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## Statin treatment and a disease-specific pattern of $\beta$ -amyloid peptides in Alzheimer's disease

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**Abstract** According to the amyloid cascade hypothesis, sporadic Alzheimer's disease (AD) is caused by the production and aggregation of  $\beta$ -amyloid ( $A\beta$ ), and the production of  $A\beta$  has recently been linked to the metabolism of cholesterol. We have previously published clinical studies where the effect of statin treatment on  $A\beta$  production has been investigated. No effect on  $A\beta$  was found, which is in disagreement with cell and animal studies. In the present study we investigated the effect of statin treatment on a disease-specific pattern consisting of a C-terminally-truncated quintet of  $A\beta$  peptides. Nineteen patients with AD were treated with simvastatin for 12 months and the quintet of  $A\beta$  peptides were analysed in cerebrospinal fluid before and after treatment. Also included was a group of 15 untreated patients with AD. We found that the  $A\beta$  peptide pattern at baseline was in agreement with earlier findings; however, we did not find any change in the  $A\beta$  peptide pattern after statin treatment. We suggest that clinical studies with extended treatment periods are performed where higher dosages of statins are used. We also believe that the pleiotropic effects of statins should be investigated further in order to elucidate the connection between Alzheimer's disease and statin treatment.

**Keywords** Alzheimer's disease ·  $A\beta$  ·  $A\beta$  peptide pattern · APP · Cholesterol · Statins

### Introduction

The processing of amyloid precursor protein (APP) results in the production of  $\beta$ -amyloid ( $A\beta$ ) peptide, a major constituent of senile plaques (SP), a pathological hallmark in Alzheimer's disease (AD). According to the amyloid cascade hypothesis, the production and aggregation of  $A\beta$  peptides are central events in the aetiology of sporadic AD. Evidence for this hypothesis comes from several lines of inquiry: (1) the disease-causing mutations found in APP, Presenilin 1 (PS1) and Presenilin 2 (PS2) genes all lead to an upregulation of  $A\beta_{40}$  and/or  $A\beta_{42}$  peptides (Scheuner et al 1996); (2) individuals with trisomy 21 (with three APP genes) develop AD pathology in their fourth or fifth decade of life (Wisniewski et al 1985; Iwatsubo et al 1995); (3) allelic variation of the apolipoprotein E (ApoE) gene is a risk factor for sporadic AD, and since ApoE binds to  $A\beta$  (Strittmatter et al 1993a, 1993b), it may be involved in the formation of SP.

APP is ubiquitously expressed in all cells and is secreted by both brain and peripheral cells into extracellular fluids. The initial cleavage of APP is made by either  $\alpha$ - or  $\beta$ -secretase, producing the soluble fragments  $\alpha$ sAPP or  $\beta$ sAPP and the corresponding C-terminal fragment C83 or C99 (Andreasen and Blennow 2002). The C-terminal fragments remain membrane-bound and are substrates for the subsequent intramembranous cleavage by the  $\gamma$ -secretase complex, producing p3 or  $A\beta$  (Andreasen and Blennow 2002). The cleavage by  $\alpha$ -secretase occurs after Lys16 within the  $A\beta$  sequence, thereby precluding the formation of  $A\beta$ . The identity of  $\alpha$ -secretase is still not clear, but three candidates have been suggested: tumour necrosis factor- $\alpha$ -converting enzyme (TACE), also called ADAM17, ADAM10 (a disintegrin and metalloprotease) and MDC9 (metallo/disintegrin/cystein-rich

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proteins, also called ADAM9) (Black et al 1997; Moss et al 1997; Buxbaum et al 1998; Koike et al 1999; Lam-mich et al 1999). The  $\beta$ -secretase has been identified as BACE ( $\beta$ -site APP cleaving enzyme) (Sinha et al 1999; Vassar et al 1999; Yan et al 1999) and it cleaves APP at two different positions: at Met1 and after amino acid 10 ( $A\beta$  numbering). In addition, a BACE homologue, BACE 2, has been identified (Farzan et al 2000). The identity of the  $\gamma$ -secretase is not known, but accumulating evidence suggests that the  $\gamma$ -secretase is a high molecular weight complex formed by several proteins—APH1b, PEN2, Nicastrin and PS1 (Yu et al 2000)—and PS1 has been identified as an essential co-factor for  $\gamma$ -secretase activity (De Strooper et al 1998).

