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A Selected Reaction Monitoring (SRM)-Based Method for Absolute Quantification of $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ in Cerebrospinal Fluid of Alzheimer's Disease Patients and Healthy Controls

Josef Pannee[a,*], Erik Portelius[a], Madalina Oppermann[b], Alan Atkins[c], Martin Hornshaw[c], Ingrid Zegers[d], Peter Höjrup[e], Lennart Minthon[f,g], Oskar Hansson[f,g], Henrik Zetterberg[a,h], Kaj Blennow[a] and Johan Gobom[a]

[a]*Department of Psychiatry and Neurochemistry, Institute of Neuroscience and Physiology, The Sahlgrenska Academy, University of Gothenburg, Mölndal, Sweden*
[b]*Thermo Scientific, Kungens Kurva, Stockholm, Sweden*
[c]*Thermo Scientific, Hemel Hempstead, UK*
[d]*Institute for Reference Materials and Measurements, Joint Research Centre, European commission, Geel, Belgium*
[e]*Department of Biochemistry and Molecular Biology, University of Southern Denmark, Odense M, Denmark*
[f]*Department of Clinical Sciences, Lund University, Lund, Sweden*
[g]*Memory Clinic, Department of Neurology, Skåne University Hospital, Malmö, Sweden*
[h]*UCL Institute of Neurology, Queen Square, London, UK*

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Abstract. Cerebrospinal fluid (CSF) biomarkers for Alzheimer's disease (AD) are increasingly used in research centers, clinical trials, and clinical settings. However, their broad-scale use is hampered by lack of standardization across analytical platforms and by interference from binding of amyloid-β (Aβ) to matrix proteins as well as self-aggregation. Here, we report on a matrix effect-resistant method for the measurement of the AD-associated 42 amino acid species of Aβ ($A\beta_{42}$), together with $A\beta_{40}$ and $A\beta_{38}$ in human CSF based on mass spectrometric quantification using selected reaction monitoring (SRM). Samples were prepared by solid-phase extraction and quantification was performed using stable-isotope labeled Aβ peptides as internal standards. The diagnostic performance of the method was evaluated on two independent clinical materials with research volunteers who were cognitively normal and AD patients with mild to moderate dementia. Analytical characteristics of the method include a lower limit of quantification of 62.5 pg/mL for $A\beta_{42}$ and coefficients of variations below 10%. In a pilot study on AD patients and controls, we verified disease-association with decreased levels of $A\beta_{42}$ similar to that obtained by ELISA and even better separation was

*Correspondence to: Josef Pannee, Clinical Neurochemistry Laboratory, Department of Psychiatry and Neurochemistry, Institute of Neuroscience and Physiology, The Sahlgrenska Academy at University of Gothenburg, Sahlgrenska University Hospital, Mölndal, SE-431 80 Mölndal, Sweden. Tel.: +46 31 3432410; Fax: +46 31 3432426; E-mail: Josef.Pannee@neuro.gu.se.

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obtained using the $A\beta_{42}/A\beta_{40}$ ratio. The developed assay is sensitive and is not influenced by matrix effects, enabling absolute quantification of $A\beta_{42}$, $A\beta_{40}$, and $A\beta_{38}$ in CSF, while it retains the ability to distinguish AD patients from controls. We suggest this SRM-based method for Aβ peptide quantification in human CSF valuable for clinical research and trials.

Keywords: Alzheimer's disease, amyloid-β, cerebrospinal fluid, mass spectrometry, selected reaction monitoring

INTRODUCTION

Alzheimer's disease (AD), the main cause of dementia, affects 36 million people worldwide and is a growing problem in the ageing population [1]. Neuropathologically, the disease is characterized by distinct changes in the brain including synaptic loss, aggregation of amyloid-β (Aβ) peptides into plaques, and accumulation of neurofibrillary tangles, consisting of hyperphosphorylated forms of the tau protein [2]. Since its discovery in plaques, the 42 amino acid form of Aβ ($A\beta_{42}$) has been the subject of extensive research [3]. It is today widely believed that abnormal accumulation of the peptide in the brain lies at the core of AD pathogenesis [4].

Cerebrospinal fluid (CSF) abundance of $A\beta_{42}$ is approximately 50% lower in AD patients, which probably reflects sequestration of the peptide in senile plaques in the brain [5]. Several studies have shown that the combined measurement of CSF $A\beta_{42}$ and tau protein (phosphorylated forms and total concentrations that reflect tangle pathology and cortical axonal degeneration, respectively) provides high diagnostic accuracy of AD in cross-sectional case control studies and longitudinal studies of patients with mild cognitive impairment [5]. These CSF biomarkers have been incorporated in novel AD definitions and diagnostic criteria [6–9] and are increasingly used in the diagnostic workup at specialized memory clinics worldwide [5].

Currently, CSF $A\beta_{42}$ is measured using several different types of immunoaffinity methods such as ELISA and newer multiplexed techniques [10]. However, there is systematic bias in the concentrations determined using these techniques [11], which to a large extent depends on differences in assay calibration and sensitivity to matrix effects. These include $A\beta_{42}$-interacting proteins and other factors such as oligomerization that may influence the fraction of CSF $A\beta_{42}$ exposed to the antibodies used for measurements [12]. An external quality control program, launched by the Alzheimer's Association to identify sources of variability for measurement of $A\beta_{42}$ [13], concluded that while intra-laboratory CVs are generally low, the concentrations reported in different studies vary considerably, even when the same analytical platform is used, with mean $A\beta_{42}$ levels in AD patients in some studies exceeding those in controls in other studies [14]. This variation presents a problem for the use of $A\beta_{42}$ as biomarker in clinical routine because it is not possible to establish generally applicable cut-off values for diagnosis making, and for research because results from studies performed in different laboratories cannot be readily compared.

