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Distinguishing Closely Related Amyloid Precursors Using an RNA Aptamer

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From the Astbury Centre for Structural Molecular Biology and School of Molecular and Cellular Biology, University of Leeds, Leeds LS2 9JT, United Kingdom

Background: Altering the co-polymerization of proteins into amyloid fibrils provides an opportunity for manipulating fibril assembly.

Results: NMR and kinetic analysis showed that an RNA aptamer distinguishes between two highly similar co-aggregating proteins.

Conclusion: RNA aptamers are specific and discriminatory probes able to modulate amyloid formation.

Significance: Aptamers can be used as tools to differentiate amyloid precursors that are closely related and alter assembly.

Although amyloid fibrils assembled in vitro commonly involve a single protein, fibrils formed in vivo can contain multiple protein sequences. The amyloidogenic protein human β2-microglobulin (hβ2m) can co-polymerize with its N-terminally truncated variant (ΔN6) in vitro to form hetero-polymERIC fibrils that differ from their homo-polymERIC counterparts. Discrimination between the different assembly precursors, for example by binding of a biomolecule to one species in a mixture of conformers, offers an opportunity to alter the course of co-assembly and the properties of the fibrils formed. Here, using hβ2m and its amyloidogenic counterpart, ΔN6, we describe selection of a 2’F-modified RNA aptamer able to distinguish between these very similar proteins. SELEX with a N30 RNA pool yielded an aptamer (B6) that binds hβ2m with an EC50 of ~200 nM. NMR spectroscopy was used to assign the 1H-15N HSQC spectrum of the B6-hβ2m complex, revealing that the aptamer binds to the face of hβ2m containing the A, B, E, and D β-strands. In contrast, binding of B6 to ΔN6 is weak and less specific. Kinetic analysis of the effect of B6 on co-polymerization of hβ2m and ΔN6 revealed that the aptamer alters the kinetics of co-polymerization of the two proteins. The results reveal the potential of RNA aptamers as tools for elucidating the mechanisms of co-assembly in amyloid formation and as reagents able to discriminate between very similar protein conformers with different amyloid propensity.

Despite the array of different proteins and peptides with distinct amino acid sequences that are known to be able to assemble into amyloid fibrils in vitro and/or in vivo, the precise mechanism(s) by which these different proteins/peptides self-assemble into amyloid fibrils and how the assembly process results in disease remain unclear. Amyloid formation commences with the generation of aggregation-prone monomeric precursors. These species can be unfolded/disordered, partially structured or even native-like (3) and their structural properties, even though potentially similar to their non-amyloidogenic counterparts, dictate the fate of amyloid assembly (4). This is exemplified by the observation that the same amino acid sequence can form conformationally distinct amyloid structures in vitro by varying the temperature, altering the agitation conditions, adding co-solvents, metal ions or other molecules, or even changing the surface properties of the incubation vessel (reviewed in Ref. 5). An extra level of complexity is added by the ability of different protein/peptide precursors to co-polymerize, resulting in new fibril polymorphs with different amyloid architectures, stabilities, and/or different kinetics of assembly than those formed by each protein alone (4, 6, 7). Indeed, there are multiple examples of amyloidogenic proteins that are able to co-polymerize such as islet amyloid polypeptide and Aβ (6, 8), Tau and α-synuclein (9), and insulin and transthyretin (10). Although the importance of identifying and characterizing rarely populated amyloidogenic precursors is widely appreciated, this remains a significant challenge because of the transient nature and heterogeneity of assembly intermediates (11). The development of reagents able to discriminate aggregation-prone species among a pool of structurally similar molecules is crucial to deciphering the mechanisms of protein assembly into amyloid and to inform the design of therapeutic/diagnostic strategies able to target individual amyloid precursors (12).

Human β2-microglobulin (hβ2m) is a small protein that forms amyloid deposits in collagen-rich osteoarticular sites, which were targeted by the aptamer B6 in this study. The structural and functional properties of this protein, and its clinical relevance, were discussed in the context of the findings presented in this paper.

