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Folding events in the 21–30 region of amyloid β-protein (Aβ) studied in silico

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Contributed by H. Eugene Stanley, March 10, 2005

Oligomeric assemblies of the amyloid β-protein (Aβ) have been implicated in the pathogenesis of Alzheimer’s disease as a primary source of neurotoxicity. Recent in vitro studies have suggested that a 10-residue segment, Ala-21–Ala-30, forms a turn-like structure that nucleates the folding of the full-length Aβ. To gain a mechanistic insight, we simulated Aβ(21–30) folding by using a discrete molecular dynamics algorithm and a united-atom model incorporating implicit solvent and a variable electrostatic interaction strength (EIS). We found that Aβ(21–30) folds into a loop-like conformation driven by an effective hydrophobic attraction between Val-24 and the butyl portion of the Lys-28 side chain. At medium EIS (1.5 kcal/mol (1 cal = 4.18 J)), unfolded conformations almost disappear, in agreement with experimental observations. Under optimal conditions for folding, Glu-22 and Asp-23 form transient electrostatic interactions (EI) with Lys-28 that stabilize the loop conformations. Glu-22–Lys-28 is the most favored interaction. High EIS, as it occurs in the interior of proteins and aggregates, destabilizes the packing of Val-24 and Lys-28. Analysis of the unpacked structures reveals strong EI with predominance of the Asp-23–Lys-28 interaction, in agreement with studies of molecular modeling of full-length Aβ fibrils. The binary nature of the EI involving Lys-28 provides a mechanistic explanation for the linkage of amino acid substitutions at Glu-22 with Alzheimer’s disease and cerebral amyloid angiopathy. Substitutions may alter the frequency of Glu-22 or Asp-23 involvement in contact formation and affect the stability of the folding nucleus formed in the Aβ(21–30) region.

Alzheimer’s disease (AD) is a neurodegenerative disorder characterized pathologically by the extracellular deposition of amyloid fibrils and the intracellular formation of neurofibrillary tangles. Amyloid fibrils are composed of the amyloid β-protein (Aβ), which exists predominantly in vivo as a 40- or 42-residue protein produced by cleavage from the Aβ precursor. Amyloid fibrils were shown to be neurotoxic (1), but subsequent biophysical, biological, and clinical data indicated that smaller assemblies also were neurotoxic (2–4). More recent studies addressed the toxicity of soluble oligomeric Aβ assemblies (5–9). Taken together, these data suggest that small oligomers, not fibrils, may be the proximate toxin that causes neurodegeneration. An attractive strategy for drug development suggests itself: Prevent the formation of toxic oligomers. To do so, knowledge of the structure and dynamics of Aβ monomer under conditions that favor oligomerization is necessary.

Recent limited proteolysis experiments on Aβ(1–40) and Aβ(1–42) identified protease-resistant segments under conditions favoring oligomerization (10). A 10-residue segment, Ala-21–Ala-30, was highly resistant to proteolytic attack, indicating the presence of a folded structure. Lazo et al. (10) postulated that this structure nucleates the intramolecular folding of Aβ monomer. Notably, the homologous decapeptide Aβ(21–30) showed similar protease resistance when studied in monomeric solution, lending support to the hypothesis. Determination of the solution structure of Aβ(21–30) by NMR yielded two families of structures containing a turn-like motif centered at residues Gly-25–Ser-26. Putative stabilization factors are (i) intrinsic turn propensities of Gly-25, Ser-25, and Asn-27; (ii) hydrophobic interaction between Val-24 and the butyl portion of the Lys-28 side chain; and (iii) electrostatic interactions (EI) between Glu-22 and Lys-28 or between Asp-23 and Lys-28. These latter interactions defined the two families and led to the question: Which of the two families of structures is preferred? Lazo et al. also postulated that partial unfolding of the Ala-21–Ala-30 region may be necessary for the subsequent fibrillization of Aβ. How might this unfolding occur?

