

# The $\beta$ -amyloid protein precursor of Alzheimer disease has soluble derivatives found in human brain and cerebrospinal fluid

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**ABSTRACT** In this study, we use antisera to synthetic  $\beta$ -amyloid protein precursor ( $\beta$ APP) peptides to identify, in human brain and cerebrospinal fluid (CSF), soluble  $\approx 125$ - and  $\approx 105$ -kDa derivatives of the  $\beta$ APP that lack the carboxyl terminus of the full-length, membrane-associated forms. We show that the soluble  $\approx 125$ -kDa  $\beta$ APP derivative contains the Kunitz protease inhibitor domain, whereas the  $\approx 105$ -kDa form does not, and we confirm that these two proteins are soluble  $\beta$ APP derivatives by purifying each from human CSF and directly sequencing its amino terminus.

The principal proteinaceous component of the amyloid deposited in senile plaques and cerebral blood vessels in Alzheimer disease (AD) is a 39- to 42-residue polypeptide (the  $\beta$ -amyloid protein  $\beta$ AP) (1-3) derived from a much larger  $\beta$ -amyloid protein precursor ( $\beta$ APP) (4-7). As shown in Fig. 1, the  $\beta$ APP gene produces at least three mRNAs (8-10) through alternative splicing of two exons (8). One of these exons encodes a 19-amino acid domain; the other encodes a 56-amino acid domain that is highly homologous to the Kunitz family of serine protease inhibitors. In each full-length precursor, the 39- to 42-residue  $\beta$ AP occurs as an internal sequence (Fig. 1), which extends from the extracellular region into the putative membrane-spanning domain (5, 11). Thus, it appears that proteolytic cleavage of the  $\beta$ APP at both the amino and carboxyl termini of the  $\beta$ AP is necessary to generate the  $\beta$ AP found in amyloid deposits.

In previous studies (12, 13), we identified a set of  $\approx 110$ - to  $\approx 135$ -kDa membrane-associated proteins that represent full-length forms of the  $\beta$ APP. Proteolytic cleavage of these full-length forms at either the amino or carboxyl terminus of the  $\beta$ AP (Fig. 1) would be expected to generate large soluble derivatives that could be functionally significant. There is, in fact, evidence that some membrane-associated proteins with structures similar to the  $\beta$ APP undergo limited proteolysis close to their membrane-spanning domain to generate soluble amino-terminal derivatives that are functionally important [e.g., prepro-epidermal growth factor (14, 15) and growth hormone receptor (16)]. Thus, a reasonable first step in evaluating both the process of amyloid deposition in AD and the normal function of the  $\beta$ APP is to determine whether soluble derivatives are produced from the membrane-associated forms of this protein. In this study, we examine this question by using antisera to synthetic  $\beta$ APP peptides to identify soluble  $\beta$ APP derivatives, which are then isolated and sequenced. Our results show that soluble Kunitz protease inhibitor (KPI)-containing ( $\approx 125$  kDa) and KPI-free ( $\approx 105$  kDa) derivatives of the  $\beta$ APP are readily detected in human brain and cerebrospinal fluid (CSF). Some of these findings have previously been reported in preliminary form (17).

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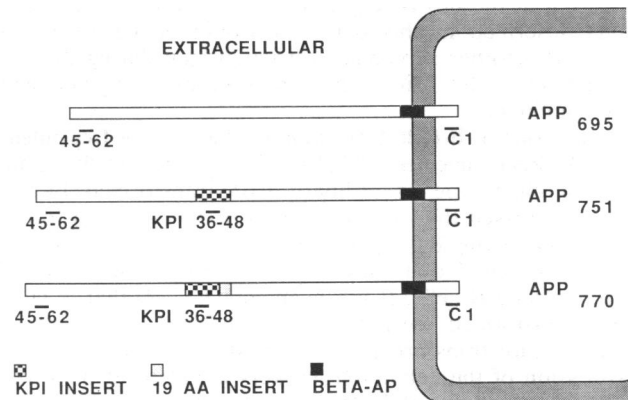


FIG. 1. Schematic structure of full-length 695-, 751-, and 770-residue forms of  $\beta$ APP based on the model of  $\beta$ APP<sup>695</sup> proposed by Kang *et al.* (5). AA, amino acid.

## MATERIALS AND METHODS

**Antisera.** To prepare antisera to KPI-containing forms of the  $\beta$ APP (anti-KPI), keyhole limpet hemocyanin was linked to a synthetic peptide (Peninsula Laboratories) corresponding to amino acids 36-48 (KPI<sup>36-48</sup>) in the KPI insert (9, 10). Production of antisera to the 20 carboxyl-terminal residues of the full-length  $\beta$ APP (anti-C<sub>1</sub>) has been described (12), as has (13) the production of antisera to amino acids 45-62 ( $\beta$ APP<sup>45-62</sup>) in the  $\beta$ APP sequence (anti-N).

