

RESEARCH ARTICLE

Structural Analysis and Aggregation Propensity of Pyroglutamate A β (3-40) in Aqueous Trifluoroethanol

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Citation: Dammers C, Gremer L, Reiß K, Klein AN, Neudecker P, Hartmann R, et al. (2015) Structural Analysis and Aggregation Propensity of Pyroglutamate A β (3-40) in Aqueous Trifluoroethanol. PLoS ONE 10(11): e0143647. doi:10.1371/journal.pone.0143647

Editor: Surajit Bhattacharjya, Nanyang Technological University, SINGAPORE

Received: September 25, 2015

Accepted: November 6, 2015

Published: November 23, 2015

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Data Availability Statement: All relevant data are within the paper and its Supporting Information files.

Funding: We gratefully acknowledge support of CD from the International NRW Research School BioStruct, granted by the Ministry of Innovation, Science and Research of the State North Rhine-Westphalia, the Heinrich Heine University of Düsseldorf, and the Entrepreneur Foundation at the Heinrich Heine University of Düsseldorf. DW was supported by grants from the "Portfolio Technology and Medicine", the "Portfolio Drug Research" and the Helmholtz-Validierungsfonds of the "Impuls und

Abstract

A hallmark of Alzheimer's disease (AD) is the accumulation of extracellular amyloid- β (A β) plaques in the brains of patients. N-terminally truncated pyroglutamate-modified A β (pEA β) has been described as a major compound of A β species in senile plaques. pEA β is more resistant to degradation, shows higher toxicity and has increased aggregation propensity and β -sheet stabilization compared to non-modified A β . Here we characterized recombinant pEA β (3–40) in aqueous trifluoroethanol (TFE) solution regarding its aggregation propensity and structural changes in comparison to its non-pyroglutamate-modified variant A β (1–40). Secondary structure analysis by circular dichroism spectroscopy suggests that pEA β (3–40) shows an increased tendency to form β -sheet-rich structures in 20% TFE containing solutions where A β (1–40) forms α -helices. Aggregation kinetics of pEA β (3–40) in the presence of 20% TFE monitored by thioflavin-T (ThT) assay showed a typical sigmoidal aggregation in contrast to A β (1–40), which lacks ThT positive structures under the same conditions. Transmission electron microscopy confirms that pEA β (3–40) aggregated to large fibrils and high molecular weight aggregates in spite of the presence of the helix stabilizing co-solvent TFE. High resolution NMR spectroscopy of recombinantly produced and uniformly isotope labeled [U -¹⁵N]-pEA β (3–40) in TFE containing solutions indicates that the pyroglutamate formation affects significantly the N-terminal region, which in turn leads to decreased monomer stability and increased aggregation propensity.

Introduction

The pathology of Alzheimer's disease (AD) is characterized by the presence of intracellular neurofibrillary tangles consisting of accumulated hyperphosphorylated tau protein and extracellular plaques containing amyloid- β (A β) as major component [1, 2]. A β is derived by

Vernetzungsfonds der Helmholtzgemeinschaft". The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

processing of the amyloid precursor protein by β - and γ -secretases [3, 4]. Multiple possible cleavage positions of γ -secretase combined with various posttranslational modifications of the cleaved products result in different A β isoforms with heterogeneity in length as well as N- and C-terminal sequences [5, 6]. Pyroglutamate-modified A β (pEA β) peptides have been reported to be the dominant component of all N-terminal truncated A β variants in AD plaques as up to 20% of the total A β are pEA β variants [7–9]. pEA β deposits in the brains of presymptomatic AD patients [10] and was shown to play a dominant role in plaque formation and to provoke neurodegeneration in mouse models [11, 12]. Formation of pEA β is based on N-terminal truncation leading to N-terminal E3 or E11 and subsequent cyclization of the accessible E amino group with the side chain carboxy group leading to pyroglutamate. *In vivo* it was suggested the cyclization is catalyzed by the enzyme glutaminyl cyclase [13, 14]. pEA β starting at position 3 (pEA β (3-x)) represents the major fraction of N-pyroglutamate modified A β species in intracellular, extracellular and vascular accumulations in AD brains [15–18]. The cumulative deposition of pEA β in AD brains coincides with increased protease-stability since the pyroglutamate modified N-terminus is inaccessible to aminopeptidases [19, 20]. The loss of two negative charges (side chain carboxyl groups of D1 and E3) and one positive charge (E3 amino group) at physiological pH result in higher hydrophobicity of pEA β (3-x) [19, 21]. Aggregation of pEA β (3-x) is up to 250-fold accelerated [22] and its neurotoxicity is enhanced [23, 24] when compared with the corresponding wild type A β species independent of the C-terminal length.