To address these questions, we used an in silico approach to visualize the folding/unfolding of Aβ(21–30). Computer simulations, particularly molecular dynamics (MD) simulations, can provide information that cannot be obtained by experimental methods, including conformational transitions that occur at every step along the folding/unfolding pathway. MD simulations also can contribute to a better understanding of the forces (e.g., electrostatic versus hydrophobic) controlling protein folding. Discrete MD (DMD) combined with a coarse-grain protein model has been used to study protein folding (11–13) and aggregation (14–17, 22). We present here results of studies of the conformational dynamics of Aβ(21–30) folding obtained by using DMD simulations in conjunction with a united-atom model and implicit solvent. The results agree with NMR-determined structures for monomeric Aβ(21–30) in aqueous solution, provide a theoretical basis for understanding the pathologic effects of mutations at position 22, and suggest that our model will be useful for in silico testing of mechanistic hypotheses about Aβ folding and its therapeutic control.

Methods

Protein Model. Our united-atom model, which is an extension of a recently used DMD model (18), represents all protein atoms except hydrogen. Of relevance to our study are the atomic interactions implemented, namely (i) backbone hydrogen bonds, (ii) effective interactions mimicking EI between charged atoms of the side chains, and (iii) implicit solvent effects mediated by hydrophobic interactions between side chain atoms.

MD. We performed DMD simulations and monitored the time evolution of Aβ(21–30) trajectories. We simulated the conformational changes of Aβ(21–30) for 10⁶ time units (=50 ns with the selected energy scale). This time span is much smaller than typical folding times of isolated hairpins in solution (19). However, we can effectively sample the conformational space of Aβ(21–30) because of our implicit treatment of solvent and hydrogen atoms, thus increasing the conformational freedom of the peptide and reducing the complexity of the energy landscape (20). We simulated Aβ(21–30) folding at six different EI

Abbreviations: Aβ, amyloid β-protein; AD, Alzheimer’s disease; MD, molecular dynamics; DMD, discrete MD; EI, electrostatic interaction(s); EIS, EI strength; SASA, solvent-accessible surface area.

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Table 1. 1-loop and 2-loop radii for amino acids of the distal hairpin of the c-Crk Src homology 3 (SH3) domain

<table>
<thead>
<tr>
<th>Aβ(21–30)</th>
<th>1-loop, r1</th>
<th>2-loop, r2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glu-22</td>
<td>6.1 ± 0.9</td>
<td>—</td>
</tr>
<tr>
<td>Asp-23</td>
<td>5.1 ± 1.0</td>
<td>8.6 ± 4.3</td>
</tr>
<tr>
<td>Val-24</td>
<td>4.7 ± 0.9</td>
<td>10.2 ± 8.7</td>
</tr>
<tr>
<td>Gly-25</td>
<td>6.0 ± 1.6</td>
<td>13.4 ± 14.4</td>
</tr>
<tr>
<td>Ser-26</td>
<td>6.3 ± 0.9</td>
<td>8.3 ± 2.5</td>
</tr>
<tr>
<td>Asn-27</td>
<td>5.1 ± 1.1</td>
<td>8.3 ± 4.4</td>
</tr>
<tr>
<td>Lys-28</td>
<td>5.2 ± 1.2</td>
<td>10.9 ± 5.2</td>
</tr>
<tr>
<td>Gly-29</td>
<td>5.6 ± 1.6</td>
<td>—</td>
</tr>
</tbody>
</table>

Data are shown as mean ± SD. Standard error of the average equals the SD divided by \sqrt{N_{idp}} = 7.9.