**Brain Tissue.** The tissue used in this report was dissected at autopsy, flash frozen, and stored at  $-80^{\circ}\text{C}$ . Cerebral cortex in Figs. 3B and 4 and the nucleus basalis of Meynert in Fig. 4B and C are from the brain of a control patient [age, 89 years; postmortem interval (PMI), 3 hr]; cerebral cortex used in Fig. 3A is from an AD patient (age, 85 years; PMI, 2 hr). For preparation of soluble and membrane-associated proteins, tissue was homogenized in 2 vol of TS buffer (50 mM Tris-HCl/150 mM NaCl/5 mM EDTA/2 mM phenylmethylsulfonyl fluoride/1  $\mu\text{g}$  of leupeptin per ml/10  $\mu\text{g}$  of aprotinin per ml/0.1  $\mu\text{g}$  of pepstatin per ml/1  $\mu\text{g}$  of 7-amino-1-chloro-3-tosylamido-2-heptanone per ml, pH 7.6), and the homogenate was centrifuged at  $100,000 \times g$  for 1 hr. The supernatant, which contains soluble proteins, was removed. In an effort to remove residual soluble forms from the pellet, it was homogenized in 2 vol of TS, centrifuged 1 hr at  $100,000 \times g$ , the supernatant was discarded, and the resulting pellet was rinsed with TS. Membrane-associated forms were then extracted by homogenizing the washed pellet in 2 vol of TS buffer containing 2% Triton X-100 and centrifuging for 1 hr at  $100,000 \times g$ .

Abbreviations: AD, Alzheimer disease;  $\beta$ AP,  $\beta$ -amyloid protein;  $\beta$ APP,  $\beta$ APP precursor; KPI, Kunitz protease inhibitor; CSF, cerebrospinal fluid; PMI, postmortem interval.

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**CSF.** CSF in Fig. 3D is from two living AD patients (ages, 69 and 67 years) and two controls (ages, 66 and 76 years). CSF in Fig. 4A was collected (i) postmortem from a patient with AD (age, 71 years; PMI, 3.5 hr) and (ii) from a living control (age, 71 years). CSF samples were dialyzed against 1 mM phosphate buffer (pH 7.4), and the desalted protein was concentrated 20:1.

**Transfected Cell Lines.** The human 293 embryonic kidney cells stably transfected with a  $\beta$ APP<sup>695</sup> expression construct (see Fig. 3C) have been described (12). Transcription in these cells is driven by the human cytomegalovirus immediate early gene enhancer/promoter unit. The construct also contains the simian virus 40 t-splice and late polyadenylation signal. Cells that express recombinant  $\beta$ APP<sup>751</sup> cDNA (see Fig. 2) were prepared similarly.

**SDS/PAGE.** Proteins were electrophoresed on 7% or 5–20% SDS/polyacrylamide gels (18) and then transferred to nitrocellulose (19). The nitrocellulose blots were analyzed by using 5% nonfat dry milk (Carnation) to block nonspecific binding of primary antibody and goat anti-rabbit IgG coupled to alkaline phosphatase (Promega) for immunodetection. To demonstrate specific immunolabeling, 50  $\mu$ g of the appropriate unconjugated peptide was incubated at 4°C overnight with 1  $\mu$ l of antiserum diluted, as indicated in the figure legends, with Tris-buffered saline containing 0.05% Tween 20 and 1 mg of bovine serum albumin per ml. The absorbed antiserum was then centrifuged at 16,000  $\times$  g for 5–10 min, and the supernatant was applied to blots.

**Purification and Sequencing.** To purify the  $\approx$ 105-kDa protein, we used CSF obtained at autopsy from a patient with AD (age, 82 years; PMI, 3 hr) and stored at  $-80^{\circ}\text{C}$ . The  $\beta$ APP derivatives were separated from the bulk (75%) of the CSF protein by ammonium sulfate fractionation: (i) 59.3 g of  $(\text{NH}_4)_2\text{SO}_4$  was added slowly to 151 ml of CSF (60% saturation) at 4°C; (ii) the mixture was allowed to stir for 30 min and was then centrifuged at 10,000  $\times$  g for 30 min; (iii) the resulting pellet was resuspended in 20 mM sodium phosphate (monobasic) buffer (pH 6.8) to a final volume of 2.5 ml and was desalted with a Pharmacia column PD-10. The resuspended desalted  $(\text{NH}_4)_2\text{SO}_4$  pellet was then loaded onto a Mono Q column (Pharmacia) and the bound proteins were eluted with a linear gradient of 20 mM phosphate buffer, pH 6.8/0.05% Tween 20 and 20 mM phosphate buffer, pH 6.8/0.05% Tween 20/1 M NaCl. The soluble  $\beta$ APP derivatives eluted from the column together in a well-defined peak at  $\approx$ 60% (0.6 M NaCl) of the gradient. The fractions comprising this peak were pooled, concentrated, desalted, and subjected to preparative SDS/PAGE on an 8% gel. The  $\approx$ 125- and  $\approx$ 105-kDa derivatives were then separately excised and electroeluted. After concentration and desalting, the recovered  $\approx$ 125- and  $\approx$ 105-kDa proteins were loaded into separate lanes for SDS/PAGE on an 8% gel. The proteins were transferred to Immobilon for 1 hr at 0.5 A and visualized with Coomassie blue R-250 as described by Matsudaira (20). The more abundant  $\approx$ 105-kDa protein was then sequenced by using the Applied Biosystems 477A Sequenator. To obtain sufficient protein to sequence the  $\approx$ 125-kDa form, we pooled CSF from five patients: three with AD (ages, 89, 87, and 68 years; PMI, 3, 3, and 3.5 hr); one control (age, 67 years; PMI, 4 hr); and one live patient undergoing aneurysm repair (age, 44 years). Purification and sequencing were performed as described for the  $\approx$ 105-kDa protein with the following modifications: ammonium sulfate fractionation was performed at 62.5% saturation, 5–15% gradient gels were used for SDS/PAGE, and transfer to Immobilon proceeded for 1.5 hr.

