

Histidine-13 Is a Crucial Residue in the Zinc Ion-Induced Aggregation of the A β Peptide of Alzheimer's Disease[†]

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ABSTRACT: Metal ions such as Zn²⁺ and Cu²⁺ have been implicated in both the aggregation and neurotoxicity of the β -amyloid (A β) peptide that is present in the brains of Alzheimer's sufferers. Zinc ions in particular have been shown to induce rapid aggregation of A β . Rat A β binds zinc ions much less avidly than human A β , and rats do not form cerebral A β amyloid. Rat A β differs from human A β by the substitution of Gly for Arg, Phe for Tyr, and Arg for His at positions 5, 10, and 13, respectively. Through the use of synthetic peptides corresponding to the first 28 residues of human A β , rat A β , and single-residue variations, we use circular dichroism spectroscopy, sedimentation assays, and immobilized metal ion affinity chromatography to show that the substitution of Arg for His-13 is responsible for the different Zn²⁺-induced aggregation behavior of rat and human A β . The coordination of Zn²⁺ to histidine-13 is critical to the zinc ion induced aggregation of A β .

Alzheimer's disease (AD) is characterized pathologically by the deposition of amyloid, the major component of which is a 40–42 residue peptide known as the β -amyloid peptide (A β) (1). A β is proteolytically derived from a ubiquitous cell surface protein called the amyloid precursor protein (APP) (2). The deposition of amyloid appears to be a critical factor in the development of AD, and A β itself has been reported to be neurotoxic (3–6). Neurotoxicity appears to require A β to be in the form of β -sheet aggregates (7–9), although the degree of aggregation of the neurotoxic species is unknown (10, 11).

A β is present in AD brain in both soluble and insoluble forms (12–14) and interacts with a variety of materials. Amyloid found in AD brain is complexed with several proteins, including apolipoprotein E (apoE) (15), APP (16) and heparin sulfate proteoglycan (17). ApoE has been proposed to act as an antiaggregation agent (18, 19), while this and other proteins have also been suggested to facilitate the conversion of soluble A β to the toxic aggregates and fibrils (20, 21). Other factors that influence the aggregation state of A β in vivo include pH (22–24), peptide concentration (22, 25), incubation time (26), salt concentration (26), glycation (27), and the presence of certain metal ions (28–30).

Zinc and copper ions have been implicated in both A β aggregation and neurotoxicity. A β preferentially and saturably binds Zn²⁺ (28), and Zn²⁺ induces synthetic A β aggregation in a pH-dependent and reversible manner (31).

Zn²⁺ also selectively induces the rapid aggregation of endogenous A β in cerebrospinal fluid (CSF). In addition, a possible mechanism for A β toxicity is free radical-induced oxidative damage initiated by a metal ion–A β -induced Fenton reaction (32). High concentrations of zinc have been found in neurones in regions of the brain that are vulnerable in AD, such as cortex and the hippocampus (33). Up to 300 μ M Zn²⁺ is released into the extracellular space during neurotransmission in the hippocampus (34, 35), which may be sufficient to induce aggregation of A β . After transient forebrain ischemia, which has been associated with amyloid deposition, degenerating neurons show a large increase in chelatable Zn²⁺ (36, 37). The Zn²⁺ binding site on A β is unknown, although it appears to be between the residues 6 and 28 (38). Because Zn²⁺ binding is abolished by acidic pH and by chemical modification of the histidines with diethyl pyrocarbonate, then one or more histidine side chains are probably involved in binding (29).

