Cathepsin D is involved in the clearance of Alzheimer's β-amyloid protein

Hideaki Hamazaki*

Department of Biology, Kitasato University School of Medicine, Sagamihara, Kanagawa 228, Japan

Received 10 September 1996

Abstract The cerebral deposition of 39–42 residue amyloid β -protein $(A\beta)$ is a histopathological characteristic of Alzheimer's disease. The present study is aimed at finding proteinases responsible for the intracellular clearance of $A\beta.$ The $A\beta$ -degrading proteinase was purified from rat brain. Aminoterminal sequence analysis indicated the $A\beta$ -degrading proteinase was cathepsin D. Purified cathepsin D hydrolyzed $A\beta$ between Phe19 and Phe20. Cathepsin D is likely to be involved in the intracellular clearance of aggregatable $A\beta,$ since $A\beta$ fragments with Phe20 at the amino-terminus have been reported to be secreted from several lines of cultured cells.

Key words: Alzheimer's disease; β-Amyloid; Amyloidosis; Cathepsin D; Rat brain; Aspartic proteinase

1. Introduction

One of the hallmarks of Alzheimer's disease is the cerebral deposition of 39–42 residue amyloid β -peptide (A β). A β is produced by proteolytic processing from β -amyloid precursor protein (β APP), a 110–130 kDa type I integral membrane glycoprotein. A β is secreted from most cells including neurons and the overproduction of A β is likely to lead to the formation of neuritic plaques and vascular deposits in the brain microvessels (see [1] for review). Therefore, it is critically important to maintain the normal balance between production and clearance of A β to prevent the cerebral deposition of A β .

The proteolytic processing of β APP has been studied using cultured cells and three endoproteinases designated α -, β -, and γ -secretases have been proposed to be engaged in the processing. The α -secretase has been shown to be present at or near the cell surface [2] and cleaves β APP within the A β region (at Lys¹⁶-Leu¹⁷ of A β) to produce a large secreted derivative (APPs) and a 9 kDa membrane-associated fragment, neither of which can produce amyloid because they do not contain the entire A β [3,4]. The β -secretase cleaves β APP at the NH₂-terminus of A β , producing a 10 kDa COOH-terminal fragment, which is further cleaved at the COOH-terminus of A β by γ -secretase. It has been described that A β formation occurs at least in part in the endosomes/lysosomes [5,6] after cell surface β APP has been reinternalized via clathrin-coated pits [7–9].

In addition to the cleavage after Lys¹⁶ of Aβ region, other

*Corresponding author. Fax: (81) (427) 78-8441.

Abbreviations: A β , amyloid β -peptide; β APP, β -amyloid precursor protein; FAD, familial Alzheimer's disease; HCHWA, hereditary cerebral hemorrhage with amyloidosis; RP-HPLC, reverse phase high performance liquid chromatography; TBS, Tris-buffered saline; TFA, trifluoroacetic acid; PAGE, polyacrylamide gel electrophoresis

cleavages are also suggested to be important to eliminate $A\beta$ generation. For instance, Busciglio et al. reported that CHO cells secreted $A\beta$ fragments with a heterogeneous NH_2 -terminal sequence, reflecting cleavages after Lys¹⁶, Phe¹⁹, and Val²⁴ [10] and Haass et al. described that kidney 293 cells secreted $A\beta$ -related peptides, reflecting cleavages after Lys¹⁶, Leu¹⁷ and Phe¹⁹ [11]. It is interesting that both cell lines produce $A\beta$ -related peptides with Phe²⁰ at the NH_2 -terminus. However, proteinase(s) that cleave after Phe¹⁹ of the $A\beta$ region have not been identified.

The present work was aimed at finding proteinases responsible for the degradation of $A\beta$ in the brain and it was found that cathepsin D (EC 3.4.23.5) was the major proteinase that hydrolyzed $A\beta$ in the middle of the sequence to eliminate the amyloidogenic peptide. The involvement of cathepsin D in the elimination of $A\beta$ has been suggested by the observations that the proteinase specifically cleaves full-length $A\beta$ between Phe¹⁹ and Phe²⁰.

2. Materials and methods

2.1. Materials

Synthetic $A\beta_{1-42}$ and $A\beta_{1-28}$ were purchased from American Peptide Co. (Sunnyvale, CA, USA). The purity of all synthetic peptides was above 98% on RP-HPLC. Pepstatin A, leupeptin, and E-64 were purchased from Sigma (St. Louis, MO, USA). Pepstatin A was coupled with Affi-Gel 10 (BioRad) by incubating the mixture of 0.05 mmol of pepstatin A, 0.05 mmol of diisopropylcarbodiimide, 0.06 mmol of hydroxybenzotriazole, and aminoethyl-Affi-Gel 10 (packed volume; 2 ml) in 2.5 ml of dimethylformamide at room temperature for 15 h. After coupling gels were successively washed with dimethylformamide, 1 M acetic acid, and 0.5 M borate buffer, pH 9.5.