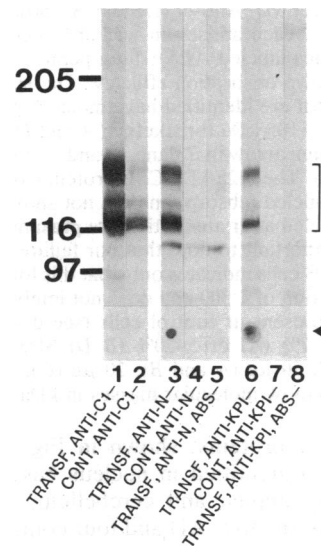
**RESULTS**

To identify KPI-containing forms of the  $\beta$ APP, we raised a rabbit antiserum to the KPI domain (anti-KPI) and evaluated this antiserum by using whole cell homogenates from a

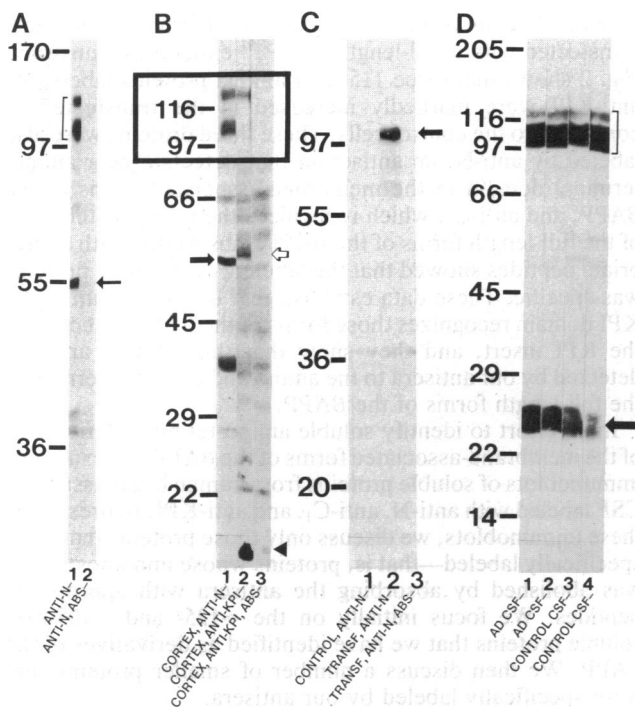
human 293 embryonic kidney cell line that had been stably transfected with a full-length  $\beta$ APP<sup>751</sup> expression construct. Fig. 2 shows that three 115- to 140-kDa proteins labeled by anti-KPI were markedly increased in the transfected as compared to the control cells. These three proteins were also labeled by anti-N, an antiserum that detects a near amino-terminal domain in the membrane-associated forms of the  $\beta$ APP, and anti-C<sub>1</sub>, which recognizes the carboxyl terminus of the full-length forms of the  $\beta$ APP. Absorption with appropriate peptides showed that the labeling of the three proteins was specific. These data establish that our antiserum to the KPI domain recognizes those forms of the  $\beta$ APP that contain the KPI insert, and they show that these forms are also detected by our antisera to the amino and carboxyl termini of the full-length forms of the  $\beta$ APP.

In an effort to identify soluble amino-terminal derivatives of the membrane-associated forms of the  $\beta$ APP, we examined immunoblots of soluble proteins from human brain tissue and CSF labeled with anti-N, anti-C<sub>1</sub>, and anti-KPI. In presenting these immunoblots, we discuss only those proteins that were specifically labeled—that is, proteins whose immunostaining was abolished by absorbing the antisera with appropriate peptides. We focus initially on the  $\approx$ 125- and  $\approx$ 105-kDa soluble proteins that we have identified as derivatives of the  $\beta$ APP. We then discuss a number of smaller proteins that were specifically labeled by our antisera.