In recent years, several studies have indicated that elevated intracellular cholesterol levels might affect the processing of APP, promoting the production of  $A\beta$ . Changing the cholesterol and lipid compositions of cellular membranes have been shown to affect both  $\alpha$ - and  $\gamma$ -secretase (Bodovitz and Klein 1996; Urmonait et al 1998; Kojro et al 2001; Runz et al 2002; Wahrle et al 2002). Other cell studies and animal studies have revealed that increased levels of cholesterol increases the production of  $A\beta$ , while lowering cholesterol levels with statins (de novo cholesterol synthesis inhibitors) decreases the production of  $A\beta$  (Simons et al 1998; Fassbender et al 2001). Epidemiological studies suggest that statin treatment lowers the incidence of AD (Jick et al 2000; Wolozin et al 2000; Rockwood et al 2002; Yaffe et al 2002). The effect of statin treatment on APP processing and the production of  $A\beta$  has also been investigated in clinical studies (Friedhoff et al 2001; Tokuda et al 2001; Fassbender et al 2002; Simons et al 2002; Ishii et al 2003), but with contradictory results. Animal studies have also shown contradictory results (Park et al 2003). Our group has published two studies (Sjögren et al 2003; Höglund et al 2004) where patients treated with statins have shown no changes in cerebrospinal fluid (CSF) or plasma levels of  $A\beta$ 1-40 or  $A\beta$ 1-42.

Recently, a peptide pattern of a quintet of  $A\beta$  peptides truncated at the C-terminal ( $A\beta$  1-37/38/39/40 and 42) has been found in AD (Wiltfang et al 2001, 2002), where the relative order of abundance differed in abso-

lute and relative terms. This result has been further confirmed by SELDI-TOF (Lewczuk et al 2003). The pattern appears to be specific, indicating a tightly regulated pathway.

We present an open biochemical study where patients with AD were treated with simvastatin (20 mg/day) for 12 months; a group of untreated patients with AD were also included. CSF samples were taken at baseline and after 12 months of treatment (endpoint) with simvastatin. The main aim of this study was to investigate whether treatment with simvastatin for 12 months affects the disease-specific peptide pattern. Our first step was to confirm previous findings (Wiltfang et al 2001, 2002; Lewczuk et al 2003). We also wanted to evaluate the two methods used for analysis of  $A\beta$ , the Luminex system and the western blot. We show that the peptide patterns in the untreated and treated groups at baseline are in agreement with earlier findings by Wiltfang et al (2002). However, we did not find any significant change in the peptide pattern after treatment with statins when comparing baseline with endpoint. A comparison of the absolute values of  $A\beta$ 1-42 from the western blot analysis revealed a high correlation with the  $A\beta$ 1-42 values quantified using xMAP technology on the Luminex system.

## Materials and methods

### Patients

Nineteen patients with AD were treated with 20 mg/day of simvastatin for 12 months, and CSF and plasma samples were collected at baseline and endpoint (12 months). One patient was excluded from the present study because western blot analysis failed. Fifteen untreated patients with AD were also included in the study, and only CSF samples, no plasma, were taken at baseline and endpoint from this group. Demographic data for both the untreated and treated groups are shown in Table 1. All patients underwent a thorough clinical investigation, which included medical history; physical, neurological and psychiatric examinations; screening laboratory tests; an electroencephalogram; and a com-

**Table 1** Demographics of the untreated and treated AD groups

	Untreated AD		Treated AD	
	Baseline	Endpoint	Baseline	Endpoint
Number (M/F)	15 (5/10)	15 (5/10)	18 (9/9)	18 (9/9)
Age (years)	78 (66–85)	79 (67–86)	77 (67–87)	78 (68–88)
Duration (years)	2.1 (0.5–6)		2.7 (1–6)	
APOE	2/13	2/13	9/8	9/8
MMSE	24 (18–27)	22.6 (12–28)	21 (14–28)	18 (10–26)*
ADAS-Cog	ND	ND	19.5 (4–37)	22.6 (7–48)

Data is given as mean (range)

*Baseline* before treatment, *Endpoint* after 12 months of treatment, *M* male, *F* female, *APOE* number of non-carriers of the APOE4 allele/carriers of the APOE4 allele, *MMSE* Mini Mental State Examination, *ADAS-Cog* Alzheimer's Disease Assessment Scale-Cognition, *ND* no data

\*  $p = 0.003$

puterized tomography scan of the brain. The diagnosis of probable AD was made according to the criteria of the National Institute of Neurological and Communicative Disorders and Stroke and Alzheimer's Disease and Related Disorders Association (McKhann et al 1984). No patient with AD had a family history of dementia suggestive of autosomal dominant AD. The cognitive status was examined using the Mini Mental State Examination (MMSE) (Folstein et al 1975) and the Alzheimer Disease Assessment Scale-Cognition (ADAS-Cog) was used to examine cognitive function (Mohs and Cohen 1988).