The abbreviations used are: hβ2m, human β2-microglobulin; TEM, transmission electron microscopy; rmsd, root-mean-square deviation; SELEX, systematic evolution of ligands by exponential enrichment; DR, dialysis-related amyloidosis.
resulting in the disorder-dissociated amyloidosis (DRA) (13, 14). Despite the propensity of hβ₂m to form amyloid fibrils in vitro, conditions that destabilize the native structure of hβ₂m such as low pH (15), the presence of SDS (16), or other co-solvents or metal ions (17, 18), are required for fibril formation on an experimentally tractable time scale in vitro. Removal of the N-terminal six residues from hβ₂m (the sequence IQRTPK), creating the variant ΔN6, disrupts the thermodynamic and kinetic stability of hβ₂m and, as a result, ΔN6 can self-assemble into amyloid fibrils rapidly and spontaneously without the need to add detergents, metal ions, or other reagents (19, 20). ΔN6 retains a native-like structure, displaying a backbone r.m.s.d. of only ~1.5 Å compared with hβ₂m (19), and contains a non-native trans X-Pro-32 (see Fig. 1, A and B), which has been shown to be vital for fibril formation (21, 22). Isomerization of the X-Pro-32 bond results in structural reorganization of the side chains in the apical region of hβ₂m, resulting in a protein with different surface hydrophobicity and electrostatic properties (19). ΔN6 can also promote the aggregation of hβ₂m even when added in trace amounts (19), resulting in co-polymerization of both proteins into hetero-polymeric amyloid fibrils (4). This interaction allows amyloid formation of hβ₂m to be investigated in the absence of additives at physiologically relevant pH values (4).

The design of molecules able to bind hβ₂m or its amyloidogenic counterpart, ΔN6, would offer an opportunity to increase understanding of the interaction between these co-assembling monomers and explore the aggregation pathway that leads to their co-polymerization into amyloid fibrils. However, such a task is hindered by the high sequence and structural homology (see Fig. 1A) of the two proteins and their dynamic nature (19). In this study, we used in vitro selection to identify an RNA aptamer able to bind hβ₂m preferentially to ΔN6 and to alter fibril co-assembly. Nucleic acid aptamer selection has been previously used to generate RNA aptamers able to discriminate fibrillar hβ₂m (~1 mg) was biotinylated (EZLink™ Sulfo-NHS-LC-biotin, Pierce Biotechnologies) at pH 7 using a 20-fold molar excess of biotin over the total protein concentration, according to the manufacturer’s instructions. The biotinylated monomer was then immobilized on 1-μm streptavidin-coated microspheres (Dynabeads™, Invitrogen) using the manufacturer’s instructions.

**In Vitro Selection**—A Biomek 2000 laboratory automation workstation (Beckman Coulter) was used to perform 12 rounds of in vitro selections with an N30 library of 2'F-modified pyrimidine RNA, encompassing ~10¹⁵ potential sequences, and transcribed using the Y639F/H784A variant of T7 RNA polymerase (32), using minor modifications of the protocols described previously (30). Selections were carried out in 50 mM MES buffer containing 120 mM NaCl, pH 6.2. Negative selections were carried out at each round of SELEX using streptavidin Dynabeads coated with Tris-inactivated linker. Stringency was increased after round 5 by decreasing the number of beads containing monomeric hβ₂m by half and increasing the number of washes from 10 to 13. The reverse transcriptase-PCR products were analyzed by native PAGE after each group of five rounds of selection to confirm the isolation of products for the next round of selection. Individual aptamer clones were produced by in vitro transcription using 10 mM final concentrations of each nucleotide triphosphate using 2'F-CTP and 2'F-UTP for production of modified RNAs. RNA concentrations were determined using the following extinction coefficients: B6, 1026.3 mM⁻¹ cm⁻¹; B6 minimized (B6min), 553.2 mM⁻¹ cm⁻¹; B9, 1054.2 mM⁻¹ cm⁻¹.

**Synthesis of Minimized B6**—B6min (5'-GGG AUA UCU GAC CUA CUC CCU UUU GGG GCC UAU GAU UCC CG-3') was synthesized with and without 2'F-modified pyrimidine nucleotides (named 2'F B6min and 2'OH B6min, respectively) on an ABI 394 RNA synthesizer at a 1 μM scale using the protocols described previously (33). The phosphoramide used for synthesis of 2'F-B6min were as follows: N-benzoyl-protected adenosine, N-dimethylformamidinyl-protected guanosine, N-acetyl-protected-2'-fluoro deoxyctydine, and 2'-fluoro-deoxyuridine. For synthesis of 2'OH B6min N-acetyl-protected-2'-fluoro deoxyctydine and 2'-fluoro-deoxyuridine were replaced with N-acetyl-protected-cytidine and uridine phosphoramidites (Link Technologies, Ltd.). Cyanosyl-(N,N'-disopropyl) and t-butyldimethylsilyl groups were present on the 3'- and 2'-hydroxy groups. Treatment with ammonia-saturated methanol at room temperature for 24 h was used to remove protecting groups and to cleave RNA from controlled pore glass resin. Methanol was removed under vacuum and the RNA pellet re-suspended in anhydrous dimethyl

**EXPERIMENTAL PROCEDURES**

**Protein Preparation**—hβ₂m and ΔN6 were expressed and purified as described previously (19). For NMR experiments, ¹H- and ¹³C-labeled hβ₂m and ΔN6 were prepared as described in Ref. 31.