Structural analysis of pEA β monomers is essential to uncover its aggregation mechanism and to reveal, why it is more prone to self-assembly than A β wild type. In a previous NMR study, we analyzed pEA β (3–40) in aqueous buffer conditions at neutral pH and compared it with given A β (1–40) data [25]. Most chemical shifts were nearly identical except of the very N-terminal region and both peptides were shown to be unstructured.

Since structural studies of A β peptides are often limited due to their high aggregation tendency, solvent conditions need to be carefully chosen. α -helical A β monomers are predominantly formed in micelles [26], hexafluoroisopropanol (HFIP)/water [27] and 2,2,2-trifluoroethanol (TFE)/water [28] mixtures. In a previous NMR study we compared pEA β (3–40) with A β (1–40), both chemically synthesized with natural carbon and nitrogen isotope abundance, in aqueous solution containing 40% TFE [29]. The results indicated that both A β isoforms formed α -helical structures in two regions (aa 14–22 and aa 30–36) connected by a flexible and disordered linker. However, pEA β (3–40) exhibited a decreased helix propensity in agreement with its higher hydrophobicity and faster aggregation kinetics.

Here, we analyzed the solvent conditions for the transition of pEA β (3–40) from TFE-induced α -helices to β -sheets by gradually lowering the TFE concentrations. We expand the data by investigations of recombinantly produced [U - 15 N]-pEA β (3–40) regarding structure and aggregation in 20% TFE, where A β (1–40) is still in a predominantly α -helical monomeric state, while pEA β (3–40) forms a β -sheet dominated secondary structure, starts to aggregate and forms large fibrils.

Materials and Methods

Peptides and sample preparation

Expression and purification of uniformly isotope labeled [U - 15 N]-pEA β (3–40) and [U - 15 N]-A β (1–40) as well as non-labeled pEA β (3–40) were performed as described recently [25, 30]. Synthetic non-labeled A β (1–40) was purchased from Bachem (Heidelberg, Germany). Samples were prepared in Protein LowBinding tubes (Eppendorf AG, 230 Hamburg, Germany). The A β peptides were dissolved in HFIP (1,1,1,3,3,3-hexafluoro-2-propanol, Sigma-Aldrich,

Hannover, Germany) and monomerized for 3 days at room temperature. Samples were lyophilized and stored at -20°C.

CD spectroscopy

Lyophilized peptides were dissolved in aqueous buffer containing different TFE concentrations (20–25% TFE in 50 mM potassium phosphate, pH 2.8) to a final concentration of 25 μ M. UV CD measurements were performed in 1 mm path-length cuvettes at 20°C. CD spectra were recorded on a Jasco J-1100 spectropolarimeter from 260 to 187 nm with 0.5 nm step size, 50 nm/min scan speed, 1 nm bandwidth and 10 scans per sample. Background correction was performed by subtraction of corresponding buffer spectra.

ThT assay

Lyophilized peptides were dissolved to a final concentration of 25 μ M in buffer (20–25% TFE in 50 mM potassium phosphate, pH 2.8) containing 10 μ M ThT. Aggregation assays were performed in black non-binding 96-well plates (Sigma-Aldrich, Germany) at 20°C with a total volume of 100 μ l per well. Each reaction was performed fivefold and background corrected by subtraction of the buffer control. Fluorescence was monitored in 10 min steps using a microplate reader (PolarStar Optima, BMG, Offenburg, Germany) with 440 excitation and 492 nm emission filters, respectively, in bottom-read mode. Wells were shaken 30°s prior to measurement.