Mass spectrometric quantification of $A\beta_{42}$ by selected reaction monitoring (SRM) may overcome many of the problems associated with antibody-based quantification methods [15]. A central difference is the use of stable isotope labeled (heavy) $A\beta_{42}$ as internal standard. The heavy peptide is added to the neat CSF prior to any sample preparation. Being chemically equivalent to endogenous $A\beta_{42}$, the heavy peptide has identical yield through all sample purification steps, as well as the same ionization efficiency and fragmentation behavior in the mass spectrometer, and therefore accounts for any variations in the analytical procedure. Thereby, quantification is largely unaffected by variations in the sample preparation. Furthermore, the high selectivity of detection using SRM alleviates the need for extensive sample purification. For $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$, CSF sample preparation can be performed with a single step of solid-phase extraction (SPE) [16]. Thus, using SPE allows for quantification of Aβ species in denatured samples without the need of antibodies. Most antibody-based methods are influenced by matrix effects and measure only the so-called free fraction of $A\beta_{42}$, i.e., not oligomerized or protein-bound forms, as revealed by the non-linearity of antibody-based methods upon dilution of samples [11, 12]. When SPE is performed under denaturing conditions, for example by adding guanidine hydrochloride (GdnHCl), non-linear dilution effects are much less pronounced indicating that a larger proportion of the analyte may be available for quantification (total fraction).

The aim of the current study was to develop a reliable SRM-based assay with reduced matrix effect for quantification of $A\beta_{42}$, $A\beta_{40}$, and $A\beta_{38}$ in human CSF. The developed assay was evaluated with regards to linearity, coefficient of variation, limit of quantification, and correlation with an established ELISA method. Its

diagnostic accuracy was verified in a study of two independent clinical materials with 15 AD patients and 15 cognitively normal controls in each set.

MATERIAL AND METHODS

Participants and CSF collection

In the present study we analyzed CSF samples from 15 AD patients, mean age ± SD: 75.6 ± 6.6 years, and 15 healthy controls, mean age ± SD: 66.3 ± 9.8 years. A second set of CSF samples from 15 AD patients (mean age ± SD: 81 ± 5.0 years) and 15 healthy controls (mean age ± SD: 63.9 ± 9.4 years) were analyzed. All patients have undergone a thorough clinical investigation, including a medical history, physical, neurological and psychiatric examination, screening laboratory tests, and computerized tomography (CT) of the brain. AD patients fulfilled the DSM-IIIR criteria of dementia [17] and the criteria of probable AD defined by NINCDS-ADRDA [18]. The control individuals were cognitively normal research volunteers. The ethics committee at the University of Lund has approved analyses of Aβ variants in CSF from AD patients and controls, and all patients (or their nearest relatives) and controls gave informed consent for research, which was conducted according to the provisions of the Helsinki Declaration. The first 10–12 mL of CSF was collected in polypropylene tubes, gently mixed to avoid possible gradient effects and aliquoted in 500 μL portions in polypropylene cryo tubes. The CSF samples were stored at −80°C pending analysis.

Sample preparation

CSF was thawed at room temperature and vortexed. A 200 μL aliquot was transferred to a 1.5 mL polypropylene tube (LoBind, Eppendorf) containing 200 μL 5 M GdnHCl for protein denaturation. The heavy peptide standards (1 mg), $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$, uniformly labeled with ^{15}N (rPeptide), were dissolved in 1 mL of 20% acetonitrile (ACN) and 1% NH_4OH in water, aliquoted and stored at −80°C in 0.5 mL polypropylene tubes (Eppendorf). Upon analysis, the internal standards were diluted with 20% ACN and 1% NH_4OH in water to a concentration of 12 nM. GdnHCL treated CSF samples (400 μL) were spiked with 8 μL of the diluted standard and mixed at room temperature for 45 mins followed by addition of 200 μL 4% phosphoric acid (H_3PO_4).

To evaluate if the method is sensitivity to matrix effects, a CSF pool with an $A\beta_{42}$ concentration of 1000 pg/mL determined by ELISA was serially diluted with PBS four times. Four replicates of each dilution were prepared.

Calibrators

The reverse curve method for calibration was used to determine the concentrations of unknown samples as described elsewhere [19]. A pool of human CSF was spiked with a mixture of heavy labeled $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ to final concentrations of 5000 pg/mL, 10000 pg/mL, and 2000 pg/mL, respectively. The spiked CSF samples were serially diluted (1 : 2) five times with CSF from the same pool (Fig. 1a). Three replicates of each dilution were analyzed.

The performance of the method including sensitivity and linearity was evaluated by the reverse curve method with heavy $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ peptides spiked in at 2000 pg/mL and serially diluted down to 62.5 pg/mL.

Intra assay coefficients of variation (CV) were determined by analyzing 6 separately prepared CSF samples from one CSF pool (1214 pg/mL) and 6 samples from another CSF pool (350 pg/mL).

Solid-phase extraction

Extraction of Aβ peptides was performed using a mixed mode cation exchange SPE 96 well plate (Oasis MCX μElution, Waters) as described elsewhere [16]. Briefly, the plate was washed with 200 μL methanol followed by 200 μL 4% H_3PO_4 in water before adding 600 μL pretreated CSF. After washing with 200 μL 4% H_3PO_4 in water followed by 200 μL 10% ACN, the samples were eluted with 2×50 μL 2.5% NH_4OH in 75% ACN into 0.75 mL polypropylene tubes (Micronic). The extracted samples were dried using vacuum centrifugation and stored at −80°C. Prior to analysis the dried samples were dissolved in 25 μL 1% NH_4OH in 20% ACN, vortexed for 30 min at room temperature, and centrifuged briefly (Fig. 1b).