Fig. 3A shows that anti-N labeled soluble  $\approx$ 125- and  $\approx$ 105-kDa proteins in human brain. The labeling of these proteins was specific because it was abolished by absorption with the appropriate N-terminal peptide. The  $\approx$ 125- and



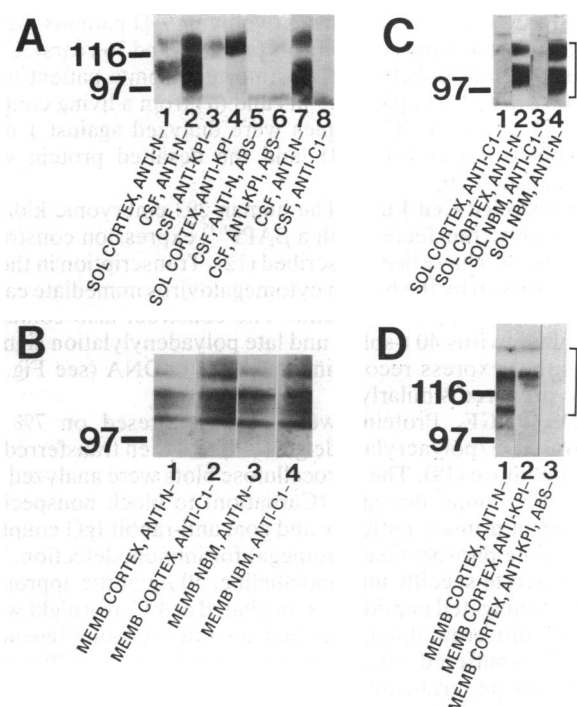
**FIG. 2.** Immunoblotted whole cell extracts of control human 293 embryonic kidney cells and 293 cells stably transfected with a full-length  $\beta$ APP<sup>751</sup> expression construct. Dilution was 1:200 for anti-N and anti-KPI and 1:300 for anti-C<sub>1</sub>. In lanes labeled ABS, the antiserum was absorbed with the appropriate peptide; 1  $\mu$ g peptide dots (arrowhead) were used to confirm absorption efficacy. The three large proteins (bracket) detected by anti-C<sub>1</sub>, anti-N, and anti-KPI have calculated molecular masses of  $\approx$ 140,  $\approx$ 125, and  $\approx$ 115 kDa. It is evident from the anti-C<sub>1</sub> immunolabeling (lanes 1 and 2) that the various membrane-associated forms of the  $\beta$ APP are present at low levels in control cells and are markedly augmented in the transfected cells. Thus, the failure of anti-N (1:200) and anti-KPI (1:200) to detect the  $\beta$ APP in control 293 cells indicates only that the level of the  $\beta$ APP is sufficiently low that it is not detected by these antisera at the dilution used. Although not shown in this figure, anti-C<sub>1</sub> labeled a  $\approx$ 14-kDa protein that was markedly increased in the transfected as compared to the control cells. Gel is 5–20% SDS/polyacrylamide; all lanes loaded with 75  $\mu$ g of protein. Bars show molecular masses in kDa.



**FIG. 3.** (A) Anti-N (1:200) soluble proteins from human cerebral cortex. (B) Anti-KPI (1:100) vs. anti-N (1:100) soluble proteins from human cerebral cortex. (C) Anti-N (1:300) soluble proteins from control 293 cells vs. 293 cells transfected with a full-length  $\beta$ APP<sup>695</sup> expression construct. (D) Anti-N (1:100) CSF proteins. To evaluate labeling specificity, each antiserum was absorbed with the appropriate peptide (lanes labeled ABS); 1  $\mu$ g peptide dots (arrowhead) were used to confirm absorption efficacy. The specifically labeled soluble proteins that are identified have molecular masses centered on  $\approx$ 125 kDa and  $\approx$ 105 kDa (brackets in A and D; box in B; arrow in C),  $\approx$ 58 kDa (open arrow in B, lane 2), and  $\approx$ 55 kDa (solid arrows in A and B, lane 1). The  $\approx$ 25-kDa CSF protein (solid arrow in D) is also specifically labeled (absorption data not shown). Proteins that continue to be labeled after absorption are presumably unrelated to the  $\beta$ APP. It is important to note that our failure to detect soluble  $\beta$ APP in control 293 cells indicates only that this form is not detected by anti-N at a dilution of 1:300 and does not imply that this form of the  $\beta$ APP is not present in control cells (see discussion in Fig. 2 legend). Gels are 7% (A) or 5–20% (B–D) SDS/polyacrylamide. Lanes loaded with 70  $\mu$ g (A and B), 20  $\mu$ g (C), or 130  $\mu$ g (D) of protein. Numbers show molecular masses in kDa.

$\approx$ 105-kDa soluble proteins, shown in Fig. 3A in cerebral cortex, were also identified in nucleus basalis of Meynert (Fig. 4C), hippocampus, and cerebellum, and they were present in each of the four AD and four control patients that we examined. Fig. 3B shows that anti-KPI labeled a protein that comigrated with the soluble  $\approx$ 125-kDa protein labeled by anti-N and that the labeling of this protein by anti-KPI was abolished after absorption with KPI<sup>36–48</sup>. The fact that the  $\approx$ 125-kDa soluble protein is specifically detected by two different antisera known to detect the  $\beta$ APP, one directed against the KPI domain and the other against an amino-terminal domain, provides strong evidence that this protein is a derivative of the  $\beta$ APP that contains the KPI domain.

