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Disassembling peptide-based fibres by switching the hydrophobic–hydrophilic balance†

Joris T. Meijer, Marloes J. A. G. Henckens, Inge J. Minten, Dennis W. P. M. Löwik* and Jan C. M. van Hest

Received 12th June 2007, Accepted 10th July 2007

First published as an Advance Article on the web 19th July 2007

DOI: 10.1039/b708847g

Amyloid-like model peptides, modified on the N-terminus with an alkyl tail and on the C-terminus with a PEG chain, yielded fibres that were susceptible to triggered disassembly by removal of the alkyl chain, which affected the hydrophobic–hydrophilic balance.

Alkylated peptides represent a versatile class of self-assembling building blocks, due to the subtle interplay between directional hydrogen-bonds and hydrophobic interactions.^{1–3} This versatility has recently been explored in a variety of applications. For example, Stupp *et al.* have demonstrated the usefulness of peptide amphiphile assemblies for the construction of bioactive materials.^{4,6} Furthermore, well defined peptide aggregates have also been used to direct and organize assemblies of synthetic polymers to enhance material properties.^{7–9} One of the interesting aspects of peptide assembly is that it can be affected by changing the balance between the non-covalent forces that govern the supramolecular architecture. Previously, we have shown that introduction of a hydrophobic tail to a fibril-forming peptide increases the stability of the fibrils and renders the assemblies amenable to manipulation.^{10,11} Induction of peptide assembly has in this respect already been shown using light,^{12–14} chemical switches^{15,16} and enzymes.^{17,18} In all of these cases, subtle changes in hydrophobicity lead to an increased affinity for aggregation.

To our knowledge, only examples in which peptides have been manipulated to promote self assembly have been described in the literature so far. The other possibility, disassembly of peptide aggregates by changing non-covalent interactions *in situ*, has not been exploited yet. This concept is worthwhile pursuing, since it could lead to new release mechanisms and controlled degradation processes for *e.g.* biomedical applications.¹⁹ In this communication we report on a convenient methodology to disassemble peptide fibre assemblies by manipulating the hydrophobic–hydrophilic balance (Fig. 1). For this purpose, peptides were modified with both a hydrophilic and a cleavable hydrophobic moiety, for which the overall balance of non-covalent interactions was still in favour of peptide assembly. After cleaving off the hydrophobic tail, the peptide fibres spontaneously disassembled.

In previous reports we discussed the stabilization of assemblies of the amyloid-forming hexapeptide Ac-Lys-Thr-Val-Ile-Ile-Glu-NH₂. It was shown that the introduction of a hydrophobic moiety

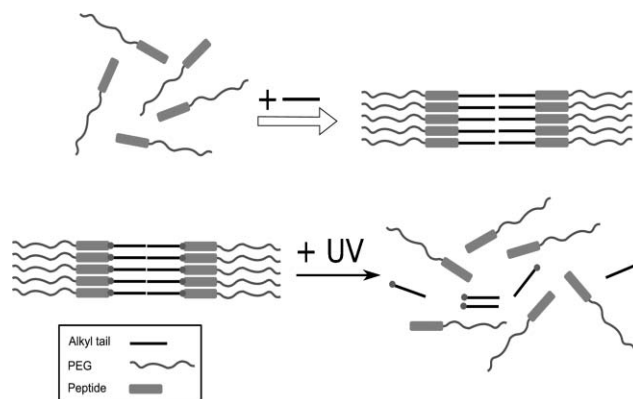


Fig. 1 Control of peptide fibril stability. Stabilization of PEGylated peptide fibrils by introduction of a hydrophobic tail (top). Destabilization of peptide fibrils by cleaving off a hydrophobic tail *in situ* (bottom).

led to a complete absence of fibre disassembly, even at elevated temperatures (up to 90 °C), whereas the unmodified peptide could be disassembled upon heating.^{10,20} We then wanted to investigate whether the opposite effect could be achieved by introduction of a hydrophilic group. Therefore a PEG chain was introduced C-terminally in the peptide sequence using a resin with an immobilized PEG moiety (Fig. 2).