It has been reported that rats do not form cerebral A β amyloid (39, 40). In addition, rat A β binds Zn²⁺ much less avidly and is less susceptible to Zn²⁺-induced aggregation than is the human A β sequence (28). Rat A β differs from human A β by the substitutions of Gly for Arg, Phe for Tyr, and Arg for His at positions 5, 10, and 13, respectively. The difference in Zn²⁺ binding, aggregation, and amyloid formation of rat and human A β and the fact that two of the three substitutions are within the putative N-terminal Zn²⁺ binding region indicate that at least one of these three substituted residues is crucial to Zn²⁺ binding and amyloid formation. Metals such as Cu²⁺ and Ni²⁺ were shown to displace radiolabeled zinc ions (⁶⁵Zn²⁺) from A β , indicating that the binding site is similar for these three metals (41), although this study was performed in the absence of a blocking transition metal ion to abolish low-affinity metal ion interactions. Therefore, at least one of the human A β residues Arg-

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| ¹ DAEFRHDSGYEVHHQKLVFFAEDVGSNK ²⁸ | hA β (1–28) |
| ¹ DAEFGHDSGFEVRRHQKLVFFAEDVGSNK ²⁸ | rA β (1–28) |
| ¹ DAEFGHDSGYEVHHQKLVFFAEDVGSNK ²⁸ | ⁵ G-hA β (1–28) |
| ¹ DAEFRHDSGFEVHHQKLVFFAEDVGSNK ²⁸ | ¹⁰ F-hA β (1–28) |
| ¹ DAEFRHDSGYEVRRHQKLVFFAEDVGSNK ²⁸ | ¹³ R-hA β (1–28) |

FIGURE 1: Sequence of the synthesized peptides.

5, Tyr-10, or His-13 may be critical to the metal binding of both Zn²⁺ and Cu²⁺ ions and in amyloid formation. Iodination of A β tyrosine has been suggested to attenuate Zn²⁺-mediated precipitation (28), indicating that this residue may be important for metal binding and aggregation. To test the importance of each rat substitution on metal binding and aggregation we have synthesized a series of A β (1–28) peptides based on the human sequence with individual rat substitutions, in addition to the rat [rA β (1–28)] and human [hA β (1–28)] peptides (Figure 1). A β (1–28) should be a good model for A β metal binding because the N-terminal 28 residues of A β encompass the putative 6–28 metal binding site, contain all the potentially charged A β residues, modulate the conformational behavior and pH dependence of the A β sequence (22–24), and contain all the human to rat substitutions. In addition, hA β (1–28) has been shown to form amyloid fibrils in vitro (42, 43). Therefore, this sequence should mimic the metal-binding properties of full-length A β .

MATERIALS AND METHODS

Peptide Synthesis. Peptides were synthesized by use of manual solid-phase Boc amino acid chemistry with in situ neutralization (44). Acylations were performed with 5 equiv of the Boc-protected amino acid, 4.9 equiv of HBTU, 5 equiv of HOBt, and 7.5 equiv of DIPEA. Each acylation was monitored by ninhydrin monitoring (45), and couplings were repeated if necessary. Peptides were cleaved from the resin by anhydrous hydrogen fluoride with *p*-cresol as a scavenger. After hydrogen fluoride removal, peptides were dissolved in trifluoroacetic acid (TFA) and precipitated with ether. Peptides were purified with an acetonitrile/water (0.01% TFA) gradient on a reverse-phase semipreparative Vydac HPLC column. Peptide purity and identity were confirmed by analytical HPLC, electrospray mass spectrometry, and amino acid analysis.

Circular Dichroism Spectroscopy. Circular dichroism (CD) spectra were obtained under a variety of solution conditions using a CD spectropolarimeter, model 62DS (Aviv, Lakewood, NJ). The method used was similar to that previously described for A β (23). Briefly, a stock solution of each peptide in acetonitrile and water (1:1) was prepared. The concentrations of the stock solutions were determined by quantitative amino acid analysis. A known amount of this stock solution, normally 7 μ L, was injected into 300 μ L of the appropriate CD buffer directly in the 1 mm path length quartz cell. The solution was mixed and allowed to stand for 5 min before the spectrum was acquired. Measurements were taken at 0.5 nm steps over a 190–250 nm wavelength range, the baseline was subtracted, and the resulting spectra were smoothed. For temperature denaturing studies, the temperature was controlled by a circulating water bath and spectra were recorded at 10 °C intervals from 10 to 60 °C.