To confirm that the soluble  $\approx$ 105-kDa protein labeled by anti-N but not by anti-KPI is a KPI-free derivative of the  $\beta$ APP, we examined the soluble proteins in a human 293 cell line designed to overexpress KPI-free  $\beta$ APP through stable transfection with a  $\beta$ APP<sup>695</sup> expression construct (12, 13). As shown in Fig. 3C, this cell line produces markedly increased levels of a soluble  $\approx$ 105-kDa form of the  $\beta$ APP that is specifically detected by anti-N. This observation provides strong additional evidence that the soluble  $\approx$ 105-kDa brain



**FIG. 4.** (A) Soluble brain vs. CSF proteins. (B) Anti-N vs. anti-C<sub>1</sub> labeling of membrane-associated proteins from cerebral cortex and nucleus basalis of Meynert (NBM). (C) Anti-N vs. anti-C<sub>1</sub> labeling of soluble proteins from cerebral cortex and NBM. (D) Anti-N vs. anti-KPI labeling of membrane-associated proteins from cerebral cortex. Anti-N and anti-KPI were diluted 1:100; anti-C<sub>1</sub> was diluted 1:150. Gels are 5–20% (A and D) or 7% (B and C) SDS/polyacrylamide. Lanes loaded with 65  $\mu$ g (A) or 70  $\mu$ g (B–D) of protein. Numbers show molecular masses in kDa. The soluble proteins that are specifically labeled by anti-N but not by anti-C<sub>1</sub> in A and C have molecular masses centered on  $\approx$ 125 and  $\approx$ 105 kDa. In B and D, the two larger membrane-associated proteins detected by both anti-C<sub>1</sub> and anti-N, which are also labeled by anti-KPI, have calculated molecular masses of  $\approx$ 133 and  $\approx$ 120 kDa; the two smaller proteins detected by both anti-C<sub>1</sub> and anti-N but not by anti-KPI have calculated molecular masses of  $\approx$ 115 and  $\approx$ 110 kDa. The weights of these four membrane-associated proteins are essentially identical to those previously reported (12, 13).

protein specifically detected by anti-N, but not by anti-KPI, is a KPI-free derivative of the  $\beta$ APP.

Since our data showed that there are soluble derivatives of the  $\beta$ APP in human brain tissue, we examined human CSF and found (Figs. 3D and 4A) that the soluble  $\approx$ 125- and  $\approx$ 105-kDa forms of the  $\beta$ APP are present there as well. Fig. 3D shows that anti-N labeled  $\approx$ 125- and  $\approx$ 105-kDa proteins in samples of both AD and control CSF. As shown in Fig. 4A, anti-KPI labeled the  $\approx$ 125-kDa CSF protein detected by anti-N, but it did not label the  $\approx$ 105-kDa CSF protein detected by anti-N. The observed labeling of these CSF proteins by anti-N and anti-KPI was specific because it was removed by absorption with the appropriate peptides. The  $\approx$ 125-kDa CSF protein labeled by anti-N and anti-KPI and the  $\approx$ 105-kDa CSF protein labeled by anti-N but not by anti-KPI comigrated with their counterparts in human brain tissue.

As shown in Fig. 4B, both anti-C<sub>1</sub> and anti-N readily labeled four 110- to 135-kDa membrane-associated forms of the  $\beta$ APP, as we had previously demonstrated (12, 13). Anti-C<sub>1</sub> did not, however, detect the soluble proteins that were labeled by anti-N either in CSF (Fig. 4A) or in brain tissue (Fig. 4C). Thus, our data indicate that there are soluble KPI-containing ( $\approx$ 125 kDa) and KPI-free ( $\approx$ 105 kDa) derivatives of the  $\beta$ APP that lack the carboxyl terminus of the full-length membrane-associated forms. Moreover, we dem-

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~125 kDa form:  L E V P x x g n a g l l a
~105 kDa form:  L E V P T x G N A G L L A E P Q I A M F
Predicted  $\beta$ APP: L E V P T D G N A G L L A E P Q I A M F
                  18                               37

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FIG. 5. Amino-terminal sequence (single-letter code) of the  $\approx$ 105- and  $\approx$ 125-kDa soluble proteins found in human CSF. Capital letters indicate that the amino acid signal was strong; lowercase letters indicate that the signal was weak although assignment was definite; x indicates that no amino acid could be identified. Note that the amino acid sequence predicted from  $\beta$ APP cDNA (5) begins with a 17-residue signal sequence identified by Dyrks *et al.* (11). Thus the amino-terminal residue of the mature protein is located at position 18 of the predicted sequence.

onstrate that these soluble  $\beta$ APP derivatives are readily detected both in brain tissue and in CSF.

To show definitively that the large soluble proteins identified by immunolabeling are derived from the  $\beta$ APP, we sequenced the amino termini of the  $\approx$ 105- and  $\approx$ 125-kDa soluble proteins after having purified them from human CSF by ammonium sulfate fractionation followed by fast protein liquid chromatography using a Mono Q column (see *Materials and Methods*). As shown in Fig. 5, this sequencing confirmed that the  $\approx$ 105- and  $\approx$ 125-kDa proteins are forms of the  $\beta$ APP. We sequenced 20 amino acids in the more abundant  $\approx$ 105-kDa protein, 19 were detectable, and all 19 were identical to those predicted from the published  $\beta$ APP cDNA sequence (5). In the  $\approx$ 125-kDa protein, 13 amino acids were sequenced, 11 were detectable, and all 11 were identical to those predicted.