Peptide **1** was synthesized on a resin with an immobilized PEG moiety of 3000 g mol^{−1} molecular weight by solid-phase peptide synthesis following a standard Fmoc-protection protocol.²¹ Next,

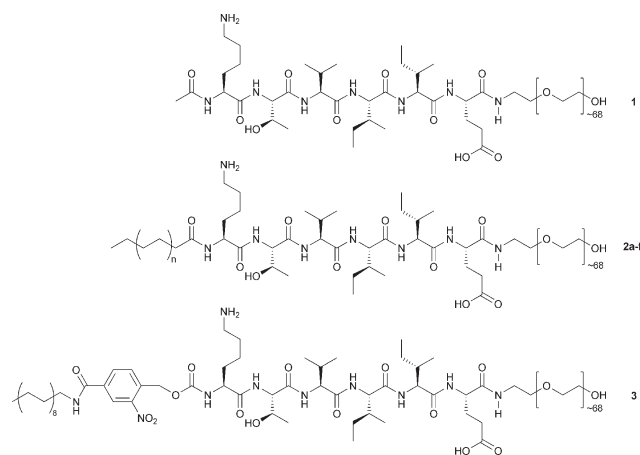


Fig. 2 PEGylated hexapeptide **1**; amphiphilic peptides **2a–f** (**a**: $n = 1$; **b**: $n = 2$; **c**: $n = 3$; **d**: $n = 4$; **e**: $n = 5$; **f**: $n = 6$); and cleavable amphiphilic peptide **3**.

Toernooiveld 1, 6525 ED, Nijmegen, The Netherlands.
E-mail: D.Lowik@science.ru.nl; Fax: +31 24 3653393;
Tel: +31 24 3652382

† Electronic supplementary information (ESI) available: Details of the synthesis, sample preparation, and measurement. See DOI: 10.1039/b708847g

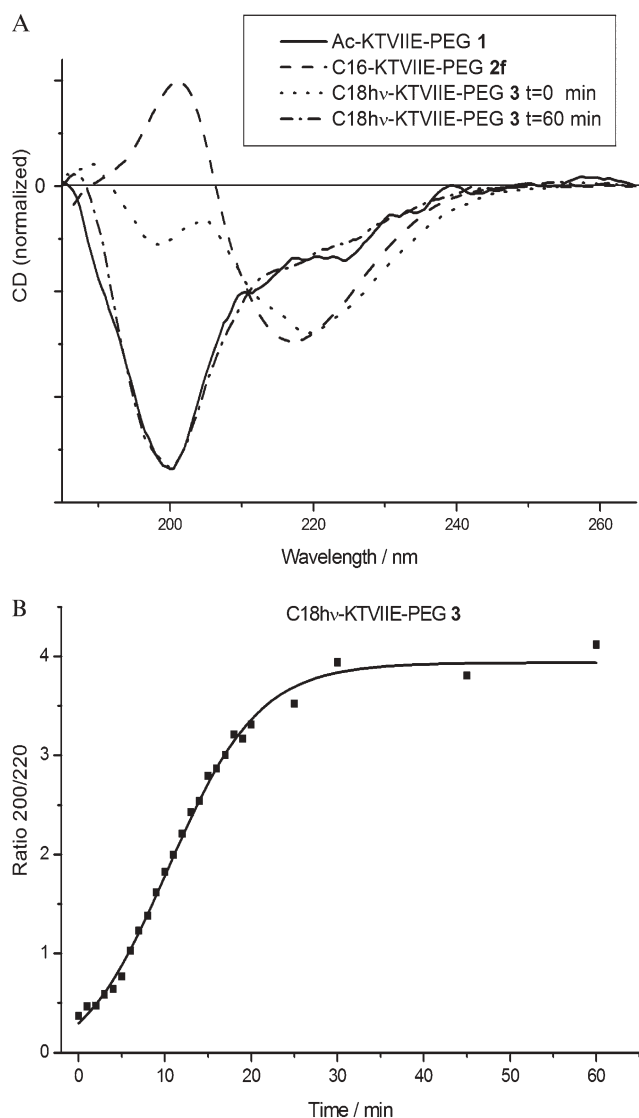


Fig. 3 A) CD spectra of peptides **1**, **2f** and **3** before and after UV irradiation. B) Ratio of the CD signals at 200 nm and 220 nm upon exposure of peptide **3** to UV radiation.

the PEGylated peptide was subjected to a previously described procedure for peptide assembly.¹⁰ The presence of fibrillar assemblies was examined using circular dichroism (CD) spectroscopy and transmission electron microscopy (TEM).²² Peptide **1** with an attached PEG tail showed a CD spectrum with a minimum at 200 nm (Fig. 3A). This spectrum indicates that the peptide is in a random coil fold and therefore in a non-aggregated state. This was in agreement with the absence of structures using TEM measurements. As expected, PEGylation was an efficient way of preventing the hexapeptide from assembling.