Sedimentation Assay. The proportion of pelletable peptide was determined by a modified literature method (46, 47). Briefly, samples were prepared from peptide stock solution by dilution with 20 mM sodium phosphate buffer (pH 7.3) containing 150 mM NaCl. For metal-induced aggregation experiments, metal ions were added from a 0.1 M metal stock solution (Ni²⁺, Zn²⁺, or Fe³⁺). The final peptide concentrations were 100 μ M, containing 0–2000 μ M metal ions with a total volume of 120 μ L. Samples were incubated for 0–24 h at 37 °C, after which insoluble aggregates were removed by centrifugation at 13000g for 10 min. The ratio of peptide concentrations, as determined by fluorescamine assay, of the supernatant relative to noncentrifuged peptide was used to calculate the levels of sedimented peptide (47). For the fluorescamine assay a Molecular Devices f-max fluorescence microplate reader with a 355 nm excitation wavelength filter and a 460 nm emission filter was used. All experiments were performed in triplicate with 200 μ L samples in 96 well plates. Control experiments were performed in parallel without the addition of metal ions and/or centrifugation.

High-Performance Immobilized Metal Ion Affinity Chromatography. High-performance immobilized metal ion affinity chromatography (HP-IMAC) was performed by a modified literature method (48, 49). HiTrap chelating Sepharose cartridges were obtained from Pharmacia and mated to a Beckman HPLC system comprising a System Gold programmable solvent module 126, a diode array detector module 168, and a Rheodyne injector. Peptide was eluted with a pH gradient and two buffers; buffer A, 20 mM potassium phosphate containing 0.5 M NaCl, pH 7.3; buffer B, 20 mM potassium phosphate containing 0.5 M NaCl, pH 4.0. Peptides were freshly prepared in buffer A and concentrations were determined by quantitative fluorescamine assay (50). The column was equilibrated with buffer A and charged with a 0.1 M solution of either NiCl₂, ZnCl₂, or CuCl₂ in buffer A until saturated. The excess metal ions were removed by a wash with distilled water and the column was reequilibrated with buffer A. Peptide was eluted with a gradient of 100% buffer A (pH 7.3) to buffer B (pH 4.0) over 15 min at 1 mL/min. Between runs, the column was removed, regenerated by washing manually with distilled water, 50 mM EDTA, and distilled water, and then reequilibrated in buffer A.

RESULTS

Secondary Structure of hA β (1–28) and rA β (1–28) in the Absence of Metal Ions. In aqueous solution at pH 7.3 both hA β (1–28) and rA β (1–28) exhibit CD spectra consistent with random coil (Figure 2). Both peptides are random coil at pH values from pH 3 to 10 and remain random coil after 24 h (data not shown). In the hydrophobic solvent trifluoroethanol (TFE), which resembles a membrane environment (51), both peptides adopt significant α -helical structure (Figure 2). On the basis of the molar ellipticity at 222 nm, the helical content of hA β (1–28) and rA β (1–28) in TFE is 48% and 47%, respectively (52). In solutions of 10%, 20%, 30%, 40%, 60%, and 90% TFE in buffer at both pH 7.3 and 5.0, the helical contents of both hA β (1–28) and rA β (1–28) were identical within experimental error (results not shown). This indicates that the helical propensity is similar for both peptides. Helical denaturing experiments performed at pH 7.3 in 60% TFE for both hA β (1–28) and rA β (1–28)

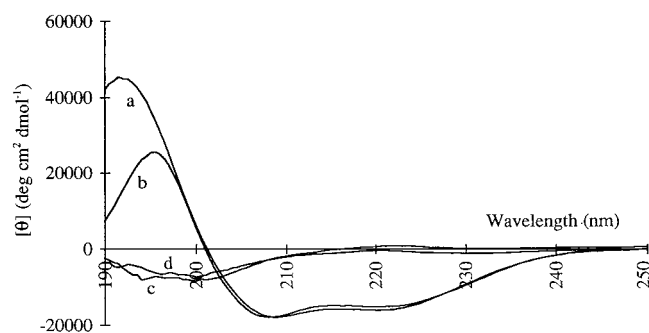


FIGURE 2: CD spectra of hA β (1–28) and rA β (1–28) in aqueous buffer at pH 7.3 and in TFE. Spectra labels correspond to (a) hA β (1–28) in TFE; (b) rA β (1–28) in TFE; (c) hA β (1–28) in 10 mM sodium phosphate buffer at pH 7.3; and (d) rA β (1–28) in 10 mM sodium phosphate buffer at pH 7.3.