SRM analysis

Samples (20 μL) were injected on a reversed-phase monolith column (ProSwift RP-4 H 1×250 mm, Thermo Scientific) heated to 50°C. A 0.2 μm particle filter (Waters), which was backflushed between sample injections, was placed in front of the column to reduce backpressure build-up. An Accela 1250 pump (Thermo Scientific) was used for delivering the

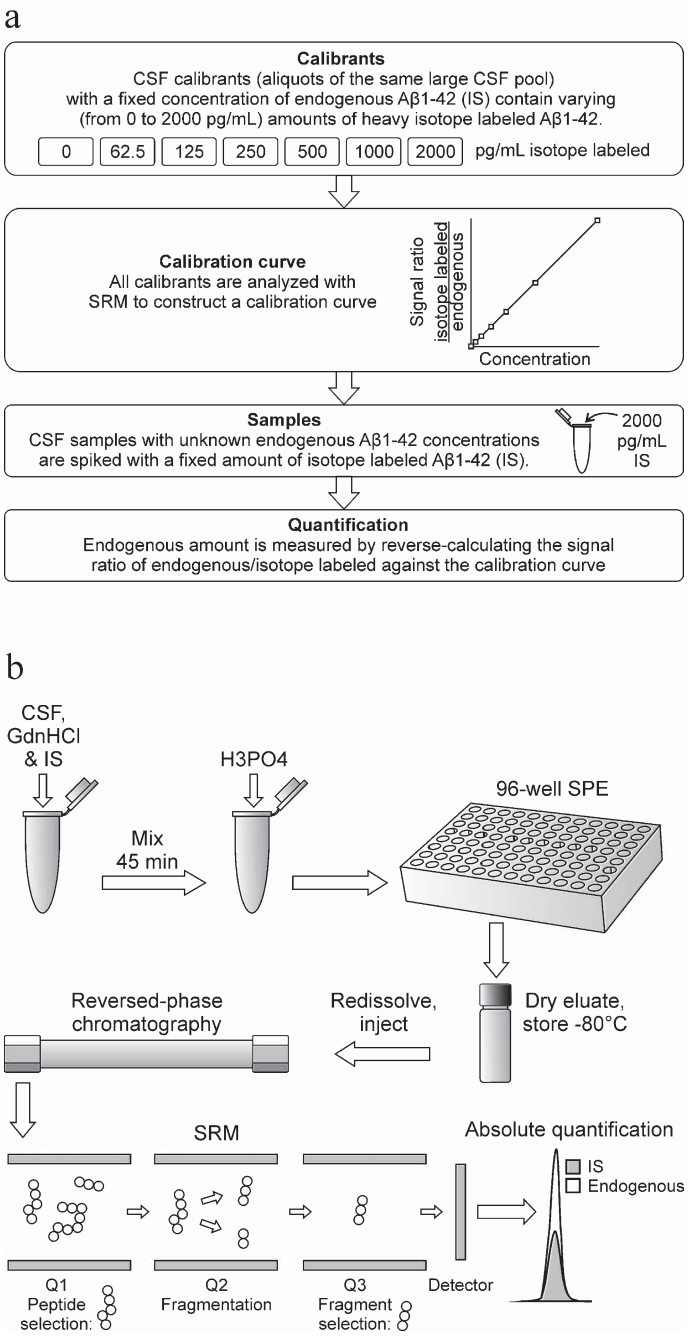

Fig. 1. a) Quantification is performed using the reverse curve method for calibration. For the calibration curve, the heavy isotope labeled peptide is varied while the light (endogenous) peptide is the internal standard (IS). With unknown samples, the heavy peptide is again used as the IS. b) Overview of the method. For each sample, 200 µL GdnHCl is added to 200 µL CSF and IS are spiked in at 2000 pg/mL. The samples are then mixed in room temperature for 45 minutes and 200 µL H_3PO_4 is added to each sample before extraction. Each SPE plate can be loaded with 96 samples in parallel. The eluted samples are dried simultaneously using vacuum centrifugation (about 45 minutes) and stored in −80°C. Prior to analysis the dried samples are redissolved with 25 µL 1% NH_4OH in 20% ACN. The samples are then injected serially on a reversed phase column which separates the peptides according to their hydrophobicity. Since the shorter Aβ peptides are less hydrophobic than the longer species, they elute earlier while co-eluting with their corresponding internal standard. The time from injection to injection is 20 minutes. The Aβ peptides are ionized using electrospray and transmitted through the first quadrupole according to their m/z values to the second quadrupole which is filled with argon. Here the peptides are fragmented as they collide with the gas atoms and only specific fragments of the Aβ peptides with predefined m/z values are transmitted through the third quadrupole and further to the detector.

mobile phases at a flow of 300 μL/min. Mobile phase A consisted of 0.1% NH_4OH and 5% ACN in water, and mobile phase B was 0.03% NH_4OH in 95% ACN. Elution was performed using the following linear gradient steps: t (min.): 0, %B: 0; t: 2, %B: 0; t: 3, %B: 10; t: 10, %B: 25; t:11, %B: 90, t: 13, %B: 90; t: 14, %B: 0; t: 21, %B: 0. SRM analysis of positively charged peptide ions was performed on a triple quadrupole mass spectrometer (TSQ Vantage, Thermo Scientific) with an IonMax source and HESI-II electrospray probe equipped with a high-flow metal needle (Thermo Scientific). The following global MS parameters were used: cone voltage 3.5 kV; vaporizer temperature 350°C; sheath gas pressure 40 psi; auxiliary gas flow 25 (a.u.); capillary temperature 350°C; CID gas pressure 1.6 mTorr. Pinpoint software version 1.1 (Thermo Scientific) was used for method optimization and data processing.