TEM microscopy

Lyophilized pEA β (3–40) was dissolved in aqueous buffer (20% TFE in 50 mM potassium phosphate, pH 2.8) and incubated for five days at 20°C. Fibrils were absorbed on formval/carbon coated copper grids (S162, Plano, Wetzlar, Germany) for 5 min and washed with water. Negative staining was performed by incubation with 1% (w/v) uranylacetate for 1 min. Images were taken with a Libra 120 transmission electron microscope (Zeiss, Oberkochen, Germany) at 120 kV.

NMR spectroscopy

Lyophilized [U - 15 N]-pEA β (3–40) and [U - 15 N]-A β (1–40) were directly dissolved in 100% TFE- d_2 -OH and diluted with 50 mM potassium phosphate, pH 2.8 to a final concentration of 25 μ M peptide in 20% TFE. NMR spectra were acquired using a TXI- or QCI-cryoprobe equipped Bruker Avance III HD 600 MHz spectrometer. 1 H, 15 N-HSQC correlation spectra were recorded according to standard Bruker pulse-sequences [31–33]. 1 H_N and 15 N Backbone resonance assignments in 30% TFE were obtained by using BEST-TROSY (BT) HNCA+-optimized pulse sequences [34, 35]. Resonance assignments of spectra recorded at 30% TFE concentration were transferred to the spectrum recorded at 20% TFE through recordings at TFE concentrations of 27% and 23%, respectively. Spectra were processed with NMRPipe [36] and evaluated with CCPNmr Analysis [37]. Analysis of C α secondary chemical shifts is based on the publication by Zhang *et al.* [38] and sequence corrected according to Schwarzsinger [39].

Results

Secondary structure analysis by CD spectroscopy

TFE is known to induce α -helical structures by lowering the solvent polarity and promoting intra-molecular hydrogen bonding [40]. Reducing the concentration of this co-solvent prevents this effect e.g. as shown for A β (1–40) [41], human carbonic anhydrase II [42], FF domain of URN1 splicing factor [43], transferrin [44], α -synuclein [45] and conalbumin [46]. The α -