2.2. Digestion of $A\beta$ by the brain extract

Rat brain (2 g, stored at -20° C) was minced in 20 ml of Trisbuffered saline (TBS; 0.15 M NaCl, 10 mM Tris-HCl, pH 7.5), and homogenized for 30 s with a Polytron homogenizer at 4°C. The brain extract was obtained as the supernatant after the homogenate was centrifuged at $10^5 \times g$ for 60 min. To estimate the pH optimum of $A\beta$ hydrolysis, $A\beta_{1-28}$ (1 nmol) was incubated with the rat brain extract (5 µl) in 20 µl of 0.1 M acetate buffer (pH 3.5 and 4.5) or phosphate buffer (pH 5.5-7.5), at 37°C for 30 min. After incubation the reaction was stopped by adding 0.1 ml of 0.05% trifluoroacetic acid (TFA) followed by heating at 100° C for 5 min. The reaction mixture was filtered through a membrane filter (0.22 µm; Amicon) and then the filtrate was chromatographed on an Inertsil 300C8 column (4.6×100 mm; GL Science Inc., Japan). The peptides were eluted at a rate of 1 ml/min with a 20-min linear gradient of 0-40% acetonitrile in 0.05% TFA and monitored by absorbance at 215 nm.

2.3. Purification of AB-degrading proteinase

Rat brain (30 g) was homogenized in 300 ml of TBS containing 0.5 mM phenylmethylsulfonyl fluoride (PMSF), 1 μ M leupeptin, and 5 mM EDTA, and centrifuged at $2 \times 10^4 \times g$ for 30 min. After the supernatant fraction was mixed with one-tenth volume of 1 M acetate buffer, pH 4.5, precipitates were removed by centrifugation at $10^5 \times g$ for 60 min. The supernatant fraction (290 ml) containing

108 units of Aβ-degrading proteinase was loaded on a column (1 ml) of pepstatin A-Affi-Gel 10 equilibrated with 0.1 M acetate buffer, pH 4.5. After the column was washed with 10 ml of the column buffer, Aβ-degrading proteinase was eluted with 0.5 M borate buffer, pH 9.6, and 0.5-ml fractions were collected, monitored by absorbance at 280 nm, and proteinase activity assayed using $A\beta_{1-28}$ as substrate. The proteinase preparation purified by affinity chromatography was loaded on a column (16×600 mm) of Superdex 75 pg column (Pharmacia Biotech) equilibrated with TBS. The column was eluted with TBS at a flow rate of 0.5 ml/min and 1-ml fractions were collected, monitored by absorbance at 215 nm, and AB-degrading activity assayed. The obtained enzyme preparation contained 34.4 units of Aβdegrading activity (specific activity: 141 units/mg protein). One unit of Aß-degrading activity was defined as the amount of proteinase required to hydrolyze 1 μmol of $A\beta_{1-28}$ after Phe^{19} in 0.1 M acetate buffer, pH 4.5, at 37°C in 1 h. SDS-PAGE was performed using 10% acrylamide gel with Tris-glycine buffer system [12] and gels were stained with Coomassie brilliant blue R-250.

2.4. Hydrolysis of A\beta by cathepsin D

 $A\beta_{1-42}$ (1 nmol) was incubated with 1.2 µg of purified brain cathepsin D in 40 µl of 0.1 M acetate buffer, pH 4.5, at 37°C for 4 h. After incubation the reaction mixture was chromatographed on an Inertsil 300C8 column (4.6×100 mm) with a solvent system containing 0.05% TFA. The peptides were eluted at a rate of 1 ml/min with a 30-min linear gradient of 0–60% acetonitrile containing 0.05% TFA and fractions with UV absorbance at 215 nm were collected for peptide sequencing.

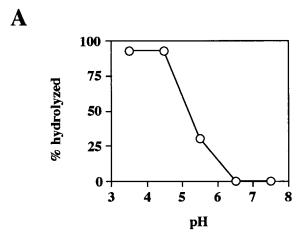
2.5. Analysis of protein sequence

Samples were spotted on polybrene-coated glass fiber disks and sequenced on an Applied Biosystems model 491 protein sequencing system. Data were analyzed using a model 610A Data Analysis Program.