To further characterize the membrane-associated forms of the  $\beta$ APP, we examined membrane-associated proteins from cerebral cortex with anti-KPI. Comparison of the membrane-associated proteins labeled by both anti-C<sub>1</sub> (Fig. 4B) and anti-N (Fig. 4B and D) with those labeled by anti-KPI (Fig. 4D) showed that anti-KPI labeled two membrane-associated proteins that comigrated with the two largest membrane-associated forms of the  $\beta$ APP. The labeling of these proteins by anti-KPI was specific because it was abolished (Fig. 4D) by absorption with the KPI<sup>36-48</sup> peptide. The fact that anti-KPI specifically labels the two largest proteins detected by anti-C<sub>1</sub> and anti-N confirms that this antiserum detects the  $\beta$ APP and shows that the two largest membrane-associated forms of the  $\beta$ APP contain the KPI insert.

In addition to the soluble and membrane-associated proteins in the  $\approx$ 105- to  $\approx$ 135-kDa range, anti-N and anti-KPI specifically detect a number of proteins with molecular masses between  $\approx$ 25 and  $\approx$ 58 kDa. Anti-N specifically detects (i) an  $\approx$ 55-kDa soluble protein in human brain (Fig. 3A and B), (ii) an  $\approx$ 55-kDa membrane-associated protein in human brain (13), and (iii) an  $\approx$ 25-kDa protein in CSF (Fig. 3D; absorption with  $\beta$ APP<sup>45-62</sup> abolished this labeling; data not shown). Anti-KPI specifically detects an  $\approx$ 58-kDa soluble protein (Fig. 3B) and an  $\approx$ 58-kDa membrane-associated protein (data not shown) that are present in human brain extracts. The fact that these proteins are detected by antisera shown to recognize full-length forms of the  $\beta$ APP suggests that the  $\beta$ APP may be highly processed to produce a number of functionally important derivatives. At this point, however, these proteins do not meet the criteria required to establish that they are  $\beta$ APP derivatives. Each of the  $\approx$ 25- to  $\approx$ 58-kDa proteins has been detected by only one antiserum, none appears to be augmented in transfected cells, and none has been sequenced. It is, therefore, possible that they are proteins, unrelated to the  $\beta$ APP, which have cross-reacting epitopes detected by anti-N or anti-KPI.

## SUMMARY AND DISCUSSION

In this report, we used three antisera—anti-N, anti-KPI, and anti-C<sub>1</sub>—to demonstrate that there are large soluble KPI-containing and KPI-free forms of the  $\beta$ APP that lack the carboxyl terminus of the full-length membrane-associated

forms. Specifically, we identify (i) a soluble  $\approx$ 125-kDa protein that is labeled by anti-N and anti-KPI but not by anti-C<sub>1</sub> and (ii) a soluble  $\approx$ 105-kDa protein that is labeled by anti-N but not by anti-KPI or anti-C<sub>1</sub>. We provide additional evidence that the  $\approx$ 105-kDa protein is a KPI-free  $\beta$ APP derivative by showing markedly increased levels of an  $\approx$ 105-kDa soluble protein specifically detected by anti-N in a transfected cell line that overexpresses KPI-free forms of the  $\beta$ APP. Both the KPI-containing ( $\approx$ 125 kDa) and KPI-free ( $\approx$ 105 kDa)  $\beta$ APP derivatives are readily detected in human brain and CSF. We confirm that the large soluble proteins in human brain and CSF are derived from the  $\beta$ APP by directly sequencing the amino terminus of both the  $\approx$ 105- and  $\approx$ 125-kDa forms. Finally, we examine the membrane-associated forms of the  $\beta$ APP by using anti-KPI, and we show that the two largest membrane-associated forms of the  $\beta$ APP contain the KPI domain.

The soluble KPI-containing and KPI-free  $\beta$ APP derivatives identified in this study are  $\approx$ 5–10 kDa smaller than the membrane-associated forms from which they are presumably derived; they are not detected by anti-C<sub>1</sub>; and they do not require detergent for solubilization. Taken together, these observations indicate that these derivatives are generated by a proteolytic event that removes a small, 5- to 10-kDa fragment containing the carboxyl terminus and some or all of the hydrophobic membrane-spanning region from the full-length membrane-associated molecule. Since the predicted size of the fragments that extend from the amino and carboxyl termini of the  $\beta$ APP through the membrane-spanning domain to the carboxyl terminus of the  $\beta$ APP are  $\approx$ 11 kDa and  $\approx$ 6.5 kDa, respectively, it is apparent that the postulated cleavage that generates soluble derivatives must occur in the vicinity of the  $\beta$ APP sequence (see Fig. 1). Thus, our data indicate that the  $\beta$ APP, like other membrane-associated proteins with similar structure (14–16), undergoes limited proteolysis releasing soluble amino-terminal derivatives that, by analogy with these other proteins, may be functionally important.