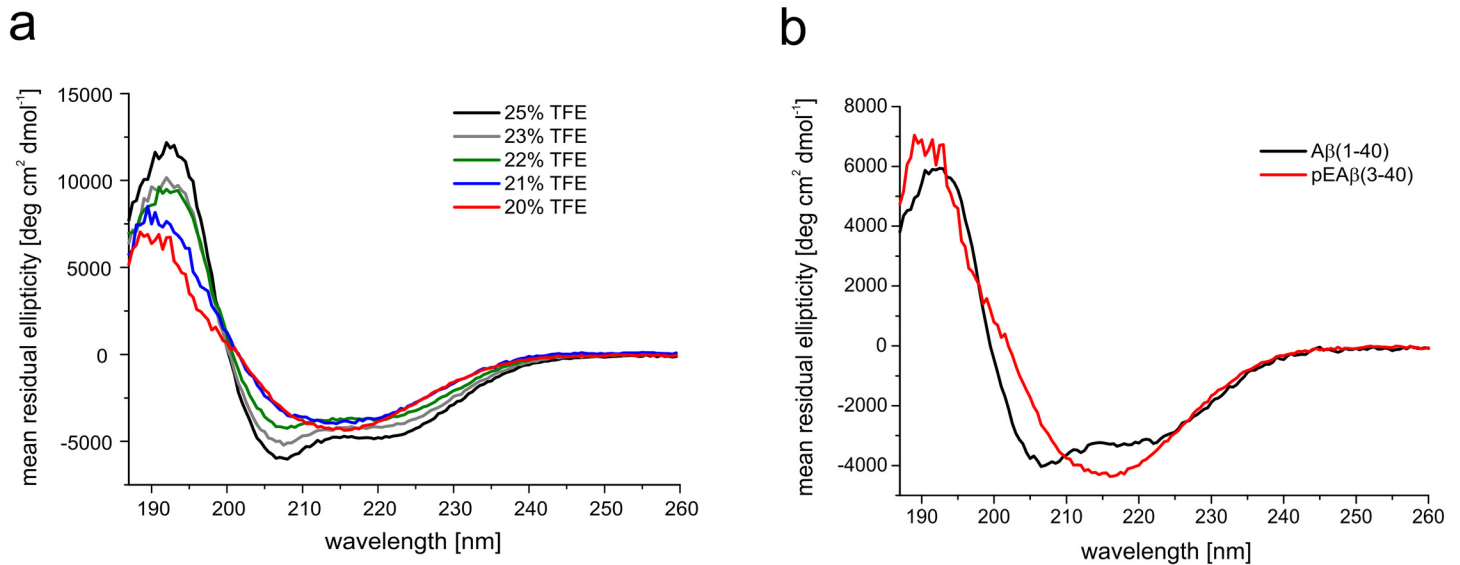


Fig 1. Far-UV CD spectra of pEA β (3-40) and A β (1-40). Peptides were dissolved in buffer (20–25% TFE in 50 mM potassium phosphate, pH 2.8). CD spectra were recorded at 20°C from 260 to 187 nm, accumulated 10 times and background corrected. (a) CD spectra of 25 μ M pEA β (3-40) in 25%, 23%, 22%, 21% and 20% TFE showed a shift from α -helical structure towards β -sheets with decreasing TFE concentrations. (b) The CD spectrum of 25 μ M A β (1-40) indicated α -helices in 20% TFE while the spectrum of 25 μ M pEA β (3-40) in 20% TFE showed mainly β -sheet rich structures.

doi:10.1371/journal.pone.0143647.g001

helices inducing effect of TFE on pEA β (3-40) and the shift towards β -sheets by lowering the TFE contents was analyzed by recording CD spectra in aqueous buffer in different TFE concentrations. CD spectra in solutions containing varying concentrations of TFE ranging from 25% to 22% at pH 2.8 indicated a mainly α -helical conformation based on minima at 208 nm and 222 nm, a maximum at 193 nm and an x-axis intercept at 200 nm. Marginally lowering the TFE concentration from 22% to 20% or 21% was sufficient to alter the α -helical protein conformation of pEA β (3-40) to a β -sheet dominated secondary structure (Fig 1a) as indicated by the evolvement of characteristic β -sheet features in the corresponding CD spectra with a single minimum at 216 nm, a x-axis intercept at 202 nm and a shift of the maximum to a lower wavelength, i.e. 190 nm. CD spectra of A β (1-40) recorded under the same condition (20% TFE) differed compared to the spectra of pEA β (3-40) by indicating α -helices (Fig 1b).

Aggregation kinetics and fibrillation

Aggregation analysis supported the CD data of pEA β (3-40) and A β (1-40) indicating different secondary structural elements in aqueous solution containing 20% TFE. Fig 2a displays the aggregation kinetics in TFE containing solutions ranging from 20% to 25% TFE at 20°C for pEA β (3-40) as monitored by ThT assay. pEA β (3-40) aggregation reaches its maximum at TFE concentrations of 20% and 21%. A distinct lag phase of 9h (20% TFE) or 14 h (21% TFE) is observable following a clear growth phase where aggregation increased indicating that β -sheet formation is not hindered by the presence of TFE. In the presence of 25% TFE no ThT fluorescence increase was observed during 72 h, which indicate that pEA β (3-40) stays monomeric at that condition. However, when the TFE concentration was lowered to 23% or 22% TFE a significant delay as well as decreased maximum was detected within 72 h exploration time. Aggregation of A β (1-40) could not be observed at all under the same conditions as no increase in fluorescence intensity was detected within 72 h (Fig 2b). Thus, fibrillation and/or ThT positive β -sheet formation of A β (1-40) seemed to be inhibited or at least significantly delayed in the presence of the helix-stabilizing fluoroalcohol TFE.