Table 2. 1-loop and 2-loop radii for amino acids of the distal hairpin of the Aβ(21–30)

<table>
<thead>
<tr>
<th>Aβ(21–30)</th>
<th>1-loop, r1 ± σ(r1)</th>
<th>2-loop, r1 ± (r2)</th>
</tr>
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<td>8.3 ± 4.4</td>
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<td>10.9 ± 5.2</td>
</tr>
<tr>
<td>Gly-29</td>
<td>5.6 ± 1.6</td>
<td>—</td>
</tr>
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</table>

1-Loop and 2-Loop Radii. We first simulated Aβ(21–30) dynamics without the hydrophobic and electrostatic components of the force field. Under these conditions, Aβ(21–30) adopts a bent conformation where the smallest and biggest average 1-loop radii, respectively, and both values are bigger than the typical 1-loop radii of a β-turn (see Methods and Table 2). The peptide tends to bend in the immediate vicinity of Val-24 and tends to adopt more locally extended conformation around Ser-26. Gly-25 and Gly-29 have the biggest standard deviations of 1-loop radii, reflecting the wider range of allowed Φ and Ψ values for Gly. Regarding the average 2-loop radii, Ser-26 and Asn-27 display the two smallest values. The emerging picture for the preferred peptide conformation under no hydrophathy and electrostatics interactions is a broad loop with the center at Ser-26 and Asn-27. The loop is broad because of the large 1-loop radius for Ser-26.

SASA. Under conditions of no hydrophathy and irrespective of the EIS, the SASA distribution shows a single peak corresponding to the sum of the separate SASA values for solvent-exposed Val-24 and Lys-28 (≈350 Å) (Fig. 1a, peak A). “Switching on” hydrophatic interactions results in an additional peak with a smaller SASA (≈245 Å, a 30% decrease) (Fig. 1b, peak B). We denote the set of conformations with SASA values within peak B as conformations of class B. For these conformations, Aβ(21–30) adopts a loop conformation centered at Ser-26 and the Val-24 propyl side chain packs against the butyl portion of the Lys-28 side chain because of an effective hydrophobic attraction. EIS modulate the population of the peaks but does not shift the average SASA values (Table 3). Thus, EIS affect the probability that the loop will form but do not alter the way in which Val-24 and Lys-28 pack against each other once the loop has formed. The Val-24–Lys-28 packing probability increases when we in-
Lys-28 show the largest distance reduction upon loop formation, emphasizing the role of electrostatic and hydrophobic interactions in the stabilization of the loop.

We estimate the loop flexibility with the standard deviation $\sigma$ of the $C^\alpha-C^\gamma$ distance (Fig. 2a). The error of a $\sigma$ value is the $\sigma$ value itself divided by $\sqrt{N_{idp}}$, ~13% of the value. Contacts Ala-21–Ser-26 and Ser-26–Ala-30 have high $\sigma$ values, indicating that the two sides of the loop [Aβ(21–26) and Aβ(26–30), respectively] are more flexible than analogous sides of a putative β-hairpin conformation. Interside $C^\alpha-C^\alpha$ distances for termini contacts Glu-22–Ala-30 (12.6 Å) and Asp-23–Gly-29 (11.1 Å) indicate rare contact formation. $C^\alpha-C^\alpha$ distances for Val-24–Lys-28 (6.4 Å) and Gly-25–Asn-27 (6.7 Å) are small enough to be associated with loops but large enough to prevent the formation of any stable hydrogen bond in the backbone. In summary, the loop has no stable hydrogen bonds in the backbone, is stable in the region Val-24–Lys-28, and fluctuates at the termini.

**α Angle.** Regardlesse of the EIS, class B conformations present a bimodal distribution of $\alpha$ values, with broad peaks at negative and positive $\alpha$ values. (Fig. 2b). We denote the set of conformations within class B with $-90^\circ < \alpha < -20^\circ$ as conformations of class $B^-$. These loop conformations feature Lys-28 pointing below the loop plane. Analogously, we construct class $B^+$ with class $B$ conformations with $20^\circ < \alpha < 90^\circ$. The population of class $B^-(B^+)$ decreases (increases) with increasing EIS (Fig. 2b and Table 3). We observe that the Glu-22–Lys-28 contact is three to five times more likely to form (the particular value depending on the applied EIS) if Lys-28 is pointing above the plane (see Table 4). In contrast, the Asp-23–Lys-28 interaction shows no preference with Lys-28 orientation. Thus, Glu-22 controls the population of the peaks in the $\alpha$ angle distribution. At optimal EI for loop stability (~1.5 kcal/mol), we observe that Glu-22 has a higher propensity to interact with Lys-28 than does Asp-23.