3. Results and discussion

To examine the effects of pH on the degradation of $A\beta$, the rat brain extract was incubated with $A\beta_{1-28}$ at 37°C for 30 min, and subsequently the degradation products were analyzed on RP-HPLC (Fig. 1A). Since AB was effectively hydrolyzed at pH 3.5-4.5, the following experiments were performed at pH 4.5. To characterize the proteinase(s) that hydrolyze A β , the brain extract was incubated with A β_{1-28} in the presence of specific proteinase inhibitors and the incubation mixture was analyzed on RP-HPLC (Fig. 1B). Neither E-64 (cysteine proteinase inhibitor) nor leupeptin (serine and cysteine proteinase inhibitor) inhibited the hydrolysis of $A\beta_{1-28}$ by the brain extract, whereas pepstatin A (aspartic proteinase inhibitor) completely inhibited the proteolysis. Neither EDTA (5 mM) nor PMSF (1 mM) inhibited the hydrolysis of $A\beta$ (data not shown). The results suggest that the major proteinase involved in the hydrolysis of Aβ is aspartic proteinase.

The A β -degrading aspartic proteinase was purified by affinity chromatography using pepstatin A as an absorbent immobilized on Affi-Gel 10 (see Section 2). After affinity chromatography, gel filtration was performed to remove a \sim 70 kDa protein which had no A β -degrading activity (Fig. 2A). By these two steps of chromatography the A β -degrading proteinase was purified approximately 3000-fold with 32% recovery. The enzyme preparation after gel filtration gave a single band on SDS-PAGE at \sim 43 kDa (Fig. 2B). The NH₂-terminal sequence of the purified A β -degrading enzyme was determined to be EPVSELLKNYLDAQY, which is consistent with the protein sequence deduced from the nucleotide sequence of rat cathepsin D cDNA cloned from a pituitary cDNA library [13]. The molecular weight and the partial pro-



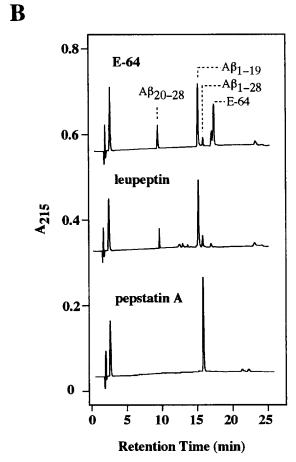


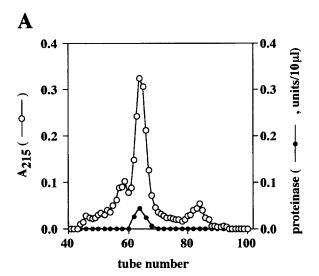
Fig. 1. Hydrolysis of $A\beta$ in the middle of the sequence with rat brain extract. A: Effects of pH on the hydrolysis of $A\beta_{1-28}$. $A\beta_{1-28}$ was incubated at 37°C for 30 min with the brain extract. B: Inhibition of $A\beta$ -degrading proteinase in the brain extract. $A\beta_{1-28}$ was incubated at 37°C with the brain extract in 0.1 M acetate buffer, pH 4.5, containing E-64 (3200 μ M), leupeptin (1200 μ M), or pepstatin A (1.5 μ M). After 30-min incubation products were analyzed on RP-HPLC.

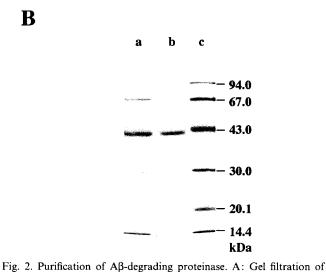
tein sequence indicated that the $A\beta$ -degrading proteinase was cathepsin D. Cataldo et al. demonstrated the presence of cathepsin D and its mRNA in human brain neurons by immunohistochemical studies and by in situ hybridization [14], sug-

gesting brain neurons produce the same cathepsin D as peripheral tissues.

To show cathepsin D is able to degrade aggregatable full-length A β , A β_{1-42} was incubated with the proteinase purified from rat brain. Fig. 3 shows that cathepsin D hydrolyzes A β_{1-42} after Phe¹⁹ and Leu³⁴, producing A β_{1-19} , A β_{20-34} , and A β_{35-42} . About 80% of A β_{1-42} was hydrolyzed in 4 h. The specific hydrolysis of A β between Phe¹⁹ and Phe²⁰ by cathepsin D suggests that this endoproteinase contributes to the generation of A β -related peptides with Phe²⁰ at the NH₂-terminus which have recently been described to be secreted from several lines of cultured cells [10,11].