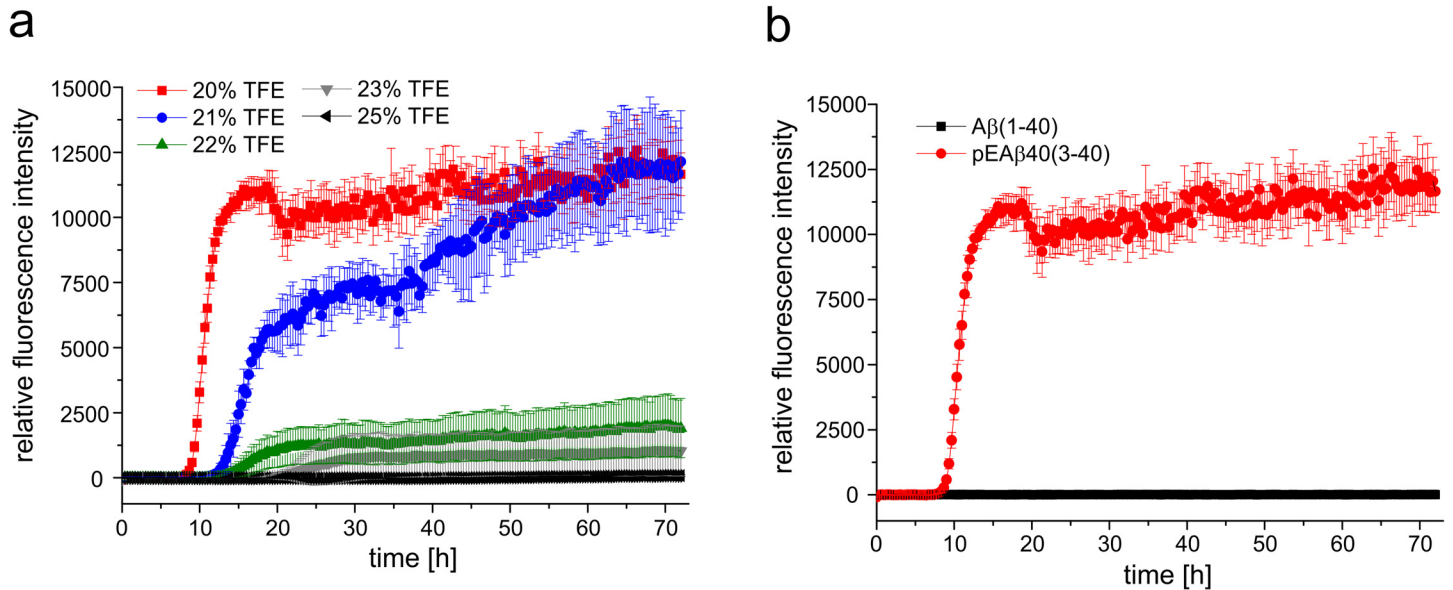


Fig 2. Aggregation kinetics of pEA β (3-40) and A β (1-40) in TFE. (a) 25 μ M of monomerized pEA β (3-40) were dissolved in buffer with various TFE contents (25%, 23%, 22%, 21% and 20% TFE in 50 mM potassium phosphate, pH 2.8) including 10 μ M ThT. pEA β (3-40) aggregated in 20% and 21% TFE but was significantly decreased in aqueous solution with higher TFE concentration. (b) 25 μ M of monomerized pEA β (3-40) and A β (1-40) were dissolved in buffer (20% TFE in 50 mM potassium phosphate, pH 2.8) including 10 μ M ThT. An increase in ThT fluorescence was observed for pEA β (3-40) but not for A β (1-40) within 72 h.

doi:10.1371/journal.pone.0143647.g002

TEM microscopy was performed to analyze the structure of pEA β (3-40) aggregation products formed after incubation of the monomerized peptide in 20% TFE (Fig 3). pEA β (3-40) built large fibrils accumulating into aggregates with several μ m in diameter. The fibrils were twisted, exhibit a rather homogeneous morphology and accumulate into plaques comparable with fibrils matured in aqueous solution [47].

NMR spectroscopy

Since pEA β (3-40) started to aggregate at room temperature and built large fibrils in 20% TFE (pH 2.8), 2D NMR spectroscopy was performed with only 25 μ M recombinantly produced [U - 15 N]-pEA β (3-40). Nonetheless, considerably protein aggregation within 2 days even at the low concentration applied impeded the recording of 3D experiments. To overcome this problem, backbone $^1\text{H}_\text{N}$ and ^{15}N resonance assignments of pEA β (3-40) in 20% TFE were obtained by a time optimized BT-HNCA+ pulse sequence performed with pEA β (3-40) in 30% TFE (S1 Fig). Transfer of the resonance assignments to the ^1H , ^{15}N -HSQC spectrum in 20% TFE was performed gradually from 30% through 27% and 23% TFE (S2 Fig). The C α secondary chemical shifts of pEA β (3-40) in 30% TFE were neighbor-corrected and plotted as a function of the aa sequence (S3 Fig). There is evidence that aa Y10-A21 and K28-V36 are involved in the α -helix formation as indicated by positive secondary chemical shifts. This is in accordance with the secondary structure of pEA β (3-40) in 40% TFE obtained from proton chemical shift data [29].