Amino acid analysis

Amino acid analysis was performed for precise determination of the concentrations of aliquoted internal standards. Polypropylene vials containing lyophilized aliquots (12.5 μg) of the heavy Aβ peptide standards were placed in separate 22 mL glass vials (Wheaton). Hydrolysis buffer (200 μL 6 N HCl, 0.1% phenol, 0.1% thioglycol acid) was added to the bottom of the glass vials. The vials were purged with argon, closed with a MiniInert valve (Pierce, $p < 5$ mbar) and the samples were incubated at 110°C for 20 h. The dried samples were redissolved in 70 μL loading buffer (pH 2.2) containing 1 nmol NorLeu and half the sample was applied to a BioChrom 31 amino acid analyzer running the sodium accelerated buffer system. The analyzer was calibrated to an r^2 value >0.999 and for every 6th sample a 1600 pmol standard was analyzed for recalibration. After analysis, integration of the chromatograms were checked manually and the integration results were analyzed using an in-house developed program AAA ver. 1.03, which corrects for intensity changes of the ninhydrin (−3.9%) and performs a best linear fit of hydrolysis data to the theoretical sequence (∼+1%).

Statistics

All statistical calculations were performed using Graphpad (version 5.02) software. For the AD versus control comparisons, the Mann-Whitney U-test was used. Linear regression was used for analyses of correlation between methods. Estimates of diagnostic accuracy were sensitivity, specificity, and the area under the receiver operating characteristics curve (AUROC). $p < 0.05$ was considered statistically significant.

RESULTS

Optimal transitions for $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ were determined through direct infusion of each peptide separately into the mass spectrometer. The most prominent precursor charge state for each of the three peptides was selected by manual evaluation of the full scan tandem mass spectrometry (MS/MS) spectra (Fig. 2a–c). For each precursor, the top 10 most prominent product ions were used for further optimization by systematically varying collision energy and collision gas pressure. The three best transitions were selected for each peptide and used for quantification (Table 1). The LC gradient was optimized for a short analysis time (20 min in total including washing and equilibration of the column) and sufficient separation for implementation of the scheduled SRM. Typical SRM chromatograms for $A\beta_{42}$, $A\beta_{40}$, and $A\beta_{38}$ in a human CSF sample are shown in Fig. 2d.

Analytical characteristics of the method includes linear results upon serial dilution of CSF (Fig. 3) and a lower limit of quantification (LLOQ) for $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ was determined to 250 pg/mL, 62.5 pg/mL, and 62.5 pg/mL, respectively, with CVs of 11%, 13%, and 5% (Fig. 4). For $A\beta_{42}$, intra-assay CVs were 12% at 350 pg/mL and 6% at 1214 pg/mL, respectively.

The influence of GdnHCl on the levels of $A\beta_{42}$ measured was tested by varying the amount of GdnHCl added to the CSF (2.5 and 6 M final concentrations). No significant difference was observed (<5%).

To test the ability of the SRM assay to separate AD patients from controls, we determined the concentrations of $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ in two sets of 15 AD and 15 control CSF samples. Aliquots of the samples were, in parallel, analyzed by $A\beta_{42}$ ELISA. A human CSF pool were analyzed every 10 samples to monitor the stability of the method. Even though the CSF $A\beta_{42}$ concentration obtained by SRM yielded an approximately two-fold higher absolute concentration compared to values obtained with ELISA, there was a statistically significant linear correlation between SRM and ELISA $A\beta_{42}$ (Fig. 5a and 6a), with an R^2 value of 0.35 ($p < 0.0001$) for set one and an R^2 value of 0.77 ($p < 0.0001$) for set two. The separation between AD patients and controls was similar using SRM with a