**Biotinylation and Immobilization of hβ₂m**—Monomeric hβ₂m (~1 mg) was biotinylated (EZLink™ Sulfo-NHS-LC-biotin, Pierce Biotechnologies) at pH 7 using a 20-fold molar excess of biotin over the total protein concentration, according to the manufacturer’s instructions. The biotinylated monomer was then immobilized on 1-μm streptavidin-coated microspheres (Dynabeads™, Invitrogen) using the manufacturer’s instructions.
were regenerated using a 20% (v/v) denaturing polyacrylamide urea gel stained with ethidium bromide. The RNA was synthesized using N-dimethylformamidinyl-protected guanosine controlled pore glass to avoid incorporation of a pyrimidine with a ribose sugar at the 3′-end. This additional guanosine has no effect on the secondary structure of 2′F-B6min or 2′-OH B6min as predicted by Mfold (35).

Surface Plasmon Resonance—A BIACore3000 instrument was used with a streptavidin-coated gold sensorchip (BIACore SA chip). A flow-rate of 10 μl min⁻¹ was used with a running buffer of 50 mM MES, 120 mM NaCl, pH 6.2, 50 μl of 50 μg ml⁻¹ of biotinylated monomer was injected over separate flow cells so that ~200 response units of protein was immobilized. RNAs were dialyzed into running buffer before injection across the surface to minimize bulk refractive index effects. Flow cells were regenerated using a 20-μl wash of 5 M NaCl. All sensorgrams were corrected by subtracting the signals of an equivalent injection across an underivatized flow cell. Data were analyzed using the manufacturer’s software (BIASevaluation).

Intrinsic Fluorescence Quenching—The fluorescence of tryptophan residues in 1 μM hβ₃m or ΔN6 was excited at 290 nm, and fluorescence emission was measured between 300 and 390 nm in the presence of increasing concentrations of 2′F B6min or 2′ OH B6min in 50 mM MES buffer containing 120 mM NaCl, pH 6.2, at 25 °C. Due to the large extinction coefficient of the RNA aptamer at 260 nm (553.2 m⁻¹ cm⁻¹), the absorbance of the hβ₃m/aptamer solution at 290 nm was measured after each addition of aptamer to ensure that the absorbance of the solution was below 0.05 at 290 nm so that inner filter effects do not contribute to the data (36). Fluorescence emission was measured using a Photon Technology International QM-1 spectrofluorimeter using 10-nm slit-widths. The data for binding of 2′F B6min to hβ₃m were normalized to a value of 0 in the absence of aptamer and a fluorescence signal of 1 obtained upon saturation. The data were then fitted to the following logistic equation to extract the half maximal effective concentration (EC₅₀) using in-house scripts,

\[ f(x) = \frac{\text{max} - \text{min}}{1 + (x/\text{EC}_{50})^{-\text{nm}}} \]  

(Eq. 1)

where max and min represent the maximum and minimum fluorescence signals, respectively, Hill is the Hill coefficient, f(x) is the fluorescence units, and x is the concentration of the aptamer in mM. For 2′F B6min to ΔN6 and 2′OH B6min to hβ₃m, no change in fluorescence was observed over the concentration range studied.

NMR Spectroscopy—Samples of ¹³C,¹⁵N-labeled protein (60 μM) in 50 mM MES buffer containing 120 mM NaCl, pH 6.2, 0.02% (w/v) sodium azide, 0.1 mM EDTA, 90% (v/v) H₂O/10% (v/v) D₂O were used for NMR experiments. Synthetic 2′F B6min or 2′OH B6min was added into the protein solution from a concentrated stock (typically 200 μM). Working at a concentration of 60 μM necessitated the use of a sensitivity optimized strategy for obtaining assignments. This was achieved using a reduced dimensionality approach based on Hadamard encoding (37). Sequential assignments were obtained from analysis of Hadamard encoded two-dimensional H(N-H)CA and H(N-H₂)(CO)CA experiments where a two-step Hadamard matrix is introduced on ¹⁵N to subdivide the peaks into two subspectra where most signals can be addressed from their ¹H shift alone and the dimensionality can be reduced to 2 to maximize sensitivity. Spectra were recorded at 25 °C on a Varian Inova 750 MHz spectrometer equipped with a cryogenic probe and were processed using NMRPipe and analyzed using Collaborative Computational Project for NMR analysis (38). To calculate the intensity profiles shown in Fig. 7, peak intensities were normalized to the number of scans and the protein concentration used for each experiment. Intensity profiles were calculated as the ratio of the normalized peak intensity of each resonance in the apo spectrum (Iₐ) versus the normalized intensity at the same position but in the aptamer-bound spectrum (Iₐ). Therefore, the loss of native signal plotted in Fig. 7 does not require full assignment of the aptamer-bound spectrum.