For reference, the spectrum of recombinant [U - 15 N]-A β (1-40) was acquired under identical conditions and both ^1H , ^{15}N -HSQC spectra were overlaid for comparison (Fig 4). The absence of the first two amino acid residues D1 and A2 and the substitution of E3 to pE3 is the only difference between pEA β (3-40) and A β (1-40). The main changes in chemical shifts are therefore expected to be primarily observed for the very N-terminal amino acid residues. Interestingly, signals of the N-terminal region up to E11 differed significantly (Fig 5). Cross-peaks further

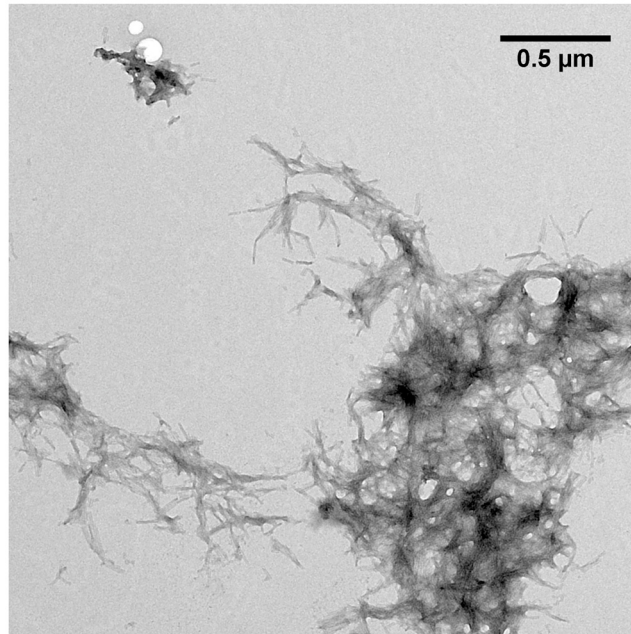


Fig 3. TEM image of pEA β (3–40) in 50 mM potassium phosphate pH 2.8 containing 20% TFE. Monomerized pEA β (3–40) (25 μ M) was incubated for fibrillation at 20°C for five days and grids were prepared by negative staining. pEA β (3–40) incubated in aqueous TFE solution formed large twisted fibrils up to several hundred nm in size which accumulate into large aggregates ranging from 1–5 μ m in diameter.

doi:10.1371/journal.pone.0143647.g003

downstream towards the C-terminus, except of the C-terminal amino acid V40, were not or only marginally changed.

Discussion

Previous data indicated that pyroglutamate-modified A β shows increased tendency to form β -sheets compared to the unstructured A β in aqueous buffer at neutral pH [22, 48, 49]. Here, we expand structural knowledge on pEA β (3–40) by showing that it forms β -sheets even in the presence of considerably amounts of the co-solvent TFE. This is consistent with data indicating that the tendency to build α -helical structures is decreased for pEA β (3–40) as compared to unstructured A β (1–40) as analyzed by proton NMR spectroscopy at higher TFE concentrations, where both peptides stay in monomeric conformation [29]. Our data indicate a change in conformation of pEA β (3–40) as a result of lowering the TFE concentration. We identified the exact TFE concentration (20% at pH 2.8) where pEA β (3–40) already is in a β -sheet conformation, whereas A β (1–40) exhibits still an overall α -helical conformation. This confirms, that TFE is not simply favoring α -helical secondary structures, but secondary structures in general [50].

The differences in the secondary structure content observed by CD spectroscopy seem to be a result of the modification from A β to pEA β , which modifies the N-terminal region significantly. ThT and TEM data support this evidence by yielding characteristic aggregation kinetics and large matured fibrils for pEA β (3–40) in 20% TFE but not for A β (1–40) under same conditions.