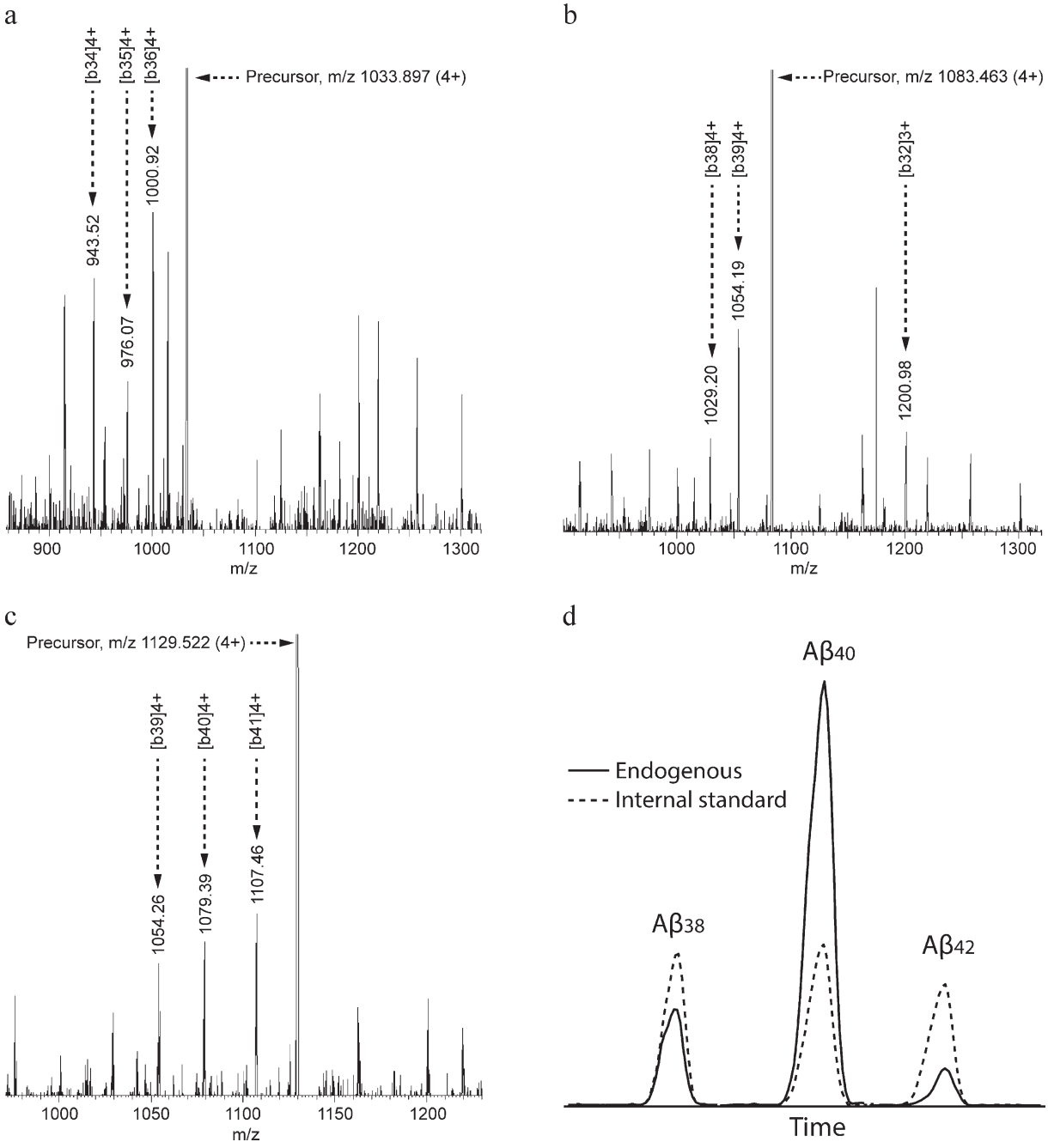

Fig. 2. MS/MS spectra for $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$. Transitions used for the assay are marked with corresponding ion type and charge state for $A\beta_{38}$ (a), $A\beta_{40}$ (b), and $A\beta_{42}$ (c). Typical SRM chromatograms for $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ (d). Absolute concentration of endogenous Aβ peptide is calculated using the area ratio for the co-eluting internal standard of known concentration.

sensitivity of 93% and specificity of 80% compared to ELISA (Fig. 5b, c) and a sensitivity and specificity of 86.7% for set two (6b, c). The ratio of $A\beta_{42}$ to $A\beta_{40}$ ($A\beta_{42}/A\beta_{40}$) further improved the separation between the diagnostic groups (Fig. 5d, e and 6d, e).

DISCUSSION

We here report on the development of an antibody-independent, matrix effect resistant assay for quantification of $A\beta_{42}$, $A\beta_{40}$, and $A\beta_{38}$ using SRM-based

Table 1
Transitions used in the SRM assay. Internal heavy standards are marked with asterisk

Peptide	Precursor ion charge state	Precursor ion m/z[a]	Product ion charge state	Product ion	Product ion m/z	Collision Energy (eV)
1–38	4+	1033.897	4+	b34	943.286	22
1–38*	4+	1045.927	4+	b34	954.392	22
1–38	4+	1033.897	4+	b35	976.085	21
1–38*	4+	1045.927	4+	b35	987.400	21
1–38	4+	1033.897	4+	b36	1000.868	20
1–38*	4+	1045.927	4+	b36	1012.416	20
1–40	4+	1083.463	4+	b38	1029.180	23
1–40*	4+	1096.626	4+	b38	1042.059	23
1–40	4+	1083.463	4+	b39	1053.960	20
1–40*	4+	1096.626	4+	b39	1067.091	20
1–40	4+	1083.463	3+	b32	1200.500	22
1–40*	4+	1096.626	3+	b32	1215.543	22
1–42	4+	1129.522	4+	b39	1057.177	22
1–42*	4+	1143.182	4+	b39	1067.091	22
1–42	4+	1129.522	4+	b40	1078.740	21
1–42*	4+	1143.182	4+	b40	1092.122	21
1–42	4+	1129.522	4+	b41	1107.000	20
1–42*	4+	1143.182	4+	b41	1120.660	20

[a] m/z = mass to charge ratio.

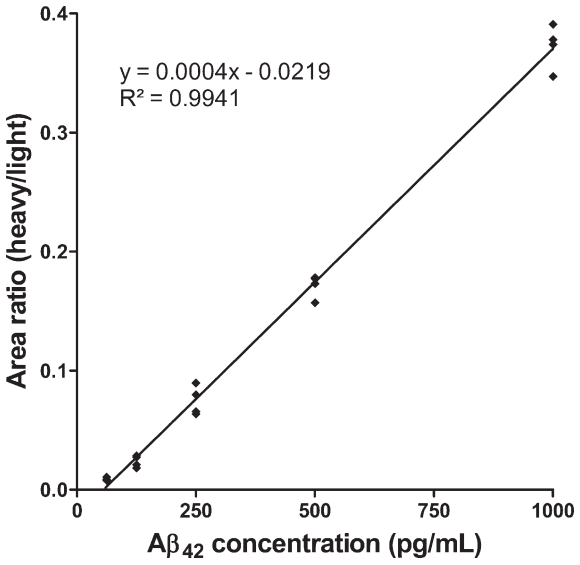

Fig. 3. Linearity of $A\beta_{42}$ measured by SRM (area ratio light/heavy) of human pool-CSF, with a concentration of 1000 pg/mL measured by ELISA, serially diluted with PBS four times.

mass spectrometry. The performance of the method was evaluated in two independent AD and control studies which showed statistically significant correlations to ELISA measurements of $A\beta_{42}$ as well as similar separations between the groups indicating that SRM-based mass spectrometry can be used as a clinically useful assay for measurement of $A\beta_{42}$ in human CSF.

For Aβ, previous studies have shown that while there is no significant change in the CSF $A\beta_{40}$ concentration between AD and controls, there is already a decrease in the $A\beta_{42}/A\beta_{40}$ in the mild cognitive impairment stage of AD. This decrease is more pronounced than the reduction in CSF $A\beta_{42}$ alone [20, 21]. Using SRM-based quantification of $A\beta_{42}$ and $A\beta_{40}$, we here replicate the finding that the CSF $A\beta_{42}/A\beta_{40}$ ratio increases the separation performance between AD and controls as compared to $A\beta_{42}$ alone. Further studies will be aimed to elucidate whether the ratio is a prognostic AD marker which can be used for AD diagnosis already at the pre-symptomatic stage of the disease.