Assembly of Amyloid Fibrils—40 μM hβ₃m and 40 μM ΔN6 in the presence or absence of two molar equivalents of 2′F B6min were co-incubated in 50 mM MES buffer containing 120 mM NaCl, pH 6.2, 0.02% (w/v) sodium azide at 600 rpm, 37 °C in a Thriller Thermoshaker incubator (Peplab). Each sample (100 μl) was incubated in 0.5-ml plastic Eppendorf tubes. Aliquots of 8 μl were removed at different time points during incubation and immediately centrifuged at 14,000 x g for 20 min. The supernatant was separated from the pellet, and both supernatant and pellet were frozen at −20 °C for subsequent analysis by SDS-PAGE.

SDS-PAGE—The effect of 2′F B6min on fibril formation was monitored using 15% polyacrylamide Tris-Tricine gels. Samples of the supernatant and pellet were thawed, and the pellet was resuspended in 8 μl of 50 mM MES buffer containing 120 mM NaCl, pH 6.2. Both the supernatant and resuspended pellet were added 1:1 to loading buffer (50 mM Tris-Cl, pH 6.8, 100 mM DTT, 2% (w/v) SDS, 0.1% (w/v) bromphenol blue, and 10% (v/v) glycerol) and boiled for 5 min before loading 15 μl into the gel. Gels were stained with Coomassie Instant Blue (Expedeon) and imaged by SnapGene software (Syngene).

Electron Microscopy—At the end of fibril assembly, 10 μl of sample were applied to a carbon-coated grid. The grid was then carefully dried with filter paper before it was negatively stained by the addition of 10 μl of 4% (w/v) uranyl acetate as described in Ref. 39. Micrographs were recorded on a Philips CM10 or a JEOL JEM-1400 electron microscope.

RESULTS

Selection of hβ₃m-specific 2′F-RNA Aptamers—Co-incubation of ΔN6 and hβ₃m results in the two proteins polymerizing into hetero-polymeric amyloid-like fibrils that are morphologically and thermodynamically distinct compared with fibrils formed by ΔN6 or hβ₃m alone (4). To control the co-assembly of these proteins, we attempted to select RNA aptamers capable
of discriminating between natively folded h\(\beta_2\)m and \(\Delta N6\) at pH 6.2 (Fig. 1A). H\(\beta_2\)m was biotinylated (predominantly at the N terminus and on Lys-7 and/or Lys-92) and immobilized as a target on streptavidin-coated magnetic beads, as described previously (30). The initial SELEX protocol used an N30 2\(\prime\)F-pyrimidine substituted RNA library to create aptamers resistant previously (30). The initial SELEX protocol used an N30 2\(\prime\)F-pyrimidine substituted RNA library to create aptamers resistant to nucleases (25, 32) and included counter-selection against the terminal loop, however, which is composed of six purine nucleotides. It appears that the loop is the motif that provides much of the binding energy for the interaction of B6 with h\(\beta_2\)m around one of the bulges (Fig. 3C). B6 differs radically at the terminal loop, however, which is composed of six purine nucleotides. It appears that the loop is the motif that provides much of the binding energy for the interaction of B6 with h\(\beta_2\)m.

Isolation of 2\(\prime\)F B6 and Characterization of the Binding Affinity to h\(\beta_2\)m—Two aptamers, B6 and B9, contained the most frequently occurring sequence motifs within the sequenced clones and showed some motif similarities (Fig. 2, A and B). To identify which aptamer to utilize for further studies, an initial binding assay was employed using surface plasmon resonance. Biotinylated h\(\beta_2\)m, \(\Delta N6\), or the non-amyloidogenic murine \(\beta_2\)m (45) were immobilized on separate flow cells and aptamer binding monitored at pH 6.2. 2\(\prime\)F B6 binds to h\(\beta_2\)m with an apparent affinity of \(\sim 500\) nM (red trace in Fig. 2C), but did not bind \(\Delta N6\) (dark green trace) or murine \(\beta_2\)m (light green trace). In contrast, binding of 2\(\prime\)F B9 was so weak that the \(K_d\) could not be determined (data not shown). The secondary structure of B6, computed via Mfold to be a stable stem loop (\(\Delta G^\circ \sim -16\) kcal/mol) (Fig. 3A) (35), was confirmed using enzymatic solution structure probing (Fig. 3B). This analysis suggests that the selected region consists of an extended base-paired stem loop interrupted by several single-stranded bulges with a terminal loop consisting of a poly-U tetraloop (highlighted in red in Figs. 2B and 3A). Note that both Mfold and enzymatic probing were of transcripts containing natural pyrimidines. B9 is predicted to have several equivalently stable structures that are all identical in the selected region, which forms a structure very similar to that of B6 around one of the bulges (Fig. 3C). B9 differs radically at the terminal loop, however, which is composed of six purine nucleotides. It appears that the loop is the motif that provides much of the binding energy for the interaction of B6 with h\(\beta_2\)m.
Trp-95 reporting on alterations within the hydrophobic core (46), whereas Trp-60 is sensitive to ligand binding (at least in proximity to this residue) at the protein surface. The fluorescence emission spectrum of monomeric hβ2m (1 μM) was monitored upon titration with 2′F B6min. The results showed a decrease in tryptophan emission intensity (with little change in $\lambda_{\text{max}}$), consistent with binding of 2′F B6min to the protein surface adjacent to Trp-60. Fitting the normalized intensity of Trp fluorescence versus the concentration of 2′F B6min added (Fig. 4A) (see “Experimental Procedures”) yielded a Hill slope of 0.99 ± 0.06, suggesting a specific one-site binding event, with an $EC_{50}$ of 223 ± 10 nM. Similar assays using 2′OH B6min showed no binding to hβ2m (Fig. 4B), indicating that the 2′F modifications to the pyrimidines are required for tight binding, consistent with the contribution of the polyU tetraloop to affinity. The fluorescence assay also showed no binding of 2′F B6min to ΔN6 monomers (Fig. 4C), consistent with the surface plasmon resonance data with full-length aptamers. These results indicate, therefore, that 2′F B6min is capable of discriminating between hβ2m and ΔN6. 2′-Fluoro-ribose is known to prefer different sugar pucker conformations compared with unmodified residues (O4′-endo versus C3′-endo, respectively (47)). This could alter the conformation of the tetraloop and hence its interaction with the protein.