**Discussion**

Recent NMR studies of Aβ(25–35) (24) show a type I β-turn centered at amino acids Ser-26 and Asn-27. Molecular modeling of fibrils formed by Aβ(1–40) (25), Aβ(12–42) (26), and Aβ(16–35) (27) predicts a turn or bend in the region Gly-25–Lys-28. In fact, this region has an intrinsic propensity to form a type I or type VII turn (28). Consistent with these results, we observe that Ser-26 and Asn-27 have a higher propensity to be at the center of a loop than any other of the amino acids in our Aβ(21–30) model when simulated in the absence of hydrophobic interactions and E1.

Addition of hydrophobic interactions induces a semistable loop conformation in Aβ(21–30), with the center at Ser-26. Hydrophobic interactions are critical for the stabilization of isolated β-hairpins (29). Espinosa et al. (30) pointed out the correlation between hairpin stability and the distance of the hydrophobic amino acids to the turn, with smaller distances leading to greater stability. We observe that Val-24 and Lys-28, two amino acids in the proximity of Ser-26, pack against each other because of the hydrophobic effect. The SASA reduction associated with Val-24–Lys-28 packing is relatively small compared with the typical SASA reduction in hairpins stabilized by the hydrophobic interaction (29), which may explain the inability of Aβ(21–30) to stabilize in a hairpin conformation during the course of our simulations.

The observed absence of backbone hydrogen bonds agrees with $^1$H NMR and the hydrogen exchange experiments of Lazo et al. (10). We argue from our results that Aβ(21–30) adopts a semirigid loop in the Val-24–Lys-28 region, whereas the termini

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**Table 3. Percent probability of observing class B conformations**

<table>
<thead>
<tr>
<th>EI, kcal/mol</th>
<th>$B^-$</th>
<th>$B^+$</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.00</td>
<td>74</td>
<td>40</td>
</tr>
<tr>
<td>1.50</td>
<td>97</td>
<td>38</td>
</tr>
<tr>
<td>2.50</td>
<td>80</td>
<td>20</td>
</tr>
</tbody>
</table>

Shown are the percent probabilities of a class B conformation (loop), class $B^-$ (Lys-28 pointing below the loop plane), and class $B^+$ (Lys-28 pointing above).
are highly flexible. Similar conclusions were made by Hou et al. (31) based on NMR experiments of Aβ(1–40) and Aβ(1–42). The finding that Lys-28 flips its orientation during the simulation is a direct consequence of the flexibility of the termini. In a hairpin configuration, a flip in the orientation of Lys-28 would require breaking three backbone hydrogen bonds, an energetically unfavorable process.

Under optimal conditions for loop stability (EI ≈ 1.5 kcal/mol), Lys-28 shows no preference to point above or below the loop plane. Lys-28 preferentially points above the loop plane at a high EIS because the bias of the Glu-22–Lys-28 interaction with Lys-28 orientation becomes prominent under these conditions. The bias is in agreement with structure calculations by Lazo et al. (10), who observed a Coulombic interaction between Glu-22 and Lys-28 for the model structure in which Lys-28 is pointing above the loop plane. In the structural model of Aβ(1–40) fibrils proposed by Petkova et al. (25), Lys-28 points above the loop plane and forms a salt bridge with Asp-23. Our results suggest that Glu-22 would inhibit formation of this salt bridge because Lys-28 preferentially interacts with Glu-22 when pointing above the plane.

EI affect loop stability differently than do hydropathic interactions. Whereas hydropathic effects are “bulky” in nature (for instance, the whole side chain of Val-24 interacting with the butyl portion of Lys-28), EI are selective because they involve only two charged atoms. Thus, we expected that EI might modulate, but not determine, the conformational dynamics of Aβ(21–30). EI stabilize the loop conformations in the range of EIS typical of interacting charged residues at the surface of proteins (32, 33) (0.0–1.5 kcal/mol). Thus, we argue that EI and hydropathic interactions cooperate to maximize the stability of loop conformations when Aβ(21–30) is solvent-exposed. Glu-22 is more likely to interact with Lys-28 than is Asp-23 (Table 4) and, thus, may be more prominent in stabilizing the Aβ(21–30) monomer fold.

