A rational design to create hybrid β-sheet breaker peptides to inhibit aggregation and toxicity of amyloid-β†

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Alzheimer’s disease is characterized by deposits of the amyloid β protein (Aβ) in the form of senile plaques and cerebral amyloid angiopathy. Deposition of Aβ into these pathological lesions is directed by step-wise aggregation of Aβ into oligomers, protofibrils and mature fibrils. Currently, all therapies are purely symptom-relieving, and an actual treatment or prevention of AD is still lacking. Since aggregated forms of Aβ are particularly neurotoxic, interference with the process of Aβ aggregation is a long-envisioned target for therapy. Based on the knowledge that both sulfated (macro)molecules and small synthetic peptides interfere with Aβ aggregation, we developed hybrid ligands to target Aβ fibrillization by a combination of peptide-peptide and sulfate-peptide interactions. A series of peptides, modified at the N-terminus with sulfated linkers, was successfully prepared by solid phase synthesis. The hybrid ligands were tested using a viability assay and an aggregation assay. Molecular modeling was applied to explain the binding of the hybrid ligands to Aβ,42. The hybrid ligands that we designed, synthesized and evaluated were found to be non-toxic to cells but displayed negligible inhibition of Aβ fibrillization and Aβ-mediated cytotoxicity compared to the beta-sheet breaker peptides known today. Further molecular modeling simulations suggested that the hybrid ligands were incorporated into the β-sheet structure of Aβ aggregates, indicating that the hybrid ligands may bind to Aβ but are unable to inhibit further aggregation. Optimization of the hybrid ligands by reducing hydrogen bond interactions of the ligand with following Aβ proteins might result in ligands, with improved binding to one Aβ protein, that could potentially disrupt further β-sheet formation. This in turn may reduce toxicity of Aβ.
oligomers and in larger fibrils, then such molecules could inhibit both the formation of toxic oligomers and of fibrils. To this end, several research groups have designed “β-sheet breakers” (BSB).8,9 BSB are based on peptide sequences that specifically interfere with β-sheets within Aβ. Two sets of peptides were effective BSB, namely the peptides LPFFD (or its analogues LVFFA or LPYFD) and KLVFF that bind to a region between amino acids 16 and 22 of Aβ.10,12,14 These compounds inhibit Aβ-mediated neurotoxicity8,10,12 and Aβ deposition in vivo and improve behavioral deficiency induced by Aβ deposition.10,12,14 However, a reasonable molar excess compared to the Aβ protein is needed to achieve such a result.10,14,15

It is known that small sulfated and sulfonated molecules have high binding affinity with Aβ, since they are designed to interfere with glycosaminoglycan/Aβ interaction.19 The binding site on Aβ for GAGs likely resides within the cluster of basic amino acids 13–16 of Aβ,19 although it remains possible that other domains within Aβ interact with GAGs as well.23 Thus, this might indicate that the binding site on Aβ for the small anionic sulfates and sulfonates also resides within the same cluster of amino acids.

Covalent linking of two separate ligands to give so-called hybrid ligands is a powerful general concept to enhance binding affinity and improve the biological activity compared to the separate molecules, a strategy that has successfully been used in medicinal chemistry in the past years.16–18 Increasing the binding affinity of a BSB peptide to Aβ might decrease the molar excess needed to affect Aβ aggregation, toxicity and deposition. Considering the relative positions of BSB peptides and GAG binding to Aβ (amino acids 16–22 and 13–16 respectively),8,10,20,22,23 it occurred to us that the covalent attachment of (poly)sulfates with the BSB peptide by a certain linker would possibly lead to a hybrid with improved binding characteristics and, thereby, possibly improved characteristics with respect to inhibition of Aβ fibrillization and Aβ-mediated cytotoxicity. Hence, we synthesized Aβ ligands that combine pentapeptide-Aβ interaction and sulfate-Aβ interaction and evaluated their effects on Aβ aggregation and Aβ-mediated cytotoxicity relative to the separate ligands.

Since BSB peptide KLVFF contains the basic amino acid lysine (K), which would result in a zwitterionic structure upon monosulfonation, BSB peptide LPFFD, lacking a basic amino acid, was chosen as starting point of our hybrid ligands. The synthetic route towards several hybrid ligands (3, 4, 5a–5d and 6a–6d) is shown in Fig. 1, and is based on standard Fmoc-based solid phase synthesis and introduction of a variety of alcohols at the N-terminus of the pentapeptide, via carbamate or urea functionality. Because cleavage of C_{10}H_{18}O_{4}-LPFFD-OH (5d (i-Pro) and 5d’ (d-Pro)) from the Breipohl resin did not result in the desired compound, likely caused by the harsh cleavage conditions, a 2-chlorotrityl resin was used instead. The milder conditions for cleavage from the 2-chlorotrityl resin successfully afforded C_{10}H_{18}O_{4}-LPFFD-OH (5d and 5d’). After cleavage from the resin, sulfate groups were introduced by sulfonation of the alcohol groups under the action of sulfuryl oxide-amine complex. Using HPLC, a purity of >95% was achieved for all synthetic sequences. In addition to the hybrid ligands shown in Fig. 1, as a control peptide Ac-LPFFD-NH_{2} (7) was also synthesized. Ac-LPFFD-NH_{2} (7) is known in literature as iAβ5p and is shown to reduce amyloid plaque formation in a transgenic mouse model.14 In our study, it served as a control to our hybrid ligands in the biological assays.