The proteolytic event that generates soluble  $\beta$ APP derivatives in human brain could occur on the amino-terminal side of the  $\beta$ APP, within the  $\beta$ APP sequence, or even on the carboxyl-terminal side of the  $\beta$ APP (Fig. 1). Cleavage on the carboxyl-terminal side of the  $\beta$ APP would be expected to shed a soluble, potentially amyloidogenic precursor into the extracellular space. This soluble  $\beta$ APP derivative would have the  $\beta$ APP at or near its carboxyl terminus and would provide an extracellular source from which the amyloid deposited in AD, which is all extracellular, could readily be derived.<sup>¶</sup>

Cleavage on the amino-terminal side of the  $\beta$ APP, on the other hand, would leave the  $\beta$ APP attached to a small mem-

<sup>¶</sup>We have been unable to label the soluble derivatives of the  $\beta$ APP by using antisera to the  $\beta$ APP. This observation cannot, however, be interpreted to mean that the soluble derivatives of the  $\beta$ APP lack the  $\beta$ APP sequence because we, and many other groups, have been unable to label full-length membrane-associated forms of the  $\beta$ APP by using antisera to the  $\beta$ APP. This failure may occur because synthetic  $\beta$ APP peptides, which spontaneously form amyloid fibrils (21, 22), have an immunogenicity that differs markedly from that of the  $\beta$ APP sequence in the native forms of the  $\beta$ APP.

brane-associated protein from which amyloid might ultimately be generated. It is interesting, in this regard, that Dyrks *et al.* (11) have shown that this small protein tends to aggregate when it is transcribed and translated *in vitro* and that Selkoe *et al.* (12) have identified an  $\approx 11$ -kDa membrane-associated protein in fresh cow and rat brain that could represent this fragment. It is apparent from the foregoing discussion that it is critically important to identify the specific site(s) at which the  $\beta$ APP is normally cleaved to generate soluble forms. It should now be possible to do this by sequencing the carboxyl termini of soluble forms purified from the large volumes of CSF available at autopsy.

By carefully evaluating  $\beta$ APP derivatives in CSF, it may be possible (i) to identify quantitative changes in  $\beta$ APP derivatives or changes in the site(s) of  $\beta$ APP cleavage that reflect significant pathogenic mechanisms operative in aging or AD and (ii) to monitor the progression of those changes in living patients. It has recently been shown that anti-C<sub>1</sub> (12), anti-N (13), and antisera to other  $\beta$ APP peptides (23) label senile plaques. These findings suggest that full-length  $\beta$ APP molecules may be processed into amyloid fibrils locally within plaques. There are typically  $>1400$  plaques per mm<sup>3</sup> in AD cerebral cortex, far more than in control cortex, and these plaques have associated microglia and astroglia potentially capable of altering  $\beta$ APP proteolysis. Thus, the process of plaque formation and amyloid deposition that occurs in AD may produce quantitative or qualitative changes in the  $\beta$ APP derivatives present in CSF. Another factor that could alter  $\beta$ APP derivatives in CSF is the selective increase in expression of the KPI-free form that we have observed in the neurons of certain populations in AD (24, 25). Finally, the loss of neurons that occurs in the AD brain might influence the level of  $\beta$ APP derivatives in the CSF since these neurons are known to express the  $\beta$ APP (26). It will, therefore, be important to analyze  $\beta$ APP derivatives quantitatively in the CSF of a large number of AD and control patients. These quantitative studies and those characterizing the carboxyl terminus of the soluble derivatives could help clarify the mechanism responsible for amyloid deposition in AD, and they are necessary to determine the diagnostic utility of the  $\beta$ APP derivatives that we have identified.

**Noted Added in Proof.** Since this report was submitted, Schubert *et al.* (27) have reported that PC12 cells secrete soluble  $\beta$ APP derivatives of 115 and 140 kDa. Weidemann *et al.* (28) have also reported the presence of soluble forms of the  $\beta$ APP in several cell lines and in human CSF. Moreover, Weidemann *et al.* have performed pulse-chase experiments that indicate that the soluble derivatives are generated from full-length membrane-associated  $\beta$ APP. Finally, Takio *et al.* (29) have independently purified and sequenced three 110- to 130-kDa membrane-associated forms of the  $\beta$ APP from newborn rat brain using a protocol similar to ours.