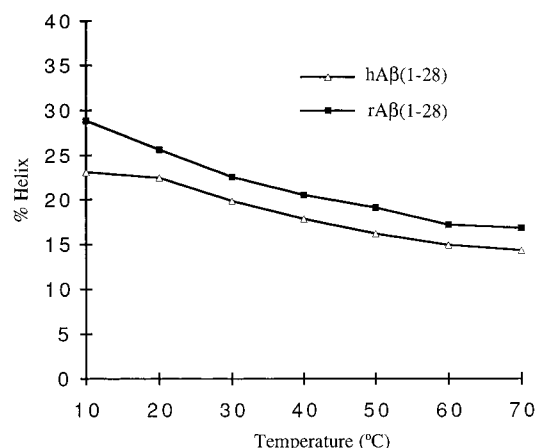


FIGURE 3: Temperature denaturing curves for hA β (1–28) and rA β (1–28) in 60% TFE in phosphate buffer at pH 7.3. Helical content for each peptide was determined from the molar ellipticity at 222 nm from CD spectra obtained at temperatures from 10 to 70 °C.

indicate that these peptides have indistinguishable helical stability (Figure 3). For the temperature range from 10 to 70 °C the slope of the temperature denaturing curve was identical within experimental error for both peptides. These results indicate that both hA β (1–28) and rA β (1–28) are random coil in aqueous solution and have similar helical content and stability in a hydrophobic environment such as TFE. No β -sheet structure or aggregation was observed for these peptides at CD concentrations in the absence of metal ions.

Metal-Induced Aggregation of hA β (1–28) and rA β (1–28). Incubation of hA β (1–28) or rA β (1–28) at concentrations of 10 and 100 μ M at pH 7.3 for 1 week showed less than 10% aggregation for both peptides at both concentrations. Aggregation was determined by centrifugation followed by fluorescamine assay determination of soluble versus total peptide. To determine the influence of different metal ions on peptide aggregation, hA β (1–28) and rA β (1–28) at concentrations of 100 μ M in pH 7.3 phosphate buffer were incubated separately with 500 μ M Zn $^{2+}$, Ni $^{2+}$, or Fe $^{3+}$ for 24 h. Controls containing no added metal ions were also incubated for the same period. All metals caused significant peptide aggregation, with a significant difference being observed between hA β (1–28) and rA β (1–28) in the presence of Zn $^{2+}$ (Figure 4). hA β (1–28) showed 80% aggregation in the presence of Zn $^{2+}$, while rA β (1–28) only exhibited 35% aggregation.

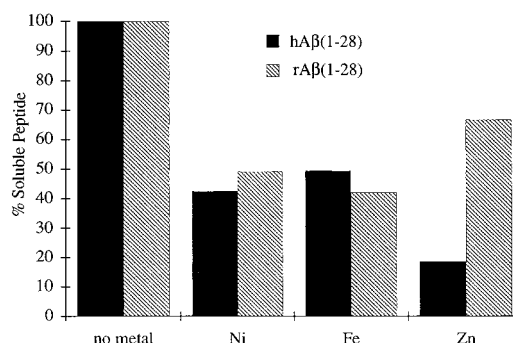


FIGURE 4: Metal-induced aggregation of hA β (1–28) and rA β (1–28). Peptides were prepared by diluting peptide stock solutions into 20 mM sodium phosphate buffer at pH 7.3, containing 150 mM NaCl. Peptide solutions (100 μ M) containing 500 μ M either Ni $^{2+}$, Fe $^{3+}$, or Zn $^{2+}$ were incubated for 1 h and then centrifuged at 13000g for 10 min. Peptide concentrations, relative to uncentrifuged control without metal, were determined by fluorescamine assay. All data points are means \pm SD, $n = 3$.