An important advantage over immunoassays is the ability to include additional peptides such as other isoforms of Aβ or other endogenous peptides to an already existing SRM assay to assemble a panel of biomarkers tailored to specific clinical questions which can be analyzed in a single run.

Several studies suggest that Aβ-binding proteins may have an impact on the measured concentration of $A\beta_{42}$ since there might be a difference in free $A\beta_{42}$ and total $A\beta_{42}$ in CSF [11, 12]. Recently, it was shown that denaturation of proteins in CSF with GdnHCl before analysis resulted in increased concentration of $A\beta_{42}$ by ELISA [12]. In the present study, using GdnHCl in the sample purification, the CSF $A\beta_{42}$ concentrations obtained with the SRM assay were approximately twice as high as the concentrations determined by ELISA, while the separation between AD patients and controls remained in spite of the denaturing conditions. Furthermore, increasing the amount of GdnHCl added to the CSF did not increase the free $A\beta_{42}$ measured in our study.

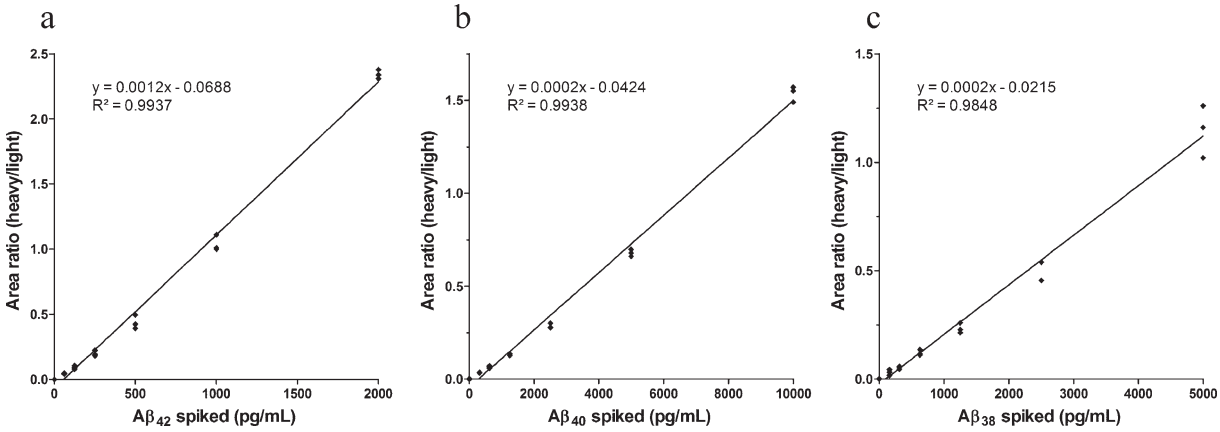

Fig. 4. Calibration curves with the SRM peak areas as a function of the peptide concentration for $A\beta_{42}$ (a), $A\beta_{40}$ (b), and $A\beta_{38}$ (c).

There are several aspects to consider including high specificity as well as robustness and stability of the method when analyzing large series of samples. While SPE purification in the 96-well format is performed in parallel with many samples, the subsequent LC-MS analysis is serial. Thus, the extracted samples will have different time delay for LC-MS. Using the described SRM method, dried extracted samples were analyzed after being stored in freezer (-20°C) for four months with minimal loss in signal (less than 1%).

A matrix effect-resistant $A\beta_{42}$ method is important to reduce the bias in CSF $A\beta_{42}$ measurements between commercially available assays. An essential component of such a method is that, e.g., the calibration of the method is performed in a matrix is identical to the sample-matrix to be analyzed. To achieve a matrix effect-resistant method, we used the reverse curve method for calibration which previously has been shown to give equal or better trueness and precision compared to traditional calibration curves or single reference point calibration [19]. For a reverse curve calibration, the heavy peptide is varied while the light (endogenous) peptide is the internal standard and is held constant. With unknown samples, the heavy peptide is again used as the internal standard by adding at a fixed amount to the samples, and the light amount is measured by reverse-calculating against the calibration curve. The method also works with calibration in artificial CSF and gives similar quantitation results as the reversed curve method in human CSF. The latter method was chosen because it avoids the risk of matrix effects that may distort results when constructing a calibration curve in a matrix different from that of the unknowns.

SRM-based quantification of $A\beta_{40}$ and $A\beta_{42}$ in human AD and control CSF was first reported by Oe et al. [22]. Their method relied on antibodies for sample purification, followed by LC-MS in a basic buffer system, and the authors showed higher concentrations of CSF $A\beta_{42}$ obtained with SRM compared to ELISA, which is in agreement with this study [22]. However, electrospray was performed in the negative ion mode, resulting in low efficiency of fragmentation, and only one transition per peptide was used for quantification, which may make the assay vulnerable to interference from other sample components (cross-talk) [23]. The current practice is to select two or more transitions per peptide for reliable quantification [24]. Furthermore, the transition chosen was neutral loss of H_2O. While sensitive, this is a non-peptide-specific loss, which increases the risk of cross-talk. In a further development, Lame et al. showed that antibody-dependent enrichment of CSF $A\beta_{38}$, $A\beta_{40}$, and $A\beta_{42}$ could be replaced by SPE without loss of detection sensitivity or precision. They also demonstrated that while using a basic buffer system, operating the mass spectrometer in the positive ion mode resulted in lower detection sensitivity compared to negative mode. This approach was still preferable because of increased selectivity for Aβ peptides together with increased stability of the Aβ signal [16]. They did not perform AD-control comparisons to test the diagnostic accuracy of the method.