In contrast, EI destabilize the loop conformations in the range of the EIS of interacting charged residues in the interior of proteins and aggregates (EI > 1.5 kcal/mol) (34). Asp-23 is more likely to interact with Lys-28 than is Glu-22, inhibiting the ability of Lys-28 to pack against Val-24 (Fig. 3a). Thus, we hypothesize that before fibril formation, the region Aβ(21–30) partially unfolds, disrupting the Val-24–Lys-28 contact. The observed prevalence of the Asp-23–Lys-28 interaction is in agreement with molecular models of fibrils formed by full-length Aβ(25) and Aβ(16–35) (27), which show stabilization through Asp-23–Lys-28 interactions and no Glu-22–Lys-28 interaction or Val-24–Lys-28 packing. In recent kinetics experiments, Sciarretta et al. (35) observed an increase of three orders of magnitude of fibrillogenesis upon stabilization of the Asp-23–Lys-28 interaction by means of an engineered lactam bridge. This observation led the authors to suggest that stabilization of the salt bridge Asp-23–Lys-28 in the core of the fibril may be the rate-limiting step in the process of fibril formation. A hypothesis that may explain this observation is a desolvation barrier upon burial of Asp-23 inside the core of the protofibril. This hypothesis rationalizes the observed increase in the rate of fibril formation (36) associated to the familial AD mutation Asp-23-Asn (Iowa mutation). The desolvation barrier for Asn may be lower than that for Asp, and Asn-23 still can form a stable hydrogen bond with Lys-28 in the core of the fibril.

Increases in the rate of fibril growth also are observed in peptides with amino acid substitutions linked to other familial AD mutations, including Glu-22-Gly (Arctic), Glu-22-Gln (Dutch), and Glu-22-Lys (Italian). However, the desolvation hypothesis barrier does not hold when applied to Glu-22, because Glu-22 is solvated in the model fibril (25). Our results suggest a different mechanism for the “protective” role of Glu-22. If fibril formation requires a rearrangement of the Aβ(21–30) region involving denaturation of the Val-24–Lys-28

Table 4. Percent probability of forming Glu-22–Lys-28 and Asp-23–Lys-28 contacts for conformations of class B, B−, and B+

<table>
<thead>
<tr>
<th>EI, kcal/mol</th>
<th>Glu-22–Lys-28</th>
<th>Asp-23–Lys-28</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>B</td>
<td>B−</td>
</tr>
<tr>
<td>0.0</td>
<td>7</td>
<td>1</td>
</tr>
<tr>
<td>1.5</td>
<td>28</td>
<td>6</td>
</tr>
<tr>
<td>2.5</td>
<td>48</td>
<td>5</td>
</tr>
</tbody>
</table>
fold, perturbations in loop stability could enhance or block fibril formation. A substitution of Glu-22 by a nonnegatively charged amino acid could enhance the model fibril formation through two different mechanisms: (i) decrease of loop stability and subsequent increase in the population of aggregation-prone unpacked conformations and (ii) increase in the rate of Asp-23–Lys-28 contact formation because Glu-22 no longer competes with Asp-23 for a stable interaction with Lys-28.

Summary

We employed discrete MD and a united-atom model to visualize the conformational dynamics of Aβ(21–30), a region of Aβ hypothesized to be the nucleation center of Aβ monomer folding. Simulations at equilibrium conditions reveal a stable loop structure in the central region (Val-24–Lys-28), which is stabilized by hydrophobic interactions, and a high degree of flexibility in other areas. Correlation of perturbations of loop stability with changes in the electrostatic component of the force field provide an energy-based interpretation for the effects of familial AD mutations causing amino acid substitution at Glu-22. Our simulations are consistent with experimental studies of Aβ(21–30) and provide mechanistic insight into how conformational changes in the structure of the Aβ monomer may affect peptide self-assembly and aggregation.

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