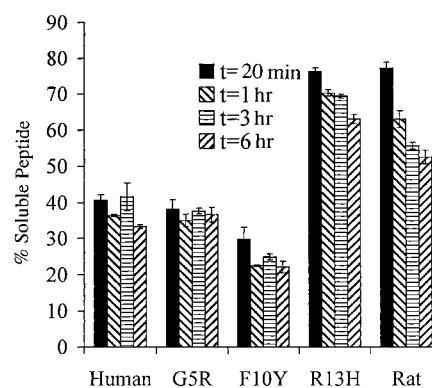


FIGURE 5: Zinc ion-induced time-dependent aggregation of hA β (1–28), rA β (1–28), 13 R-A β (1–28), 5 G-hA β (1–28), and 10 F-hA β (1–28). Peptides were prepared by diluting peptide stock solutions into 20 mM sodium phosphate buffer at pH 7.3, containing 150 mM NaCl. Peptide solutions (100 μ M) containing Zn $^{2+}$ (500 μ M) were incubated for between 20 min and 24 h and centrifuged at 13000g for 10 min. Peptide concentrations, relative to uncentrifuged controls without Zn $^{2+}$, were determined by fluorescamine assay. All data points are means \pm SD, $n = 3$.

Effect of Individual Substitutions on the Zinc Ion-Induced Aggregation of hA β (1–28). Because of the importance of Zn $^{2+}$ –A β interactions in AD and the clear difference observed for hA β (1–28) and rA β (1–28) with Zn $^{2+}$, we explored time-dependent Zn $^{2+}$ -induced aggregation of hA β (1–28), rA β (1–28), 5 G-hA β (1–28), 10 F-hA β (1–28), and 13 R-hA β (1–28). Each peptide was incubated at pH 7.3 for periods from 20 min to 6 h in the presence of Zn $^{2+}$. The hA β (1–28) peptide and the two peptides containing the individual substitutions R to G [5 G-hA β (1–28)] and Y to F [10 F-hA β (1–28)] showed 60–70% aggregation after 20 min with a slight increase in aggregation over 6 h (Figure 5). In contrast, both rA β (1–28) and the peptide containing the H to R substitution [13 R-hA β (1–28)] both showed approximately 23% aggregation after 20 min with an increase to 47% and 36% aggregation after 6 h, respectively. Both rA β (1–28) and 13 R-hA β (1–28) aggregated significantly less than the other peptides, indicating that the H to R substitution is responsible for the observed difference between hA β (1–28) and rA β (1–28) in Zn $^{2+}$ -induced aggregation. Histidine-13 is probably a coordination site for the binding of Zn $^{2+}$ by hA β (1–28).

Table 1: Elution pH of Each of the Peptides hA β (1–28), rA β (1–28), ¹³R-A β (1–28), ⁵G-hA β (1–28), and ¹⁰F-hA β (1–28) on Immobilized Iminodiacetate–Metal Chelating Chromatography^a

| | hA β (1–28) | rA β (1–28) | ¹³ R-A β (1–28) | ⁵ G-hA β (1–28) | ¹⁰ F-hA β (1–28) |
|----------------------|-------------------|-------------------|----------------------------------|----------------------------------|-----------------------------------|
| IDA–Fe ³⁺ | 7.3 | 7.3 | 7.3 | 7.3 | 7.3 |
| IDA–Zn ²⁺ | 4.0 | 7.3 | 7.3 | 4.0 | 4.0 |
| IDA–Ni ²⁺ | 4.0 | 5.0 | 5.3 | 4.0 | 4.0 |
| IDA–Cu ²⁺ | 4.0 | 4.0 | 4.0 | 4.0 | 4.0 |

^a Elution at pH 7.3 indicates no affinity, while at pH 4.0 both the peptide and metal are stripped off the column, indicating high affinity. Intermediate elution pHs indicate moderate affinity.