### Sample collection

Lumbar puncture was performed in the morning under standard conditions. A volume of 12 ml of CSF was collected, and gently mixed to avoid gradient effects. A blood sample was taken at the same time. All CSF samples with more than 500 erythrocytes/ $\mu$ l were excluded. The CSF/serum albumin ratio [CSF-albumin (mg/ml) divided by serum albumin (g/l)] was used as a measure of blood-brain barrier function. All samples were centrifuged to remove cells and debris, and the CSF was stored at  $-80^{\circ}\text{C}$  pending biochemical analyses. Due to previous analysis, all samples in the present study have been through two cycles of freezing/thawing, and a few samples have been through an additional third cycle. The local ethical committees approved the study. All the patients or their relatives gave informed consent to participate in the study, which was performed in accordance with the provisions of the Helsinki Declaration.

### Lipoproteins, APOE genotype and A $\beta$ 1-42 on the Luminex

The plasma levels of total cholesterol (TC) and triglycerides (TG) were determined enzymatically with a Modular Hitachi analyzer (Roche Diagnostics Scandinavia AB, Stockholm, Sweden). Plasma high-density lipoprotein (HDL) cholesterol was determined enzymatically after low-density lipoprotein (LDL) and very low-density lipoprotein cholesterol was selectively removed by precipitation from the plasma by magnesium sulphate and dextran sulphate. LDL cholesterol concentration was estimated using the Friedewald formula (Friedewald et al 1972). ApoE genotyping was performed by polymerase chain reaction followed by mini sequencing, as described previously (Blennow et al 2000). The CSF levels of A $\beta$ 1-42 were measured using the xMAP technology on the Luminex system (Austin, Texas, USA) as described previously (Ohlsson et al 2005).

### $\beta$ -amyloid-sodium dodecyl sulphate-polyacrylamide gel electrophoresis

Following the protocol from Wiltfang et al (2002), the synthetic A $\beta$  peptides were directly dissolved in sample

buffer I containing 0.36 M BisTris, 0.16 M bicine, 1% (w/v) SDS, 15% (w/v) sucrose, 0.004% (w/v) bromophenol blue, and heated at  $95^{\circ}\text{C}$  for 5 min. This latter buffer was also used for subsequent dilutions of the synthetic peptides. Sample buffer II was composed of 0.12 M BisTris, 0.053 M bicine, 5% sucrose, 0.5% SDS, and 0.0025% bromophenol blue containing one tablet of proteinase inhibitor cocktail Complete Mini per 10 ml. Sample buffer II was dried (SpeedVac,  $40^{\circ}\text{C}$ ) in polypropylene tubes (Eppendorf, Hamburg, Germany). The equivalent volume of CSF was added to the polypropylene tubes and vortexed until completely solubilized. After the addition of 2-mercaptoethanol to a final concentration of 2.5% v/v, the sample mix was heated at  $95^{\circ}\text{C}$  for 5 min.

The urea version of the bicine/BisTris/Tris/sulphate SDS-PAGE of Wiltfang et al (1991) was used to separate the A $\beta$  peptides. The composition of the separation gel was modified from 15%T%/5%C%8 M to 12%T%/5%C%/8 M urea, and the gel thickness was 0.5 mm, as described in Wiltfang et al (2002). The gels were run at 25 mA/gel for 1 h, using the MiniProtean II electrophoresis unit (Bio-Rad Laboratories, Hercules, CA, USA). Ten microliters of CSF were loaded per lane. All samples were run in quadruplicate and each gel carried a five-step dilution series of the synthetic A $\beta$  peptide mix. Mean values were used for subsequent calculations of A $\beta$ 1-37/38/39/40 and 42 peptides.

### Western blot

Western blot and immunostaining was performed according to the the following protocol (Wiltfang et al 2002): proteins were transferred for 30 min at 1 mA/cm<sup>2</sup> and room temperature under semi-dry conditions (Hoefer Semiphor) onto Immobilon-P PVDF membranes according to Wiltfang et al (1997). All of the following washing and incubation steps were performed at room temperature if not otherwise stated. For immunostaining, the Immobilon-P PVDF membranes were washed in deionized H<sub>2</sub>O and boiled for 3 min in PBS (phosphate buffer saline) using a microwave oven (Ida et al 1996; Wiltfang et al 1997). Blocking was performed for 1 h using Roti-Block (Carl Roth GmbH & Co. KG, Karlsruhe, Germany). Incubation with the primary antibody, which was diluted 1:200 in RotiBlock, was performed overnight at  $+4^{\circ}\text{C}$ . The membranes were washed for 30, 15 and 2 $\times$ 10 min in PBS-T (0.075% v/v Tween 20) and then incubated for 1 h with anti-mouse biotinylated IgG (H + L) antibody (Vector Laboratories, Burlingame, CA, USA) (1 mg/ml), which was diluted 1:3,000 in PBS-T. A second PBS-T wash was preformed for 3 $\times$ 10 min and then the membranes were incubated for 1 h with streptavidin-biotinylated horseradish peroxidase complex (Amersham Pharmacia Biotech, Buckinghamshire, UK) diluted 3,000-fold. Following 3 $\times$ 10 min washes, the membranes were developed for 5 min with ECL Advanced (Amersham Pharmacia