The present results give direct evidence that cathepsin D is a major proteinase in the brain that is able to degrade full-length $A\beta$ in the middle of the sequence. Since cathepsin D localizes in lysosomes and endosomes [14], where $A\beta$ is gen-





rigidal Aβ-degrading enzyme. The proteinase preparation purified by affinity chromatography was loaded on a column (16×600 mm) of Superdex 75 pg column equilibrated with TBS. The column was eluted with TBS at a flow rate of 0.5 ml/min and 1 ml fractions were collected, monitored by absorbance at 215 nm, and proteinase activity assayed every second fraction. B: SDS-PAGE of the purified enzyme. Lane a: 2 μ g of the enzyme preparation after affinity chromatography; lane b: 2 μ g of the enzyme preparation after gel filtration; lane c: molecular weight standard.

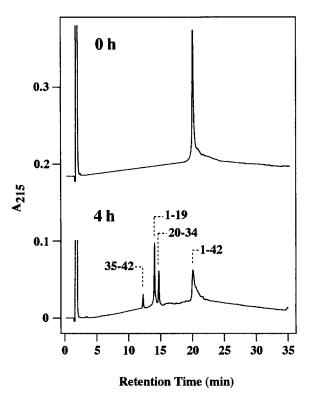


Fig. 3. Cleavage of full-length A β by cathepsin D. A β_{1-42} (1 nmol) was incubated with 1.2 μg of purified brain cathepsin D in 40 μ l of 0.1 M acetate buffer, pH 4.5, at 37°C for 4 h. After incubation the peptides were separated on an RP-HPLC and peaks with UV absorbance at 215 nm were collected for peptide sequencing.

erated by proteolytic processing [5,6], it is possible that cathepsin D eliminates $A\beta$ at the site of generation. It has been described that cathepsin D was capable of producing the cleavages resulting in $A\beta$ generation, especially when a synthetic peptide with Swedish-type mutation was used as substrate [15]. In conclusion, I would like to propose that cathepsin D is able to work as an $A\beta$ -producing enzyme especially for Swedish-type mutants and also as an $A\beta$ -eliminating enzyme by cleaving at Phe^{19} - Phe^{20} of the $A\beta$ region and that the balance between the two cleavages affects the secretion of the amyloidogenic peptide.

Acknowledgements: The author thanks Dr. Takeshi Nakamura for the use of FPLC and Katsumi Aoki, Yuko Furuse, Toshiyuki Nishimaki, and Akiko Shinozuka for their technical assistance.

References

- [1] Selkoe, D.J. (1994) Annu. Rev. Cell Biol. 10, 373-403.
- [2] Sisodia, S.S. (1992) Proc. Natl. Acad. Sci. USA 89, 6075-6079.
- [3] Sisodia, S.S., Koo, E.H., Beyreuther, K., Unterbeck, A. and Price, D.L. (1990) Science 248, 492–495.
- [4] Esch, F.S., Keim, P.S., Beattie, E.C., Blacher, R.W., Culwell, A.R., Oltersdorf, T., McClure, D. and Ward, P.J. (1990) Science 248, 1122-1124.
- [5] Haass, C., Koo, E.H., Mellon, A., Hung, A.Y. and Selkoe, D.J. (1992) Nature 357, 500-503.
- [6] Golde, T.E., Estus, S., Younkin, L.H., Selkoe, D.J. and Younkin, S.G. (1992) Science 255, 728-730.
- [7] Haass, C., Hung, A.Y., Schlossmacher, M.G., Teplow, D.B. and Selkoe, D.J. (1993) J. Biol. Chem. 268, 3021–3024.
- [8] Nordstedt, C., Caporaso, G.L., Thyberg, J., Gandy, S.E. and Greengard, P. (1993) J. Biol. Chem. 268, 608-612.

- [9] Koo, E.H. and Squazzo, S. (1994) J. Biol. Chem. 269, 17386– 17389.
- [10] Busciglio, J., Gabuzda, D.H., Matsudaira, P. and Yankner, R.A. (1993) Proc. Natl. Acad. Sci. USA 90, 2092–2096.
- [11] Haass, C., Hung, A.Y., Selkoe, D.J. and Teplow, D.B. (1994)J. Biol. Chem. 269, 17741–17748.
- [12] Laemmli, U.K. (1970) Nature 227, 680-685.

- [13] Birch, N.P. and Loh, Y.P. (1990) Nucleic Acids Res. 18, 6445–6446.
- [14] Cataldo, A.M., Barnett, J.L., Berman, S.A., Li, J., Quarless, S., Bursztajn, S., Lippa, C. and Nixon, R.A. (1995) Neuron 14, 671– 680
- [15] Ladror, U.S., Snyder, S.W., Wang, G.T., Holzman, T.F. and Krafft, G.A. (1994) J. Biol. Chem. 269, 18422–18428.