To achieve high specificity and stability over time, we analyzed the samples in the positive ion mode, and monitored three *b* ions per peptide using scheduled SRM, thereby reducing the signal-to-noise ratio while the limit of detection was improved [25]. With the one-step SPE procedure described here, the Aβ

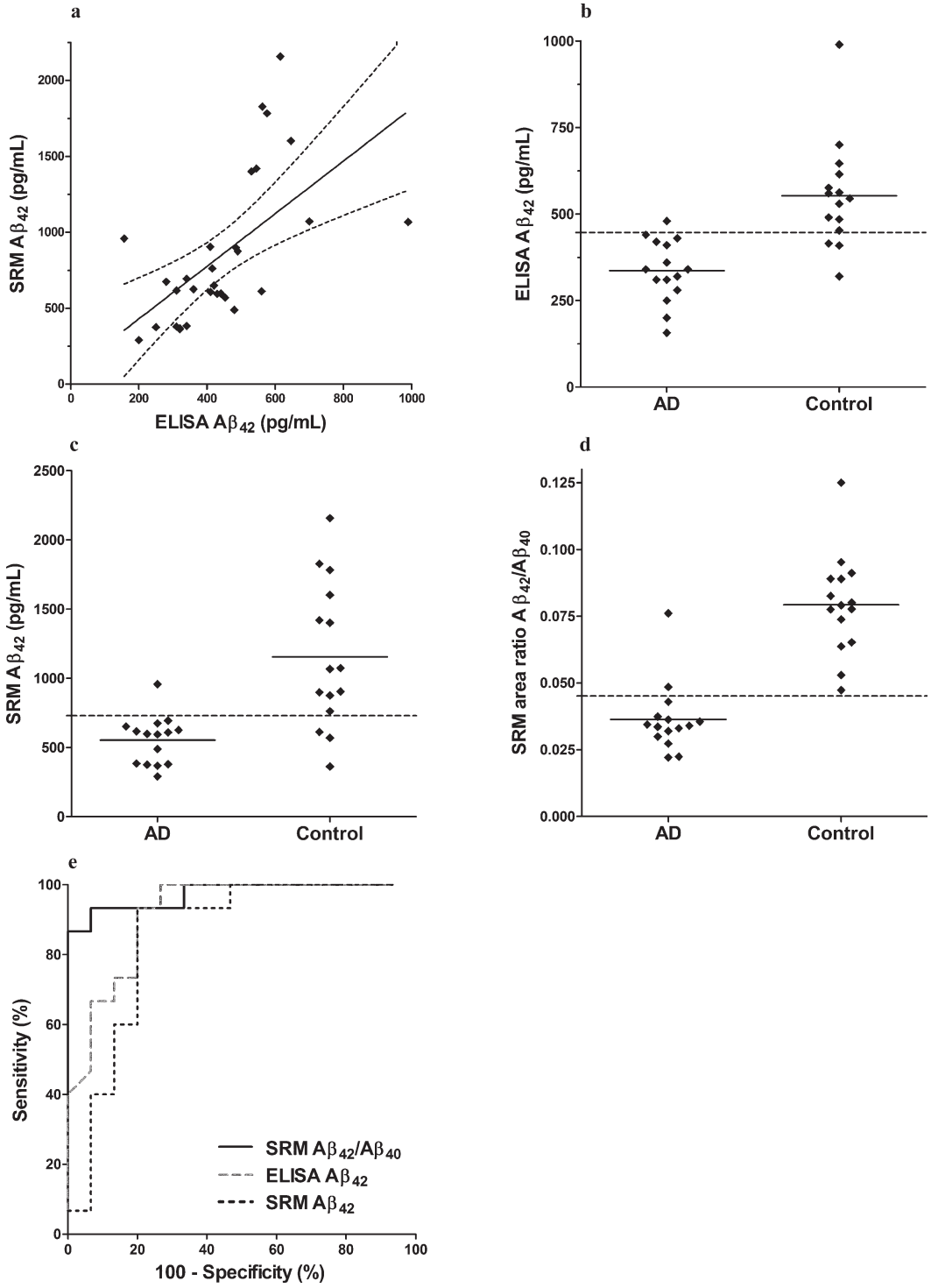

Fig. 5. Set one of 15 AD patients and 15 controls. Correlation between SRM $A\beta_{42}$ and ELISA $A\beta_{42}$ assays (a). Separation of AD and control groups for ELISA $A\beta_{42}$ ($p < 0.0001$) (b) and SRM $A\beta_{42}$ ($p = 0.0011$) (c) and separation of AD and control groups for SRM using the $A\beta_{42}/A\beta_{40}$ ratio ($p < 0.0001$) (d). The solid line represents median value for each group while the dashed line represents the optimal sensitivity and specificity for separation of AD and control groups. The sensitivity and specificity of the different methods is summarized in an ROC curve, AUC ELISA $A\beta_{42} = 0.92$, SRM $A\beta_{42} = 0.85$, SRM $A\beta_{42}/A\beta_{40} = 0.97$ (e).