Using NMR spectroscopy, we analyzed pEA β (3–40) monomers in 20% TFE (pH 2.8). Under these conditions, pEA β (3–40) slowly forms β -sheet containing aggregates that could not be observed by solution NMR. Although it was shown in a model peptide starting with a N-terminal E1 that conversion to pE1 results in altered chemical shifts only of the following two amino acids [51], pE formation of A β peptides obviously affects not only the immediately

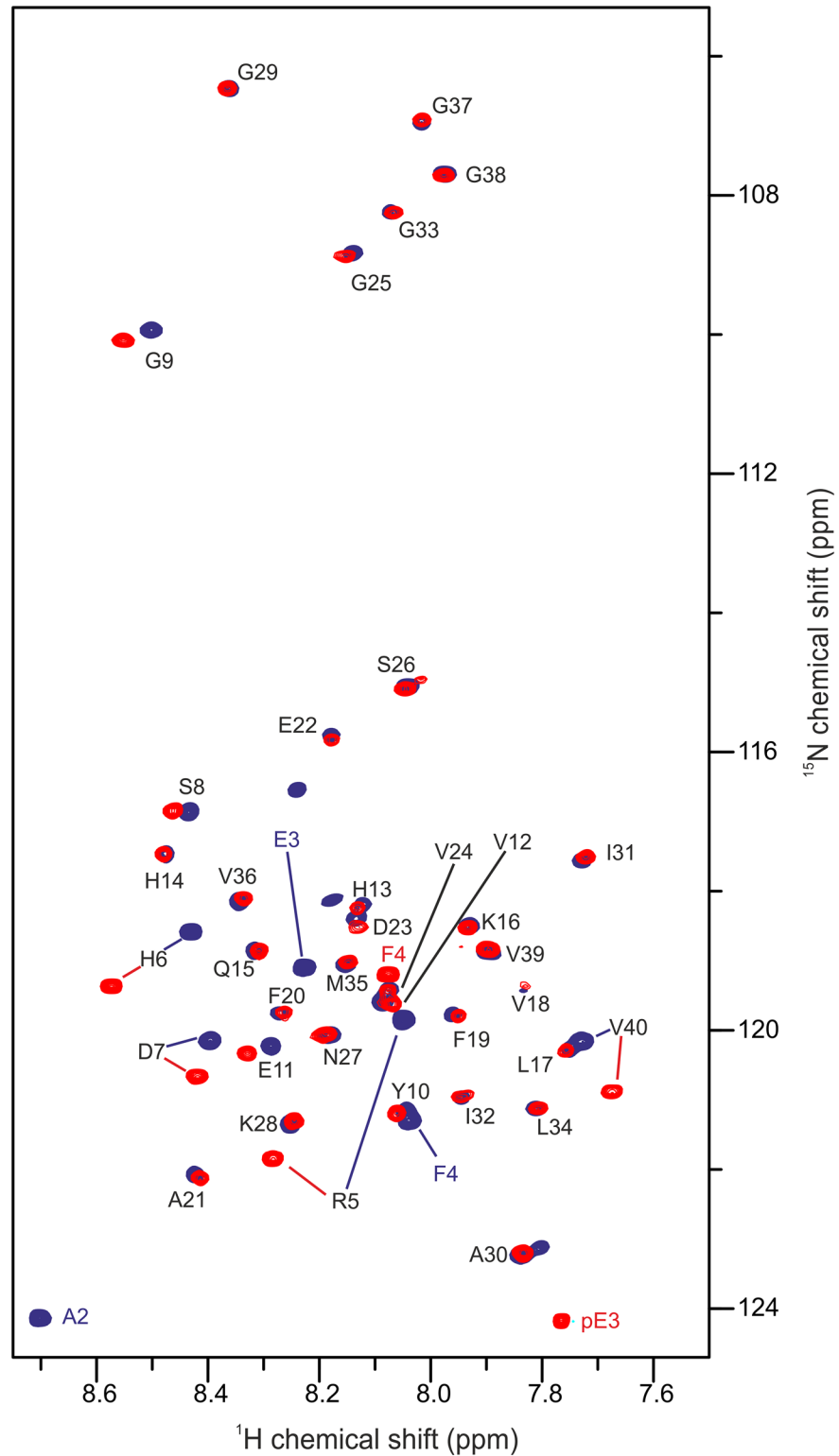


Fig 4. $^1\text{H},^{15}\text{N}$ -HSQC of pEA β (3-40) and A β (1-40). 25 μM of the monomerized peptides were dissolved in aqueous solution (50 mM potassium phosphate, pH 2.8) containing 20% TFE. Spectra were recorded on a 600 MHz Bruker spectrometer at 5°C. Overlay of the spectrum of pEA β (3-40) (red) and A β (1-40) (blue) indicate that the pyroglutamate modification affects the N-terminal signals significantly towards E11 as well as V40.

doi:10.1371/journal.pone.0143647.g004



Fig 5. Chemical shift changes $\Delta\delta(^1\text{H}, ^{15}\text{N}) = ((10 \cdot \Delta\delta^1\text{H}^{\text{N}})^2 + (\Delta\delta^{15}\text{N})^2)^{1/2}$ between pEAβ(3-40) and Aβ(1-40) plotted as a function of the pEAβ(3-40) sequence. Pyroglutamate formation affects the N-terminal amino acids with decreasing effect towards the C-terminus and, interestingly, also the C-terminal V40.

doi:10.1371/journal.pone.0143647.g005

adjacent N-terminus. It was previously shown by H_N and H_α proton chemical shift differences between pEAβ(3-40) and Aβ(1-40) in higher TFE concentrations (40%), that mostly protons of the six following amino acids from pE3 to S8 with decreasing influence towards the C-terminus were affected [29]. In the presence of only 20% TFE, we observed many resonance differences of pEAβ(3-40) compared to Aβ(1-40). Chemical shift differences of the N-terminal amino acids towards E11 as well as the C-terminal V40 were mostly affected as shown in Fig 5. Thus, it seems that the modification of Aβ(1-40) to pEAβ(3-40) not only influence the neighboring amino acids, but