**Determining the Binding Interface of B6min with Natively Folded hβ2m Using NMR**—To determine whether binding of 2′F B6 to hβ2m induces conformational changes in the protein and to map the binding site in residue-specific detail, 2′F B6min was titrated into $[^{15}N,^{13}C]$-labeled hβ2m at 0, 0.25, 0.5, 1.0, and 2.0 molar equivalents at pH 6.2, and $[^1H,^{15}N]$ HSQC spectra were recorded. The $[^1H,^{15}N]$ HSQC spectrum of the 2:1 mixture of 2′F B6min and hβ2m is shown in Fig. 4A. Addition of 2′F B6min results in the appearance of new peaks in the spectrum and the loss of resonances assigned to native apo-hβ2m, indicating that the complex is in slow exchange with the apo-protein, as expected for a high affinity complex. The chemical shift changes involve some, but not all, resonances, indicative of binding of the aptamer to a specific surface. The $[^1H,^{15}N]$ HSQC spectrum of the hβ2m-2′F B6min complex was assigned using a combination of two-dimensional and three-dimensional NMR techniques (see “Experimental Procedures”) (Fig. 6A). The low sample concentration (60 μM) and relatively large size of the complex (25.6 kDa) made assignment challenging. Of the 88 main chain resonances in the $[^1H,^{15}N]$ HSQC spectrum of hβ2m, 55 were successfully assigned. The assigned spectrum of the 2′F B6min-hβ2m complex was then used to map the binding site for 2′F B6min on the surface of the protein. Residues with the largest chemical shift differences upon aptamer binding are located on the face of hβ2m that contains the A, B, E, and D β-strands (Fig. 6B and C). A significant number of residues in this region could not be assigned unambiguously in the spectrum of the complex, suggesting that they experience large chemical shift differences upon aptamer binding or are not detected due to exchange line broadening (Fig. 6, B and C). The titration was also performed using 2′OH B6min (Fig. 5, C and D). No changes in the chemical shifts of hβ2m were observed, even at the 2:1 aptamer/hβ2m molar ratio, confirming that the presence of 2′F-modified pyrimidines is vital for high affinity binding.

Further characterization was therefore restricted to B6 and its derivatives.

A truncated 44-nucleotide version of the 110-nucleotide full-length B6 was produced encompassing nucleotides 22 to 59 with 2′OH (termed 2′OH B6min) (Fig. 3D) or 2′F pyrimidines (termed 2′F B6min) (Fig. 3E), i.e. all of the selected region defining the stem loop with some stabilizing additional base pairs. We examined the solution binding of 2′F B6min to native hβ2m and ΔN6 using fluorescence spectroscopy. hβ2m has two tryptophan residues: Trp-60, which lies in the DE loop (Fig. 1A) and is solvent exposed, and Trp-95, which lies toward the C terminus of the 100-residue protein and is buried. Tryptophan fluorescence of hβ2m can be used to probe changes in conformation or chemical environment upon aptamer binding, with...
binding. To investigate whether 2′F B6min is able to recognize ΔN6, 2 molar equivalents of the aptamer were added to 60 μM 15N-labeled ΔN6, and binding was again assessed by monitoring changes in chemical shifts (Fig. 5, E and F). In this sample, the large changes in chemical shifts observed previously in the hβm-2′F B6min complex (Fig. 5, A and B) were not detected (e.g., compare residues Lys-41 and Ala-79 in Fig. 5, B and F). For some resonances, small changes in chemical shift
To obtain more detailed information about the position of the 2′F B6min binding site on the surface of hβ2m, the intensity of each resonance was determined in the presence of a 2-fold molar excess of aptamer and compared with the intensity of its apo counterpart. The results of this analysis are shown in Fig. 7A. Resonances arising from residues in the A, B, E, and D β-strands, the AB and DE loops, residues 3–6 in the N-terminal region, and the C-terminal 6 residues (red in Fig. 7A) lose >80% of their intensity in the spectrum of the complex. These residues form a contiguous surface on hβ2m (Fig. 7A) and include the N-terminal 6 residues of hβ2m that are lacking in ΔN6 and confer increased affinity, consistent with these residues forming part of the interface between the RNA and the protein. Consistent with this, there is little or no change in intensity for residues that lie in the CC’ loop and F and G β-strands on the opposite face of hβ2m (gray in Fig. 7A). By contrast with these results, addition of a 2-fold molar excess of 2′OH B6min to hβ2m has no significant effect on the intensities of the resonances of native hβ2m (Fig. 7B), consistent with its lack of binding.