To study the balance between hydrophilic destabilization and hydrophobic stabilization of fibres, a hydrophobic tail was introduced to the N-terminus of the peptide (Fig. 2). C₁₆-functionalized peptide **2f** showed a spectrum with signals at 220 nm and at 200 nm, identical to the spectra obtained for the previously examined self-assembling amphiphilic peptides (Fig. 3A).¹⁰ On heating the solution to 90 °C the CD spectrum did not change, indicating a stable aggregate of the peptide. TEM

confirmed that fibrils were present in the sample (Fig. S2-1/2†). Next, a series of peptides was prepared with varying hydrophobicity. Solutions of the peptides with alkyl tails of C₆, C₈ and C₁₀ (**2a–c** respectively) showed the same CD spectrum as peptide **1**, indicating the absence of fibrillar aggregates. In contrast, solutions of peptides with C₁₂ (**2d**) and C₁₄ (**2e**) tails showed a CD spectrum similar to the fibril-forming peptide **2f**. Interestingly, for both samples (**2d** and **2e**) the CD signal did not change on heating the sample to 90 °C. This suggests that once a critical hydrophobicity is acquired, strong stabilization of the assemblies is established.

PEGylation of the fibril-forming hexapeptide KTVIIE seems thus to prevent aggregation, and introduction of a hydrophobic n-alkyl group longer than C₁₂ overcomes this solubilizing effect and the peptide amphiphiles form fibres in aqueous solution. Removing the stabilizing group *in situ* should now allow us to trigger the disassembly of the fibrils. In order to investigate this possibility, peptide **3** was synthesized, containing both a hydrophilic PEG moiety and an alkyl chain. In this case, however, the alkyl chain was connected to the peptide by a UV-sensitive nitrobenzyl moiety.^{23–25} Upon irradiation, this group was cleaved, thereby removing the hydrophobic tail from the peptide.

Peptide **3** containing the UV-cleavable linker formed the same fibril structures as the amphiphilic peptide **2f**, corroborated by CD spectroscopy and TEM. The CD spectrum of cleavable peptide **3** only differed at 200 nm compared to C₁₆-functionalized peptide **2f** (Fig. 3A). This is attributed to the presence of the UV-cleavable linker, which also absorbs in this region.

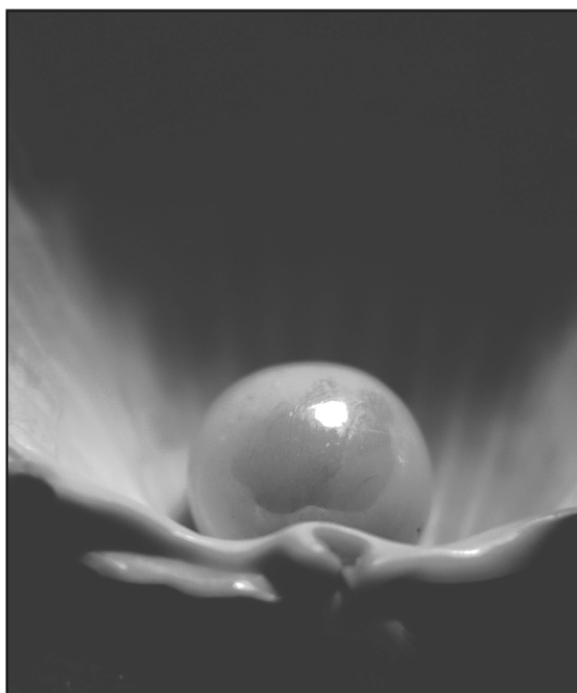
Irradiation of assemblies of **3** with a strong UV source resulted in clear changes to the CD spectrum after 3 minutes of exposure (Fig. 3B). The ratio of the peaks at 200 and 220 nm increased, characteristic for a change from β -sheet to random coil. Prolonged exposure changed the CD spectrum completely to a spectrum typical for the dissolved state, showing the destruction of the fibrils (Fig. 3A and Fig. S1-1) which was substantiated by TEM, confirming the absence of fibrillar structures. Moreover, the cleavage was established by TLC (Fig. S3-1). In a control experiment, fibres of peptide **2f** without the labile linker were exposed to the same UV source for 1 hour (Fig. S1-2). This exposure did not cause any change in the assembly of the fibrils as determined by CD spectroscopy.

In conclusion, the introduction of a hydrophilic group to a fibril-forming peptide can inhibit the formation of structured assemblies of this peptide. More interestingly, upon increasing the amphiphilic character of the peptide by introducing an additional hydrophobic group, the well-structured aggregates return. This effect on assembly led us to introduce a moiety that enables us to selectively control the presence of aggregates. We are exploring this strategy to further manipulate self-assembled peptide amphiphile architectures.

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