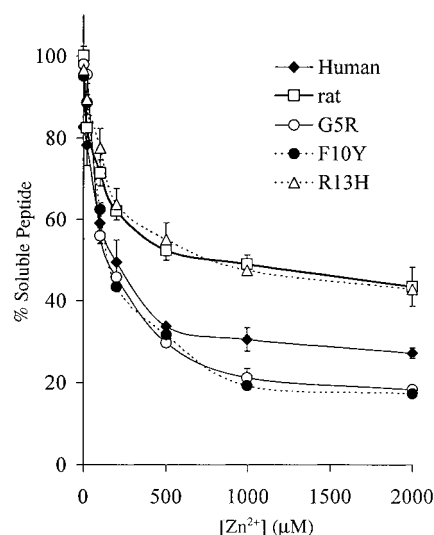


FIGURE 6: Zinc ion concentration dependence of the aggregation of hA β (1–28), rA β (1–28), ¹³R-A β (1–28), ⁵G-hA β (1–28), and ¹⁰F-hA β (1–28). Peptides were prepared by diluting peptide stock solutions into 20 mM sodium phosphate buffer at pH 7.3, containing 150 mM NaCl. Peptide (100 mM) containing Zn²⁺ (0–2 mM) were incubated for 24 h and centrifuged at 13000g for 10 min. Peptide concentrations, relative to an uncentrifuged control without Zn²⁺, were determined by fluorescamine assay. All data points are means \pm SD, $n = 3$.

To explore the importance of Zn²⁺ concentrations for metal-induced aggregation of A β , 100 μ M of each peptide was incubated at pH 7.3 with Zn²⁺ at concentrations of 25 μ M, 100 μ M, 200 μ M, 500 μ M, 1 mM, and 2 mM. All peptides aggregated in a Zn²⁺ concentration-dependent manner (Figure 6). A significant difference in the degree of aggregation for hA β (1–28) and rA β (1–28) can be seen at each concentration. In addition, ¹³R-hA β (1–28) has a similar profile to that of rA β (1–28), while ⁵G-hA β (1–28) and ¹⁰F-hA β (1–28) are similar to hA β (1–28). The results can be quantitated by calculating an EC₅₀ value for each peptide, which is defined as the concentration of Zn²⁺ needed for a 50% reduction of soluble peptide (53). The EC₅₀ values are 150 ± 50 μ M for hA β (1–28), ⁵G-hA β (1–28), and ¹⁰F-hA β (1–28) and 850 ± 100 μ M for rA β (1–28) and ¹³R-hA β (1–28). These results again clearly implicate histidine-13 as playing an important role in the Zn²⁺-induced aggregation of A β .

Affinity of hA β (1–28), rA β (1–28), ⁵G-hA β (1–28), ¹⁰F-hA β (1–28), and ¹³R-hA β (1–28) for Metal Chelates. Immobilized iminodiacetate–metal chelates (IDA–M²⁺) have been applied to the chromatography of both rat and human APP (54). In addition, both human A β (1–42) and A β (1–28) display affinity for immobilized metal chelates, including Cu²⁺, Ni²⁺, and Zn²⁺ (49). Using IDA–M²⁺ coupled with HPLC, we explored the affinity of each of the peptides

hA β (1–28), rA β (1–28), ⁵G-hA β (1–28), ¹⁰F-hA β (1–28), and ¹³R-hA β (1–28) for Fe³⁺, Cu²⁺, Ni²⁺, and Zn²⁺ metal chelates (Table 1). None of the peptides were retained on the immobilized metal chelate IDA–Fe³⁺. All peptides were strongly retained on IDA–Cu²⁺ and only eluted at pH 4.0 when the metal was stripped off the column. The peptides had intermediate affinity for IDA–Zn²⁺ and IDA–Ni²⁺, with a significant difference in affinity being observed among peptides with both metal chelates. The difference for IDA–Zn²⁺ was the most pronounced, with hA β (1–28), ⁵G-hA β (1–28), and ¹⁰F-hA β (1–28) showing strong affinity and eluting near pH 4.0 and rA β (1–28) and ¹³R-hA β (1–28) showing no affinity and eluting near pH 7.3. For IDA–Ni²⁺, ¹³R-hA β (1–28) eluted slightly before rA β (1–28) near pH 5.0, while hA β (1–28), ⁵G-hA β (1–28), and ¹⁰F-hA β (1–28) eluted later near pH 4.0. Because at pH 4.0 the metal is removed from the chelate, it is not possible to distinguish the affinity of binding for peptides that elute at this pH.