Biotech) solution according to the manufacturer's instructions. The emitted signal was detected by a CCD camera (Fluor-S Max MultiImager; BioRad), using a series of 5, 10, 15, 30, 45, 60, 75, 90, 105, 120, 135 and 150 s for data acquisition. Band intensities were quantified relative to an internal five-step dilution series of the A $\beta$  peptide standard mix using Quantity One software.

## Statistics

All statistical procedures were performed using the Statistical Package of the Social Sciences (SPSS). The Shapiro–Wilk test was performed to test the data distribution. The data was not normally distributed, so the groups were compared using the non-parametric Kruskal–Wallis test. The paired Wilcoxon test was used to investigate any significant changes between baseline and endpoint. The Spearman correlation coefficient was used for correlations. Individual A $\beta$  peptides were expressed as absolute values (ng/ml) and as percentages of the total A $\beta$  peptide concentration (A $\beta$ 1-X%, fractional A $\beta$  peptide values). For multivariate analysis, the data was transformed and the ANOVA test was used. Values of *p* lower than 0.05 were considered significant.

## Results

At baseline, the A $\beta$  quintet showed the following order of abundance in absolute and relative terms: A $\beta$ 1-40 > A $\beta$ 1-38 > A $\beta$ 1-39 > A $\beta$ 1-37 > A $\beta$ 1-42, in both the untreated group (Table 2) and the treated group (Table 3).

In the untreated group there was a slight but significant decrease in the absolute values of A $\beta$ 1-39 (*p* = 0.030) when comparing endpoint with baseline. However, this decrease was not significant when the levels of A $\beta$ 1-39 were expressed as percentages of the total A $\beta$  peptide concentration.

In the treated group there were no changes in any of the absolute peptide levels when comparing endpoint with baseline (Fig. 1a–f). Neither were there any changes in the ratios between A $\beta$ 1-42 and A $\beta$ 1-40, A $\beta$ 1-42 and A $\beta$ 1-38 or the ratio between A $\beta$ 1-38 and A $\beta$ 1-40.

However, there was a slight but significant decrease (*p* = 0.032) in the levels of A $\beta$ 1-39 when the value was expressed as a percentage of the total A $\beta$  peptide concentration.

We investigated the effect of confounding factors on changes between endpoint and baseline for the five different A $\beta$  peptides using multivariate analysis. The following confounding factors were analysed; sex, age, APOE4 and both baseline values and difference between baseline and endpoint in MMSE, ADAS-Cog and cholesterol levels. We only found effects on the A $\beta$  peptides 1–38 and 1–40. The ADAS-Cog score at baseline was significantly related to the change in A $\beta$ 1-38 (*p* = 0.036) and the change in ADAS-Cog was significantly related to the change in A $\beta$ 1-40 (*p* = 0.040). The MMSE score at baseline was significantly (*p* = 0.043) related to the change in A $\beta$ 1-40 and the decrease in MMSE was significantly related to the change in A $\beta$ 1-38 (*p* = 0.039). In addition, the decrease of cholesterol in plasma significantly influenced the change in A $\beta$ 1-40 (*p* = 0.031).

The plasma levels of cholesterol (*p* = 0.000) and LDL (*p* = 0.000) were significantly decreased (Table 4) in the treated AD group when comparing endpoint with baseline, and the plasma levels of HDL were significantly increased (*p* = 0.046) (Table 4). The CSF levels of A $\beta$ 1-42 measured by xMAP technology correlated with the levels of A $\beta$ 1-42 quantified by western blot, *r* = 0.593 (*p* = 0.000] (Fig. 2).