A similar analysis was performed to assess the possible interaction between 2′F B6min and ΔN6. As expected based on the fluorescence titration results shown in Fig. 4C, little change in intensity was observed for the vast majority of residues in this sample (compare Fig. 7, A and C), consistent with weak binding to ΔN6. Furthermore, the residues that do show a difference in resonance intensity differ from those involved in the 2′F B6min-hβ2m interface. For example, although resonances belonging to residues in the AB loop, the E strand, and the C-terminal 6 residues of native hβ2m diminish in intensity by >80% upon interaction with 2′F B6min, these resonances are largely unaffected (retaining >60% average intensity) when ΔN6 is incubated with the aptamer. Moreover, the residues in ΔN6 showing the largest decrease in intensity upon addition of 2′F B6min (red in Fig. 7C) are spread throughout the structure of the protein, suggesting that binding of 2′F B6min to ΔN6 is less specific than the 2′F B6-hβ2m interaction. These differences in binding presumably explain the insensitivity of tryptophan fluorescence observed upon addition of 2′F B6min to ΔN6.

The 2′F B6min-hβ2m interface defined by these experiments (Fig. 8, A–C) includes a large number of aromatic side chains (Tyr-10, Phe-22, Tyr-26, Phe-56, Tyr-63, Tyr-66, and Tyr-67, green in Fig. 8C), as often found in protein-RNA complexes (48). The residues involved in the binding interface might also be expected to be positively charged, but there appears to be an equal balance of positively charged residues (Arg-3, Lys-6, His-13, Lys-19, Lys-48, His-51, and Lys-94 (blue in Fig. 8C)) and negatively charged side chains (Glu-16, Asp-38, Glu-50, Asp-53, Asp-59, Glu-69, and Asp-98 (pink in Fig. 8C)). Analysis of the NMR data shows that residues 3–6 are clearly part of the binding site. This sequence is absent in ΔN6, which binds very poorly, and contains two positive charges (Arg-3 and Lys-6), but no negative charges. This region is therefore a candidate for a favorable electrostatic interaction with the aptamer. Indeed, murine β2m, which does not bind this aptamer (Fig. 2C), has a Gln substituted for Lys at residue 6 (N-terminal sequence of

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**FIGURE 4.** Binding of 2′OH B6min and 2′F B6min to hβ2m and ΔN6 measured using intrinsic tryptophan fluorescence. A, normalized tryptophan fluorescence of hβ2m (1 μM) upon addition of 2′F B6min (0–1.7 μM). The data are fitted to a logistic equation (solid line). The data are normalized (Norm.) between 0 (no aptamer) and 1 (the fluorescence signal in the presence of 1.7 μM aptamer) (see “Experimental Procedures”). B, titration of hβ2m (1 μM) with 2′OH B6min. C, titration of ΔN6 (1 μM) with 2′F B6min. No fluorescence change was observed over the concentrations of aptamer added in B and C. These data were normalized between 0 (no aptamer) and 1 (the fluorescence signal when 1.7 μM of 2′F B6min was added to hβ2m. All experiments were performed in 50 mM MES buffer, 120 mM NaCl, pH 6.2. AFU, arbitrary fluorescence units.

were observed; however, in those cases, the chemical shifts did not saturate, even in the presence of a 2-fold molar excess of 2′F B6 (e.g. residues Ser-20 and Cys-80 (Fig. 5F)). The results thus confirm a significantly lower affinity of this aptamer for ΔN6.
murine β2m is IQKTPQ), implying that Lys-6 is a likely key recognition element for hβ2m.