DISCUSSION

In this study both hA β (1–28) and rA β (1–28) showed no β -sheet structure in aqueous solution and did not aggregate significantly in the absence of metals. This is consistent with previous results where the C-terminal amino acids have been shown to be crucial for A β aggregation in aqueous solution. hA β (29–42) has been shown to adopt a β -sheet conformation in aqueous solution independently of pH (22–24). This C-terminal region contains only hydrophobic amino acids and would be expected to increase both β -sheet and aggregation propensity by increasing hydrophobicity. The side chains within this region would not be expected to be involved in metal coordination due to the absence of charged residues. Metal-induced aggregation of A β appears to be initiated by metal coordination with charged residues within the amino acid region 6–28 of A β (38). In this study we have shown that histidine-13 is involved in Zn²⁺-induced aggregation of A β and is probably involved directly in Zn²⁺ coordination. In agreement with some reports (28), but not others (55), we observed that the Zn²⁺-induced aggregation of human A β is more rapid and extensive than that of rat A β . This difference can be explained by the substitution of histidine-13 for arginine in the rat peptide.

Iodination of A β at tyrosine-10 has been reported to decrease the susceptibility of this peptide to Zn²⁺-induced aggregation (28). Because this residue is substituted with a phenylalanine in rat A β , it was suggested that tyrosine is critical in coordinating Zn²⁺ to the human peptides. However, we find that ¹⁰F-hA β (1–28) is as susceptible to Zn²⁺-induced aggregation as is hA β (1–28), and only ¹³R-A β (1–28) has a lower susceptibility similar to that of rA β (1–28). These results indicate that tyrosine is not directly involved in the coordination of Zn²⁺ with A β . The decreased susceptibility

previously observed for iodinated A β could be due to the large iodine atom either interfering sterically with the close β -sheet packing of A β or sterically inhibiting zinc binding to a nearby coordination site.

It has been reported that Cu $^{2+}$, Ni $^{2+}$, and Zn $^{2+}$ will each displace radiolabeled $^{65}\text{Zn}^{2+}$ from A β , while Fe $^{2+}$ will not (41). Using immobilized iminodiacetate-metal chelation chromatography, we have shown that hA β (1–28) is strongly retained by IDA–Cu $^{2+}$, IDA–Zn $^{2+}$, and IDA–Ni $^{2+}$, while rA β (1–28) is strongly retained by IDA–Cu $^{2+}$, weakly retained by IDA–Ni $^{2+}$, and not retained by IDA–Zn $^{2+}$. Neither hA β (1–28) nor rA β (1–28) was retained by IDA–Fe $^{3+}$. Results obtained for ^{13}R -A β (1–28) were similar to those for rA β (1–28), while those for ^5G -hA β (1–28) and ^{10}F -hA β (1–28) were similar to those for hA β (1–28) (Table 1). These results indicate that histidine-13 is involved in the A β coordination of both zinc and nickel ions and are consistent with these metals binding at the same binding site. The results for IDA–Cu $^{2+}$ may just show that A β binding to this metal is particularly strong and does not mean that the Cu $^{2+}$ binding site is different from that of Zn $^{2+}$. In addition, because two coordination sites are used for metal chelation to IDA, affinity for IDA–metal chelates is not completely analogous to metal binding in solution, which may explain why Fe $^{3+}$ -induced partial aggregation of both hA β (1–28) and rA β (1–28) (Figure 4) even though neither of these peptides was retained by IDA–Fe $^{3+}$.