## Discussion

### Disease-specific A $\beta$ peptide pattern

A disease-specific pattern of C-terminally-truncated A $\beta$  peptides in CSF has been found in AD, with decreased absolute and relative quantities of A $\beta$ 1-42 and increased relative quantities of A $\beta$ 1-38 (Wiltfang et al 2002). In nondemented controls, the A $\beta$  quintet showed the following order of abundance in absolute and relative terms: A $\beta$ 1-40 > A $\beta$ 1-38 > A $\beta$ 1-42 > A $\beta$ 1-39  $\geq$  A $\beta$ 1-37, while in patients with AD the following pattern was found: A $\beta$ 1-40 > A $\beta$ 1-38 > A $\beta$ 1-39 > A $\beta$ 1-37 > A $\beta$ 1-42. In the present study we found the same peptide pattern in both the treated and untreated groups of patients with

**Table 2** A $\beta$  peptides at baseline and endpoint in CSF from patients with Alzheimer's disease, treated with simvastatin for 12 months

	Median p25 p75											
	A $\beta$ 1-42		A $\beta$ 1-40		A $\beta$ 1-39		A $\beta$ 1-38		A $\beta$ 1-37		Total A $\beta$	
	Baseline	Endpoint	Baseline	Endpoint	Baseline	Endpoint	Baseline	Endpoint	Baseline	Endpoint	Baseline	Endpoint
Absolute values (ng/ml)	0.28	0.28	5.6	5.9	1.1	1.05	1.8	1.9	0.9	0.9	9.4	9.8
	0.21	0.21	4.5	3.6	0.96	0.72	1.5	1.3	0.7	0.6	8.4	7.3
	0.36	0.41	6.6	6.6	1.5	1.5	2.3	2.8	1.2	1.3	11.7	12.6
Percentage of total A $\beta$	3.1	3.2	55.9	57.1	11.9	10.9	20.1	18.9	9.2	9.3	100	100
	2.5	2.6	53.5	51.9	10.1	9.3	16.4	16.0	8.2	8.2		
	4.2	4.0	59.2	62.3	13.4	12.0	21.6	22.9	10.9	10.9		

**Table 3** A $\beta$  peptides at baseline and endpoint in CSF from untreated patients with Alzheimer's disease

	Median p25 p75											
	A $\beta$ 1-42		A $\beta$ 1-40		A $\beta$ 1-39		A $\beta$ 1-38		A $\beta$ 1-37		Total A $\beta$	
	Baseline	Endpoint	Baseline	Endpoint	Baseline	Endpoint	Baseline	Endpoint	Baseline	Endpoint	Baseline	Endpoint
Absolute values (ng/ml)	0.5	0.5	7.2	7.1	1.7	1.5	2.4	2.1	1.3	1.1	13.1	12.2
	0.46	0.31	5.8	6.0	1.3	1.2	2.0	1.7	1.1	0.8	11.1	10.6
	0.61	0.55	8.5	8.4	2.0	1.9	2.8	2.4	1.4	1.4	14.9	14.0
Percentage of total A $\beta$	3.9	3.7	56.1	57.7	12.8	12.4	18.2	16.9	9.4	9.4	100	100
	3.3	2.8	50.8	54.1	10.8	10.6	15.5	16.0	8.0	7.7		
	4.4	4.1	61.5	60.4	14.7	13.3	19.7	18.5	10.8	11.0		

AD at baseline, in other words A $\beta$ 1-40 > A $\beta$ 1-38 > A $\beta$ 1-39 > A $\beta$ 1-37 > A $\beta$ 1-42, suggesting that this pattern is highly regulated. In the untreated group we found a slight but significant reduction in the absolute levels of A $\beta$ 1-39. However, this did not change the relative order of abundance. The method shows the high reproducibility of the absolute and relative quantities of CSF A $\beta$  peptides measured by A $\beta$  SDS-PAGE/immunoblot when comparing endpoint with baseline.

#### Effect of statin treatment on A $\beta$ peptide pattern

When comparing endpoint with baseline in the treated AD group, no significant change was seen when the absolute levels of A $\beta$  peptides were expressed. However, upon expressing the levels of different peptides as percentages of the total A $\beta$  level, a slight decrease in A $\beta$ 1-39 was seen in the treated group when comparing endpoint with baseline, but with no change of the peptide pattern. From these results we can also conclude that there is no change in the CSF levels of A $\beta$ 1-40 or A $\beta$ 1-42, and the level of A $\beta$ 1-42 was also shown to be unchanged by xMAP technology. It has previously been shown that the level of A $\beta$ 1-42 does not decline during disease progression in untreated patients with AD (Andreasen et al 1999). The constant level of A $\beta$  observed in this study correlates with two previously published studies from our group (Sjögren et al 2003; Höglund et al 2004) where the production of A $\beta$  was studied and where statin treatment was shown to have no effect on the level of A $\beta$ . In our first study (Sjögren et al 2003), the CSF and plasma levels of A $\beta$ 1-42 were investigated in patients with AD before and after 12 weeks of treatment with simvastatin. In the second study (Höglund et al 2004), plasma levels of A $\beta$ 1-40, 1-42 and total A $\beta$  were investigated in patients with hypercholesterolemia, before and after 6, 12 and 24 weeks of treatment with either atorvastatin or simvastatin.