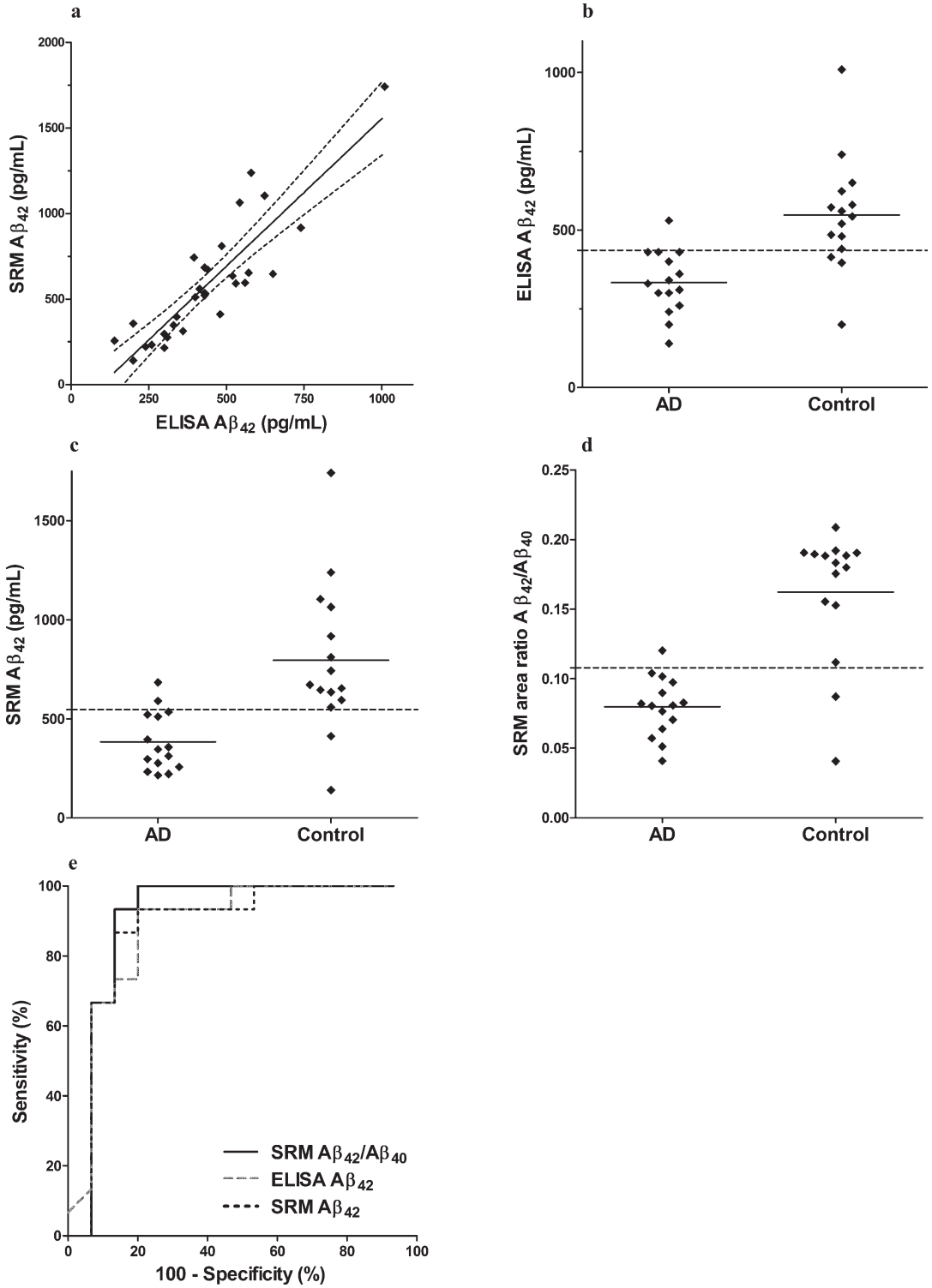

Fig. 6. Set two of 15 AD patients and 15 controls. Correlation between SRM $A\beta_{42}$ and ELISA $A\beta_{42}$ assays (a). Separation of AD and control groups for ELISA $A\beta_{42}$ ($p = 0.0004$) (b) and SRM $A\beta_{42}$ ($p = 0.0004$) (c) and separation of AD and control groups for SRM using the $A\beta_{42}/A\beta_{40}$ ratio ($p = 0.0002$) (d). The solid line represents median value for each group while the dashed line represents the optimal sensitivity and specificity for separation of AD and control groups. The sensitivity and specificity of the different methods is summarized in an ROC curve, AUC ELISA $A\beta_{42} = 0.88$, SRM $A\beta_{42} = 0.88$, SRM $A\beta_{42}/A\beta_{40} = 0.91$ (e).

samples loaded on the LC-MS system are quite crude, containing many other peptides and larger proteins, as well as aggregates and particles. These sample impurities may contaminate the system and cause degradation of the analytical performance over time. Trapping of insoluble materials on the particle filter resulted in successively increased back pressure over the filter. By implementing a routine for backflushing the filter between sample injections, the trapped particles were removed, and minimal pressure build-up over the filter was observed.

When using a silica-based C_{18} column for peptide separation, as described in previous studies [16, 22, 26], we noticed a gradual back pressure build-up over the separation column following each consecutive sample injection. This is most likely caused by irreversible binding of sample impurities to the column and resulted in the column needing to be replaced after less than 10 injections. This may have severe implications for the applicability of the method to routine work: it increases the cost per sample by over $100 and causes down-time because each new column has to be tested before use. We therefore evaluated the use of a monolith separation column based on a polystyrene divinylbenzene copolymer bed. Possessing weaker hydrophobic retention characteristics than particle-based C_{18} stationary phases, this chromatographic medium is less prone to contamination by proteins and other hydrophobic molecules. The separation column used in this study has been used for over 200 injections of human CSF samples without any increase in back pressure or degradation of performance.

While SRM has been used for over three decades, its main area of application has been small-molecule analysis, and only in recent years has the technique emerged as an alternative to immunoassays for protein and peptide quantification [27]. In this respect, the technique has distinct advantages. For one, molecular mass-based selective quantification allows one to discriminate between modified forms of a target molecule, which would be indistinguishable in an immunoassay. Assay development is generally quicker and panels of many target molecules can be assayed in one analysis. For $A\beta_{42}$, it is plausible that SRM-based assays will overcome the problem of inter-laboratory variation discussed above, because mass spectrometric quantification using stable isotope-labeled internal standards enables absolute quantification and is uninfluenced by matrix effects. This notion is currently being evaluated in a collaborative effort involving several research laboratories within the Global Consortium for Biomarker Standardization (GCBS) of the Alzheimer's Association. A positive evaluation, however, does not necessarily imply that SRM assays will likely replace immunoassays in clinical routine in the near future; LC-MS analysis is a serial, relatively time-consuming process that cannot match the sample throughput of state-of-the-art immunoassay methods. A more likely scenario is that SRM will be used as a reference technique to determine the absolute $A\beta_{42}$ levels in reference materials. Such materials have been used as 'gold standards' in other areas of laboratory medicine to reduce measurement variability and harmonize analytical results obtained in different laboratories [28].

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