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1. Glenner, G. G. & Wong, C. W. (1984) *Biochem. Biophys. Res. Commun.* **120**, 885-890.
2. Masters, C. L., Simms, G., Weinmann, N. A., Multhaup, G., McDonald, B. L. & Beyreuther, K. (1985) *Proc. Natl. Acad. Sci. USA* **82**, 4245-4249.
3. Selkoe, D. J., Abraham, C. R., Podlisny, M. B. & Duffy, L. K. (1986) *J. Neurochem.* **146**, 1820-1834.
4. Goldgaber, D., Lerman, M. I., McBride, O. W., Saffiotti, U. & Gajdusek, D. C. (1987) *Science* **235**, 877-880.
5. Kang, J., Lemaire, H.-G., Unterbeck, A., Salbaum, J. M., Masters, C. L., Grzeschik, K.-H., Multhaup, G., Beyreuther, K. & Muller-Hill, B. (1987) *Nature (London)* **325**, 733-736.
6. Robakis, N. K., Ramakrishna, N., Wolfe, G. & Wisniewski, H. M. (1987) *Proc. Natl. Acad. Sci. USA* **84**, 4190-4194.
7. Tanzi, R. E., Gusella, J. F., Watkins, P. C., Bruns, G. A. P., St. George-Hyslop, P., Van Keuren, M. L., Patterson, D., Pagan, S., Kurnit, D. M. & Neve, R. L. (1987) *Science* **235**, 880-884.
8. Kitaguchi, N., Takahashi, Y., Tokushima, Y., Shiojiri, S. & Ito, H. (1988) *Nature (London)* **331**, 530-532.
9. Ponte, P., Gonzalez-DeWhitt, P., Schilling, J., Miller, J., Hsu, D., Greenberg, B., Davis, K., Wallace, W., Lieberburg, I., Fuller, F. & Cordell, B. (1988) *Nature (London)* **331**, 525-527.
10. Tanzi, R. E., McClatchey, A. I., Lamperti, E. D., Villa-Komaroff, L., Gusella, J. F. & Neve, R. L. (1988) *Nature (London)* **331**, 528-530.
11. Dyrks, T., Weidemann, A., Multhaup, G., Salbaum, J. M., Lemaire, H.-G., Kang, J., Muller-Hill, B., Masters, C. L. & Beyreuther, K. (1988) *EMBO J.* **7**, 949-957.
12. Selkoe, D. J., Podlisny, M. B., Joachim, C. L., Vickers, E. A., Lee, G., Fritz, L. C. & Oltersdorf, T. (1988) *Proc. Natl. Acad. Sci. USA* **85**, 7341-7345.
13. Palmert, M. R., Podlisny, M. B., Witker, D. S., Oltersdorf, T., Younkin, L. H., Selkoe, D. J. & Younkin, S. G. (1988) *Biochem. Biophys. Res. Commun.* **156**, 432-437.
14. Scott, J., Urdea, M., Quiroga, M., Sanchez-Pescador, R., Fong, N., Selby, M., Rutter, W. J. & Bell, G. I. (1983) *Science* **221**, 236-240.
15. Doolittle, R. F., Feng, D. F. & Johnson, M. S. (1984) *Nature (London)* **307**, 558-560.
16. Leung, D. W., Spencer, S. A., Cachianes, G., Hammonds, R. G., Collins, C., Henzel, W. J., Barnard, R., Waters, M. J. & Wood, W. I. (1987) *Nature (London)* **330**, 537-543.
17. Palmert, M. R., Podlisny, M. B., Golde, T. E., Cohen, M. L., Kovacs, D. M., Tanzi, R. E., Gusella, J. F., Whitehouse, P. J., Witker, D. S., Oltersdorf, T., Younkin, L. H., Selkoe, D. J. & Younkin, S. G. (1989) *First International Conference on Alzheimer's Disease and Related Disorders, Las Vegas, October 6-8, 1988*, eds. Iqbal, K., Wisniewski, H. M. & Winblad, B. (Liss, New York), in press.
18. Laemmli, U. K. (1970) *Nature (London)* **227**, 680-685.
19. Towbin, H., Staehelin, T. & Gordon, J. (1979) *Proc. Natl. Acad. Sci. USA* **76**, 4350-4354.
20. Matsudaira, P. (1987) *J. Biol. Chem.* **262**, 10035-10038.
21. Castano, E. M., Ghiso, L., Prelli, B. F., Gorevic, P. D., Migheli, A. & Frangione, B. (1986) *Biochem. Biophys. Res. Commun.* **141**, 781-789.
22. Kirschner, D. A., Inoye, H., Duffy, L. K., Sinclair, A., Lind, M. & Selkoe, D. J. (1987) *Proc. Natl. Acad. Sci. USA* **84**, 6953-6957.
23. Perry, G., Lipphardt, S., Mulvihill, P., Kanclerla, M., Mijares, M., Gambetti, P., Sharma, S., Maggiora, L., Cornette, J., Lobl, T. & Greenberg, B. (1988) *Lancet* **ii**, 746.
24. Cohen, M. L., Golde, T. E., Usiak, M. F., Younkin, L. H. & Younkin, S. G. (1988) *Proc. Natl. Acad. Sci. USA* **85**, 1227-1231.
25. Palmert, M. R., Golde, T. E., Cohen, M. L., Kovacs, D. M., Tanzi, R. E., Gusella, J. F., Usiak, M. F., Younkin, L. H. & Younkin, S. G. (1988) *Science* **241**, 1080-1084.
26. Bahmanyar, S., Higgins, G. A., Goldgaber, D., Lewis, D. A., Morrison, J. H., Wilson, M. C., Shankar, S. K. & Gajdusek, D. C. (1987) *Science* **237**, 77-80.
27. Schubert, D., LaCorbiere, M., Saitoh, T. & Cole, G. (1989) *Proc. Natl. Acad. Sci. USA* **86**, 2066-2069.
28. Weidemann, A., Konig, G., Bunke, D., Fischer, P., Salbaum, J. M., Masters, C. & Beyreuther, K. (1989) *Cell* **57**, 115-126.
29. Takio, K., Hasegawa, M., Titani, K. & Ihara, Y. (1989) *Biochem. Biophys. Res. Commun.* **160**, 1296-1301.