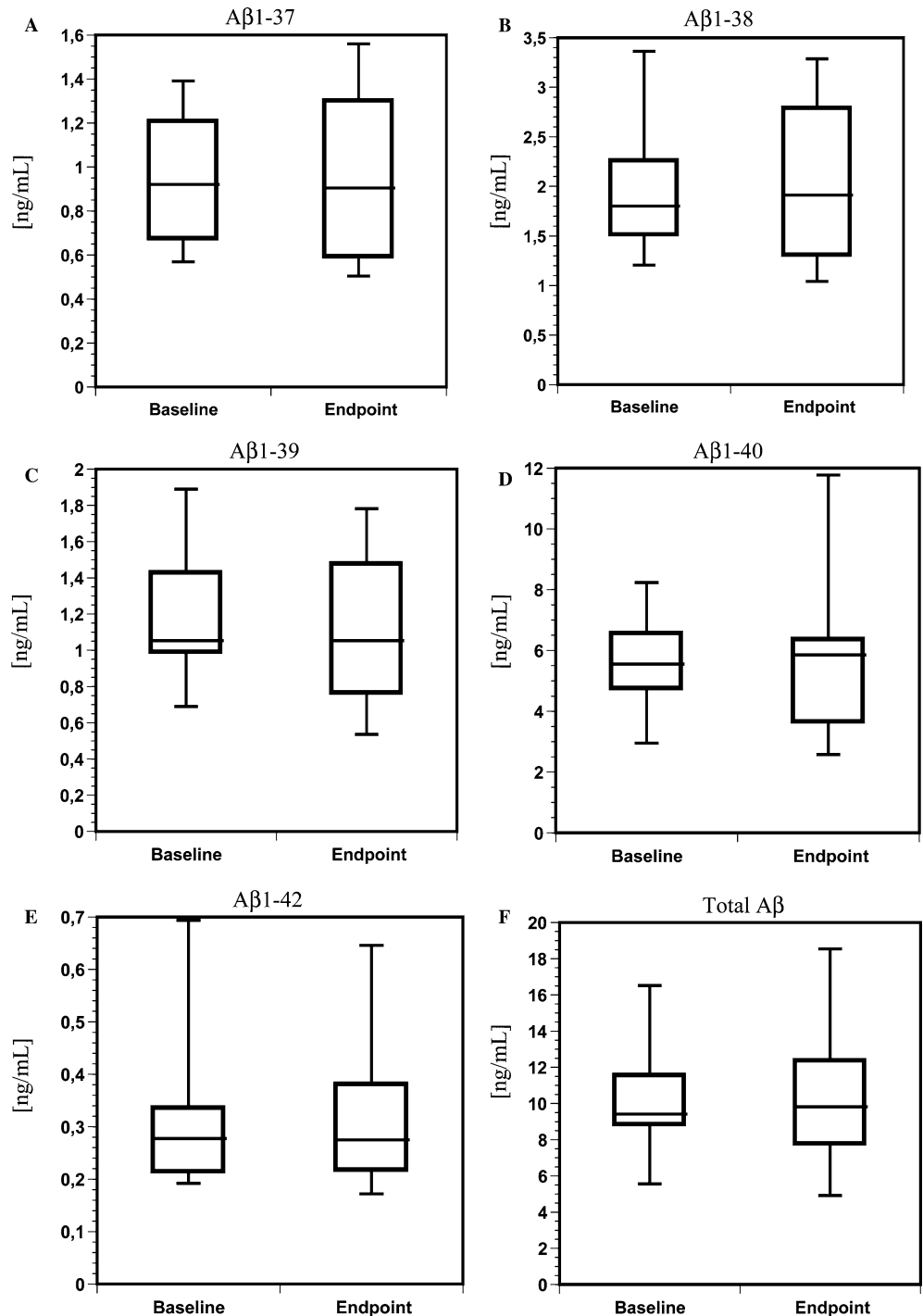
The lack of influence on the A $\beta$  pattern observed in this study could perhaps be explained by the dosage of simvastatin being too low. However, in a study performed recently by our group (Höglund et al 2005), we found that treatment with 20 mg/day of simvastatin over 12 months is sufficient to affect cholesterol