also change significantly the conformational state of at least 25% of all amino acids. This result suggests that the N-terminal modification to pEAβ has a significant effect on secondary structure elements and thus is the driving force for pEAβ(3-40) to be more likely to build β-sheet structures under exactly the same conditions when compared to Aβ(1-40). The propensity of pEAβ(3-40) to aggregate in aqueous TFE solution seems to be propagated by the modified N-terminus, but V40 obviously play also a central role, maybe due to interactions of both termini. Since C-terminally truncated Aβ peptides are less prone to aggregation, e.g. Aβ(1-38) < Aβ(1-40) < Aβ(1-42) [52, 53], it is likely that their pE modified isoforms would show an increased aggregation propensity as compared to the non-pE-modified isoforms, analogous to the results obtained within this study.

Supporting Information

S1 Fig. ^{15}N -HSQC of pEAβ(3-40) in 30% TFE.

(TIF)

S2 Fig. ^{15}N -HSQC of pEAβ(3-40) in different TFE concentrations.

(TIF)

S3 Fig. $\text{C}\alpha$ secondary chemical shifts of pEAβ(3-40) in 30% TFE.

(TIF)

Acknowledgments

Matthias Stoldt, Justin Lecher and Maren Thomaier are highly acknowledged for fruitful discussions. We gratefully acknowledge support of CD from the International NRW Research School BioStruct, granted by the Ministry of Innovation, Science and Research of the State North Rhine-Westphalia, the Heinrich Heine University of Düsseldorf, and the Entrepreneur Foundation at the Heinrich Heine University of Düsseldorf. The authors acknowledge access to the Jülich-Düsseldorf Biomolecular NMR Center. DW was supported by grants from the

“Portfolio Technology and Medicine”, the “Portfolio Drug Research” and the Helmholtz-Validierungsfonds of the “Impuls und Vernetzung-Fonds der Helmholtzgemeinschaft”.

Author Contributions

Conceived and designed the experiments: CD MS LG NS HUD DW. Performed the experiments: CD ANK KR. Analyzed the data: CD MS RH PN. Wrote the paper: CD MS LG DW.

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