11]. The reaction mixture was diluted with an equal volume of water and excess reagent extracted with 1-chlorobutane.

Peptides were separated by gel filtration and high voltage paper electrophoresis. Amino acid analyses were performed on a Durrum Amino Acid Analyzer (Model D-500). Automated Edman degradations were carried out on a Beckman Sequencer (Model 890B) by the method in [12]. SDS—urea gel electrophoresis was performed by the method in [13].

3. Results and discussion

Since amino acid analysis indicated the presence of one methionine residue/mol amino-terminal segment (residues 1–181) of factor IX_{ao} , cleavage with cyanogen bromide was expected to generate two fragments. The gel filtration profiles of products with cyanogen bromide at room temperature for 24 h and at 4°C for 7 h are shown in fig.1A and 1B, respectively. Fraction 1 in fig.1A and 1B was further separated by gel filtration on a column of Sephadex G-75 into the unreacted segment and a homogenous fragment, CB 1. Fraction 2 of fig.1B contained another homogenous fragment, CB II. Amino acid and sequence analyses indicated that CB I and CB II corresponded to residues 62-181 and 1-61 of the amino-terminal segment, respectively. Three fragments were isolated by gel filtration on a column (1.5 X 150 cm) of Sephadex G-50 superfine in 0.1 M NH₄HCO₃ from fraction 2 of fig.1A and shown to be residues 28-61. 31-61 and 37-61, respectively, by amino acid and sequence analyses. Similar analyses indicated that a fragment isolated by paper electrophoresis, at pH 6.5, from fraction 3 of fig.1A comprised residues 41-61.

As judged by SDS—urea gel electrophoresis, CB II was itself stable in 70% formic acid at room temperature for 3 days, but in the presence of cyanogen bromide under the same conditions, it was rapidly degraded. After 1, 2 and 3 days, respectively, 39%, 17% and 7% of the initial product remained.

These results suggest that cyanogen bromide or some impurity in the reagent cleaves the peptide bond at the carboxyl side of γ -carboxyglutamyl residues as shown in fig.2.

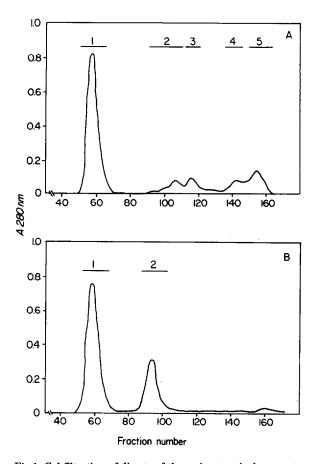


Fig.1. Gel filtration of digests of the amino-terminal segment (residues 1-181) of bovine factor $IX_{a\alpha}$ with cyanogen bromide. Digests prepared at room temperature for 24 h (A) and at 4°C for 7 h (B) were applied to a column (2.5 × 115 cm) of Sephadex G-50 Superfine in 9% formic acid and eluted at a flow rate of 24 ml/h. Fractions of 4 ml were collected and pooled as indicated.

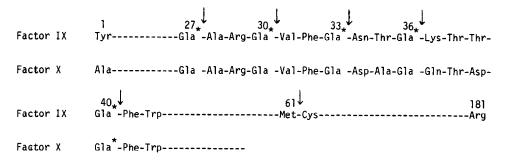


Fig.2. Partial sequence of the amino-terminal segment of bovine factor $IX_{a\alpha}$ and the sites cleaved by cyanogen bromide (indicated by arrows). The sequence of bovine factor X is shown for comparison. Gla* denotes γ -carboxyglutamyl residues tentatively identified and placed by the homology between bovine factors IX and X in this region of the molecules [5,14,15].

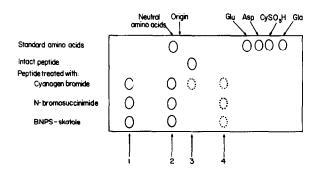


Fig.3. Cleavage of a heptapeptide (residue 5-11 of bovine factor IX) containing 2 γ -carboxyglutamyl residues. The peptide was treated with 4000 equiv. cyanogen bromide in 70% formic acid for 3 days, 2 equiv. of N-bromosuccinimide in 70% acetic acid for 30 min or 20 equiv. BNPS-skatole in 80% acetic acid for 5 h, and then the product separated by electrophoresis, at pH 6.5, for 1 h at 2000 V. Peptides were eluted and identified by amino acid analysis to be Phe-Val-Arg (labelled 1), Lys-Leu-X (2), intact peptide (3) and Lys-Leu-Gla-X (4).

In order to confirm this interpretation, a heptapeptide of known sequence containing 2γ -carboxyglutamyl residues (Gla), i.e., Lys—Leu—Gla—Gla—Phe—Val—Arg, was treated in a similar manner at room temperature for 3 days. Two major peptides (labelled 1 and 2 in fig.3) and one minor peptide (4 in fig.3) were observed. Similar results were obtained for the product of reaction with N-bromosuccinimide (fig.3); in this case, 2 equiv. reagent completely degraded the peptide in 30 min at room

temperature, generating 3 subpeptides. Amino acid analysis after acid hydrolysis indicated that the cationic peptide (labelled 1) was Phe-Val-Arg and the neutral peptide (labelled 2) Lys-Leu-X. X refers to an unknown amino acid derivative which is generated from γ -carboxyglutamyl residue during the cleavage reaction. After acid hydrolysis of the peptide, this derivative is eluted on a Durrum Amino Acid Analyzer at a position in close proximity to DL-allo-hydroxyglutamic acid, but its chemical structure is unknown. The minor peptide (labelled 4) was Lys-Leu-Gla-X.

BNPS-skatole also cleaved the heptapeptide at the sites identical to those cleaved by cyanogen bromide and by N-bromosuccinimide, but more than 10 equiv. reagent and 5 h were necessary to complete the cleavage.

The present results indicate that brominating reagents such as N-bromosuccinimide and BNPS-skatole cleave γ -carboxyglutamyl peptide bonds. The cleavage with cyanogen bromide may be due to the reagent itself or bromine pre-existent in the reagent. A hypothetical mechanism for cleavage is shown in fig.4. The γ -carboxyglutamyl residue is brominated at the γ -carbon and the peptide bond subsequently cleaved via its iminolactone. The new carboxylterminal residue, therefore, may be a lactonized form of γ -hydroxy- γ' -carboxy-glutamic acid, since the peptide Lys-Leu-X is neutral in charge, at pH 6.5.

While this observation initially complicated our analysis of the sequence of both factors IX [14] and X [15], elucidation of the site of anomalous cleavage

Fig.4. A hypothetical mechanism for the cleavage of γ -carboxyglutamyl peptide bond by bromo-reagents.

now facilitates our examination of this region of factor IX.

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