metabolism in both the peripheral body and the CNS, as indicated by reduced levels of lathosterol (a marker for cholesterol synthesis) and 24S-hydroxycholesterol (a marker for cholesterol homeostasis in the CNS). In addition, doses of between 10 and 40 mg/day of statins have been shown to significantly reduce the CSF levels of 24S-hydroxycholesterol (Fassbender et al 2002), which is a marker for brain cholesterol homeostasis (Björkhem et al 1998). In cell and animal experiments where statins were found to affect A $\beta$  production (Simons et al 1998; Fassbender et al 2001), the doses given exceeded clinically-relevant doses many times over. In epidemiological studies (Jick et al 2000; Wolozin et al 2000; Rockwood et al 2002; Yaffe et al 2002), the results were not sub-grouped by statin dosage. It has been shown that different statins have different effects (Kirsch et al 2003), which could also explain the lack of effect in the present study.

In vitro studies (Simons et al 1998; Frears et al 1999) have shown that lowering intracellular levels of cholesterol with statins affects the cholesterol content of cellular membranes. The  $\gamma$ -secretase complex believed to be responsible for the production of A $\beta$  peptides would be expected to be sensitive to changes in the cholesterol content of cellular membranes since the cleavage occurs intramembraneously. Perhaps there are alternative proteolytic pathways. An  $\epsilon$ -cleavage site has been identified (Weidemann et al 2002), located distal to the  $\gamma$ -cleavage site, and there are results indicating additional cleavages, with the A $\beta$  peptide itself as substrate (Shi et al 2003). Together these findings could form a regulated pathway, producing the different peptides 1-37/38 and 39.

In epidemiological studies (Jick et al 2000; Wolozin et al 2000; Rockwood et al 2002; Yaffe et al 2002) where statin treatment was found to reduce the prevalence of AD, longer treatment periods (2–5 years) were investigated than explored here. Reducing the synthesis of cholesterol, which must be compensated for in the long run, may result in a new equilibrium, where the cholesterol content of the membrane is slightly affected. It should be noticed that the effect of statins on the cholesterol content of cellular membranes in humans is unknown and that the full effect might not be seen after only 12 months of treatment. Although statins work

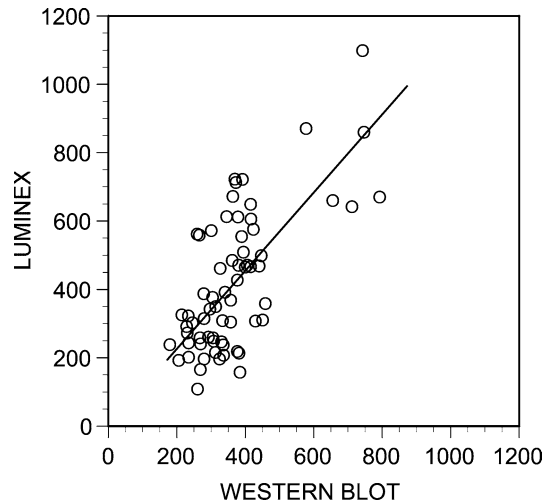
**Fig. 1a–f** Box-plots of the absolute values of the five different  $A\beta$  peptides and total  $A\beta$  in the treated group of patients with AD, at baseline and after 12 months of treatment (endpoint): **a** represents  $A\beta$ 1-37, **b**  $A\beta$ 1-38, **c**  $A\beta$ 1-39, **d**  $A\beta$  1-40, **e**  $A\beta$ 1-42 and **f** total  $A\beta$ . The values are expressed as ng/ml



preventatively against the negative impacts that  $A\beta$  has on cholesterol and lipid homeostasis (Mason et al 1999; Chochina et al 2001; Michikawa et al 2001) and on the postulated deposition of  $A\beta$  on the plasma membrane (Yamaguchi et al 2000) it may be too late to see any change in  $A\beta$  production after statin treatment in patients who have already developed AD.

Mutually exclusive regulation of the APP cleavage pathways is suggested to occur, and enhanced  $\alpha$ -cleavage may suppress  $\beta$ -cleavage at the same time (Checler 1995). However, this generally accepted

hypothesis does not appear to be valid under all circumstances (Tomita et al 1998; Mills and Reiner 1999), and the processing of APP is probably much more complicated. There are findings suggesting that APP is processed differently, depending on the cell type (Hartmann et al 1997). That the  $A\beta$  peptides produced are heterogeneous in both the N-terminal and the C-terminal further indicates complicated processing. Together these findings suggest that several proteolytical products from the processing of APP should be analysed simultaneously.