2′F B6min Alters the Co-assembly of ΔN6 and hβ2m—The NMR and fluorescence data presented above indicate that 2′F B6min binds tightly to hβ2m, but only weakly and non-specifically to ΔN6. At pH 6.2 hβ2m does not self-assemble into amyloid fibrils in vitro over a time scale of several weeks at a concentration of 40 μM, even using significant agitation (13, 49, 50).
In contrast, ΔN6 rapidly and quantitatively forms fibrils under these conditions (19, 49). When the two proteins are incubated together at this pH, they co-polymerize, forming hetero-polymeric fibrils with distinct structural properties compared with either of their homo-polymeric counterparts (4). To determine whether 2′F B6min is able to affect the co-aggregation of hβ2,m and ΔN6 (due to preferential binding of the aptamer to one of the fibrillating monomers), the two proteins were mixed (each at a concentration of 40 μM) in the presence or absence of a 2-fold molar excess of 2′F B6min (160 μM) at pH 6.2. Assembly was monitored by separating soluble and insoluble material by centrifugation and subsequent analysis of each fraction by SDS-PAGE (see “Experimental Procedures”) (Fig. 9). In parallel, a sample of the assembly products were monitored using transmission EM (TEM) to confirm whether amyloid fibrils were produced. The results of these experiments showed that in the absence of 2′F B6min, each protein remains in the soluble fraction up to the 24-h time point, after which time insoluble material containing both proteins forms (Fig. 9A). After 166 h of incubation, both proteins are also found in the pellet presumably due to their co-polymerization into fibrils (4). By contrast, in the presence of 2′F B6min aggregation occurs more rapidly, with >90% of ΔN6 and ~40% of hβ2,m forming fibrillar material after 24 h. TEM images of the samples after 166 h confirmed that the insoluble material in the pellets contains amyloid fibrils (Fig. 9, A and B), although the precise location of each protein within each fibril (i.e. the extent to which co-polymerization occurred) could not be ascertained from these experiments. Presumably, the interaction between soluble ΔN6 and hβ2,m is inhibited by 2′F B6min, leading to rapid polymerization of ΔN6, which in part co-polymerizes with hβ2,m.

**DISCUSSION**

To derive a structural mechanism of amyloid formation, the identity and structure of all assembling components must be defined, and how these species interact and form the cross-β-structure of amyloid should be determined. Here, RNA SELEX has been used to generate a specific, high-affinity aptamer (2′F B6) against monomeric hβ2,m. Importantly, despite only subtle differences in the structures of monomeric hβ2,m and its N-terminal truncation variant ΔN6 at pH 6.2 (Fig. 1, A and B), 2′F B6 is able to discriminate between these structures, showing tight and highly specific binding to the β-sheet containing the A, B, E, and D strands of hβ2,m. By contrast, weak, nonspecific binding is observed to ΔN6 that is detectable only at the high protein and RNA concentrations used for NMR (60 μM protein). The discrimination between hβ2,m and ΔN6 by 2′F B6 can be explained, at least in part, by the presence of Lys-6 in the bind-

**FIGURE 7. 2′F B6 distinguishes between two highly similar proteins.** A, plot of the loss of signal intensity of resonances in native hβ2,m upon binding to a 2-fold molar excess of 2′F B6min using data shown in Fig. 5A. Profiles were calculated as the ratio of the peak intensity in the presence (I) or absence (I') of a 2-fold molar excess of aptamer. Intensity profiles were normalized to residues 40 – 45 that are not involved in the interface. Residues with a ratio of ~0.2 are colored red, those showing a ratio between 0.2 and 0.4 are colored yellow, and those with no significant decrease in intensity are colored gray. The structure of hβ2,m drawn as a surface representation is shown on the right color-coded using the same scale. Residues with no assignments (na) are shown in blue. B, as described in A, but for the interaction of 2′OH B6min and hβ2,m. C, as described in A, but for the interaction of 2′F B6min with ΔN6. The secondary structure elements of the proteins are shown as ribbons on top of the panels.
ing interface. However, given that the binding interface appears to involve an extended region spanning the A, B, E, and D/β-H9252-strands, other residues must also contribute to affinity. Indeed, differences in the organization of residues on the surfaces of hβ2m and hN6 that result from the isomerization of the X-Pro-32 peptide bond from the native cis isomer in hβ2m to the trans isomer in hN6 (19), and/or the decreased stability (13) and increased conformational dynamics of hN6 compared with hβ2m (19), may also contribute to 2F B6 discriminating between these otherwise similar structures. For example, although the structure of the backbone is highly conserved between hβ2m and hN6 (Fig. 1), the orientation of the side chains of aromatic residues involved in the aptamer binding interface differs significantly (Fig. 10A). Furthermore, the organization of hydrophobic and charged residues on the surface formed by the A, B, E, and D-β-strands in hβ2m differs significantly from ΔN6 (Fig. 10B). Accordingly, the apical region of this surface in hβ2m is more highly positively charged than its equivalent in ΔN6 (this region contains the N-terminal six amino acids, including Lys-6) (Fig. 10B). In addition, the organization of negatively charged residues (involving the AB loop, the EF loop, and the C terminus) also differs between the two

![Diagrams showing the interaction between aptamers and hβ2m and hN6](https://example.com/diagram.png)
proteins (Fig. 10B). In total, therefore, the balance between electrostatic and hydrophobic residues, crucial for nucleic acid binding (51), is distinct in hβ2m and ΔN6, partly due to the removal of the N-terminal six amino acids, and in part due to differences in solvent exposure of hydrophobic residues in the DE and BC loops in the two proteins that occur as a consequence of X-Pro-32 isomerization.