Although a number of groups have shown that Zn $^{2+}$ will induce the aggregation of A β , there is some controversy as to the concentrations of Zn $^{2+}$ required to induce aggregation and the difference in response between rat and human A β (28, 30, 55). Although we observe a significant difference in Zn $^{2+}$ -induced aggregation between hA β (1–28) and rA β (1–28), both peptides will only aggregate at high concentrations of both metal and peptide. The high concentration of peptide needed is not surprising in light of the high aqueous solubility and low β -sheet propensities of the A β (1–28) relative to full-length A β . However, metal binding affinity should be similar for A β (1–28) and full-length A β if binding to the monomeric 6–28 sequence is the sole contributor to binding affinity. The EC $_{50}$ of $150 \pm 50 \mu\text{M}$ obtained for hA β (1–28) is consistent with the EC $_{50}$ of 120–140 μM obtained for the Zn $^{2+}$ -induced aggregation of endogenous A β (53) and the similar micromolar levels observed by other groups (30, 56). A possible explanation for the nanomolar binding levels reported by Bush et al. (28) for full-length A β is that a second binding mode dependent on secondary structure may exist. That is, Zn $^{2+}$ may also bind to the aggregated β -sheet structure, in a similar mode to the binding of Cu $^{2+}$ to the β -sheet regions of galactose oxidase and superoxide dismutase (57). This high-affinity binding site may not be present in the hA β (1–28), which forms β -structure less avidly than full-length A β . Further work is required to determine if such a structure-dependent high-affinity binding site exists for A β . In addition, because the EC $_{50}$ value obtained in this study is a measure of Zn $^{2+}$ required for aggregation rather than a direct measure of Zn $^{2+}$ binding affinity, the lower aggregation propensity of hA β (1–28) in the absence of Zn $^{2+}$ could significantly raise the EC $_{50}$ in the presence of Zn $^{2+}$ relative to full-length A β .

Although we have shown that histidine-13 is crucial to Zn $^{2+}$ -induced aggregation of A β , most probably due to the

histidine-13 side chain being a coordination site for Zn $^{2+}$, the full mechanism of A β binding to Zn $^{2+}$ remains unknown. A recent detailed study of a zinc metalloenzyme, carbonic anhydrase II (58), showed the zinc ion was liganded to the imidazole side chains of three histidine residues, with a carboxyl group from another spatially close residue coordinate with Zn $^{2+}$ as the fourth ligand, to complete a tetrahedral metal coordination polyhedron. It is expected that Zn $^{2+}$ would coordinate in a similar tetrahedral arrangement with one or more A β molecules. The importance of histidine-13 also implicates the adjacent histidine-14 in the coordination of Zn $^{2+}$. If each zinc ion coordinates with one A β peptide, then one could envisage coordination to the three histidine side chains at positions 6, 13, and 14, and a carboxyl group from a glutamic acid or aspartic acid residue. Such an arrangement could potentially stabilize β -sheet formation and thus aggregation. The recent solid-state NMR study by Benzinger et al. (59) predicts a parallel rather than an antiparallel β -sheet arrangement for A β amyloid. All the parallel β -sheet arrangements that were consistent with the NMR data placed histidine-13 and histidine-14 of each strand within coordinating distance of the equivalent histidine residues in an adjacent strand. In such a parallel arrangement it is possible that each zinc ion is coordinated to four histidine residues on two A β strands, stabilizing intermolecular β -sheet structure and providing a seed for amyloid formation. Further work is needed to fully define the binding site of Zn $^{2+}$ and other divalent metals.

The importance of histidine-13 for metal-induced aggregation of A β , which may be an important mechanism of amyloid formation in vivo, provides potentially useful information toward the mechanism-based design of aggregation inhibitors. A therapeutic strategy can be envisaged where inhibitors are designed to bind to the amino acid sequence near residue 13 and inhibit metal coordination to this residue.

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