**Fig. 2** Illustration of the correlation between  $A\beta_{1-42}$  levels measured by western blot and Luminex. The level of  $A\beta_{1-42}$  is expressed as pg/ml

The pathological significance of the  $A\beta$  peptide pattern relevant to AD is still not clear and must be further elucidated. However, considering that the CSF level of  $A\beta_{1-42}$  is a biochemical marker for AD (Blennow and Hampel 2003), we believe that changes in CSF are able to reflect those in the brain. We also believe that further investigations of  $A\beta$  peptides that are truncated in both the C-terminal and N-terminal are important if we are to elucidate the role of  $A\beta$  in AD.

#### Confounding factors

It is important to be cautious when interpreting the results from the multivariate analyses in the present study, since only 18 patients were included in the study and the multivariate analyses included several factors. We investigated the effects of the following confounding factors on changes in the different  $A\beta$  peptide levels between endpoint and baseline: sex, age, APOE4, baseline values of MMSE, ADAS-Cog and cholesterol, and finally changes in MMSE, ADAS-Cog and cholesterol. We did not find any effects of sex, age or APOE4 genotype on the change between baseline and endpoint

**Table 4** The plasma levels of cholesterol, LDL and HDL in the group with treated patients

	Treated AD	
	Baseline	Endpoint
Cholesterol	224 (198–247)	154 (145–184)*
LDL	142 (116–172)	74 (60–90)*
HDL	60 (42–70)	62 (45–79)**

Data is given as median (inter-quartile range) (p25–p75), cholesterol, LDL and HDL in mg/dl. No plasma was taken from the untreated group

\*  $p = 0.000$

\*\*  $p < 0.046$

for the five different peptides. For the  $A\beta$  peptide 1–40, a less pronounced decrease in plasma cholesterol was significantly related to a more pronounced decrease of  $A\beta_{1-40}$ . We also found that both the change in ADAS-Cog and MMSE and the baseline values of ADAS-Cog and MMSE could be related to decreases in  $A\beta_{1-38}$  and 1–40. There were no correlations, but when looking at the plots we see that: (1) a more affected cognitive state at baseline (that is, low MMSE and high ADAS-Cog) is linked to a more pronounced decrease in  $A\beta_{1-38}$  and  $A\beta_{1-40}$ , and (2) those patients who did not deteriorate as much as others during the 12 months of treatment had a more pronounced decrease in the CSF levels of  $A\beta_{1-38}$  and  $A\beta_{1-40}$ . These two groups of patients—the ones with a more affected cognitive state at baseline and the ones who did not deteriorate as much—are more or less the same patients. This indicates that  $A\beta_{1-38}$  and  $A\beta_{1-40}$  may be related to severity of dementia. In agreement with this, Lue et al (1999) and McLean et al (1999) suggest that the soluble fraction of  $A\beta$  peptides is more closely correlated to the severity of dementia, compared to the insoluble  $A\beta$  peptides aggregated in plaques. Interestingly, in the study by Wiltfang et al (2002) there were also indications that  $A\beta_{1-38}$  and  $A\beta_{1-40}$  are connected to severity of dementia. In that study, the connection was found when the peptides were expressed as percentages of total  $A\beta$ . This may not be comparable to this study but is an interesting finding.

There is a significant difference in the number of carriers of the E4 allele of ApoE between the treated and untreated group. Even though ApoE is a risk factor for AD, there seems to be no connection between presence of the ApoE4 allele and cognitive decline (Bunce et al 2004).

#### Correlation between Luminex and western blot

One potential drawback when measuring  $A\beta$  in the Luminex system is that the measurement can be affected if other proteins bind to  $A\beta$ . In the present study we measured the CSF levels of  $A\beta_{1-42}$  using both western blot analysis and xMAP technology on the Luminex system. Using the western blot method, potential protein complexes are dissolved upon subjecting the proteins to sodium dodecyl sulphate and heating. The levels of  $A\beta_{1-42}$  measured by the Luminex system and the levels of  $A\beta_{1-42}$  quantified by western blot showed a high correlation, and the absolute values of  $A\beta_{1-42}$  also corresponded when comparing the two methods, so the methods seem to be comparable.

In conclusion, the disease-specific peptide pattern of  $A\beta_{1-37/38/39/40}$  and 42 was confirmed in the present study. However, despite an effect on both peripheral and CNS cholesterol synthesis after 12 months of treatment with simvastatin (20 mg/day), we found no effect on the  $A\beta$  peptide pattern. We suggest that clinical studies with extended treatment periods are performed, where different statins in higher dosages are used. We also believe

that the pleiotropic effects of statins should be investigated in order to further elucidate the connection between AD and statin treatment.

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