The role of ΔN6 in DRA is not currently understood. Although ΔN6 is present in the amyloid deposits found in patients with DRA (52), it remains unknown whether the N-terminal truncation of hβ2m occurs pre- or post-fibril formation. Additionally, the interaction between hβ2m and ΔN6 in vitro is complex, with ΔN6 possessing the ability to convert monomeric hβ2m into an amyloidogenic conformation (4, 19, 53) and to act as a fibrillar seed able to be elongated with hβ2m monomers (19, 49). The aptamer selected here may be useful as an analytical probe to derive greater clarity in understanding the early stages of hβ2m and ΔN6 co-assembly into amyloid. Given the complexity of amyloid formation, where self-assembly can be initiated by one or more rare conformers that may differ subtly in structure, and that different oligomeric species may exhibit profoundly different cytotoxicity (54, 55), RNA aptamers offer unique potentials as reagents for the analysis of, and interference with, amyloid formation.

The specific and tight binding of 2′F B6 to hβ2m alters the course of amyloid assembly in mixtures of hβ2m and ΔN6 at pH 6.2. Thus, aptamer binding to hβ2m disfavors the incorporation of hβ2m into amyloid fibrils during co-assembly with ΔN6 and results in more rapid fibril formation. In the presence of the aptamer, hβ2m molecules will become incorporated into fibrils only after aptamer dissociation, possibly by cross-seeding with preformed ΔN6 fibrils (4, 49). Alternatively, ΔN6 may promote conversion of hβ2m to an amyloidogenic conformation once 2′F B6min dissociates (4, 19, 53), pulling the equilibrium toward co-assembly into fibrils. Given that amyloid formation is under kinetic control, the development of aptamers able to bind their targets with slow off-rates (even for the same apparent $K_d$) would provide an effective strategy to control assembly. Such aptamers could be isolated by increasing the length of the time of the elution steps in SELEX as stringency is increased. Alternatively, coupling of the RNA aptamer to a molecule with known affinity to the target could provide a route to achieving this goal by exploiting avidity effects. Doxycycline, a small molecule tetracycline analog, has been shown to modulate the formation of hβ2m fibrils in vitro (56), to reduce articular pain and improve movement in DRA patients (57), and to correct a locomotory defect in Caenorhabditis elegans expressing hβ2m (58). Analysis of the hβ2m-doxycycline complex using NMR suggests that the highest affinity binding site (IC$_{50}$ ~ 50 µM (56)) involves residues that lie in the C-terminal region of strand A, the N-terminal region of strand B, and the central residues of the AB loop (56). A second, lower affinity binding site involves the N-terminal region and residues in the BC and DE loops. An intriguing possibility, therefore, would be to create an aptamer linked to doxycycline such that the relatively tight and specific binding of 2′F B6 can be exploited to enhance binding of doxycycline to its target interface. Creation of such bipartite molecules has been shown to be a highly effective strategy, not just for enhancing the effectiveness of RNA aptamers as delivery vehicles (59–61), but in many other applications (62–64).

In conclusion, the biophysical and biochemical studies presented here demonstrate that RNA aptamers can be highly specific and discriminatory probes, modulating co-polymerization reactions and controlling the course of amyloid assembly. How the 2′F B6-hβ2m complex changes as fibril formation proceeds and the effect of the aptamer on hetero-polymorphic fibril structure and stability will require further studies, for example, by exploiting the powers of solid-state NMR to analyze fibril structures (65, 66). Further characterization and modification of 2′F B6 will potentially allow the affinity of the aptamer for hβ2m to be increased, and selection of aptamers specific for ΔN6 will also allow detailed biophysical analysis of the role of ΔN6 in hβ2m-ΔN6 co-polymerization. Understanding this process further may shed light on the molecular mechanisms of fibril formation and how the protein precursors of hetero-polymorphic assemblies can be modulated to tailor the extent, rate, and structure of amyloid fibrils.

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Amyloid Precursors and RNA Aptamers

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Claire J. Sarell, Theodoros K. Karamanos, Simon J. White, David H. J. Bunka, Arnout P. Kalverda, Gary S. Thompson, Amy M. Barker, Peter G. Stockley and Sheena E. Radford

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