Two kinds of assays were used to determine the biological activity of the hybrid ligands. First of all, hybrid ligands were screened for in vitro activity in inhibition of amyloid fibril formation. Fibril formation was quantified with a fluorescence assay based on the specific binding of thioflavin T (Th-T) to β-sheet amyloid aggregates.24 By binding to the β-sheets in Aβ aggregates, a fluorescent signal is produced which is proportional to the amount of fibrils formed. The effect of the hybrid ligands on β-sheet formation of Aβ_{42} in the first 48 h of incubation was analyzed and compared to the inhibitory effect of Ac-LPFFD-NH_{2} (7) alone. In earlier studies (unpublished data) it became apparent that co-incubation of (monomeric) Aβ with Ac-LPFFD-NH_{2} (7) in a molar ratio of 1 : 20 resulted in approximately 50% inhibition of the aggregation of Aβ. Therefore, we have used this molar ratio to study the hybrid ligands in the aggregation assay. Secondly, toxicity of Aβ in cell culture has been reported to be related to the formation of β-sheet-rich aggregates8 and has been used in several studies to screen diverse compounds to prevent amyloid neurotoxicity. Degeneration of smooth muscle cells (SMCs) and pericytes by Aβ (aggregation) is a prominent feature of CAA. We, therefore, developed a model of Aβ-mediated degeneration of cultured human brain pericytes (HBPs) and SMCs.25,26 These cells were isolated from human brain capillaries and leptomeningeal vessels, respectively, from control and AD brains obtained at autopsy. In this model the aggregation of wild-type Aβ_{1–42}, is cytotoxic for HBP and SMC cultures.8 The effect of the hybrid ligands on Aβ_{42}-mediated cell death after 6 days of incubation was analyzed and compared to the inhibitory effect of Ac-LPFFD-NH_{2} (7) alone. In earlier studies (unpublished data) it became apparent that co-incubation of (monomeric) Aβ with Ac-LPFFD-NH_{2} (7) in a molar ratio of 1 : 5 resulted in approximately 50% inhibition of the cytotoxicity of Aβ. Therefore, we have used this molar ratio to study the hybrid ligands in the viability assay.

Co-incubation of Aβ_{42} with Ac-LPFFD-NH_{2} (7) resulted in an inhibition of the toxicity and aggregation of Aβ_{42} (Fig. 2), which confirms earlier research.10 However, no significant effect was found of either hybrid ligand both on toxicity and aggregation of Aβ_{42}. In Table 1 (supporting materials) an overview of the hybrid ligands in the aggregation assay. Fig. 2 shows a representative figure for all hybrid ligands. Co-incubation of Aβ_{42} with Ac-LPFFD-NH_{2} (7) in a molar ratio of 1 : 20 resulted in 66% decrease in fluorescent signal (p < 0.01; Fig. 2A), i.e. Ac-LPFFD-NH_{2} (7) seems to inhibit the fibril formation of Aβ_{42}, which confirms earlier research.23 However, co-incubation of Aβ_{42} with C_{10}H_{18}O_{4}-LPFFD-OH (5d) or the bisulfonlated analogue C_{10}H_{18}N_{3}O_{4}S_{2}-LPFFD-OH (6d) in a molar ratio of 1 : 20 resulted in a fluorescent signal comparable to the signal of Aβ_{42} alone (Fig. 2A). Incubation of buffer alone or the compounds themselves did not result in a fluorescent signal. In addition, a significant difference was observed in cell death between HBPs treated with 10 μM Aβ_{42} either alone (25% cell death) or with Ac-LPFFD-NH_{2} (7; 11.3% cell death; p < 0.001; Fig. 2B) in a molar ratio of 1 : 5 for 6 days, which also confirms earlier research.10,12 However, again no significant effect was observed when co-incubating Aβ_{42} with 5d or 6d in a molar ratio of 1 : 5 for 6 days compared to incubation with Aβ_{42} alone.
Incubation of the compounds alone resulted in cell death comparable to control levels. Thus, N-terminal chain extension of peptide LPFFD with an aliphatic alcohol or sulfonlated alcohols, via urea or carbamate functionality, consequently leads to derivatives with reduced activity with respect to Ac-LPFFD-NH₂ (7) itself.

To find a possible explanation for these results, a molecular modeling approach was applied to the hybrid ligands (3, 4a–4d and 5a–6d) and the NMR structure deposited in RCSB Protein Data Bank under the ID number 2BEG as a model for the Aβ fibrils (see supporting materials). In earlier studies, the binding site of LPFFD on Aβ was determined and we used this binding site to align our...
hybrid ligands to the Aβ42 protein. As can be seen in Fig. S1, a nice β-sheet was observed when aligning several Aβ42 proteins. According to the obtained model, it was rationalized that a spacer of three carbon atoms should be sufficient to target His13 and/or His14 in the Aβ42 protein with a sulfate group of the hybrid ligand, Fig. S1. Based on this insight, our synthetic compounds could simultaneously target the binding domains of GAGs (binding to Aβ amino acids 13–16) and of pentapeptides (binding to Aβ amino acids 16–22).

After alignment, molecular dynamics was performed with the assumption that the phenylalanine (amino acid 3) of the hybrid ligand adopts the same orientation as the phenylalanine (amino acid 18) of the Aβ42 protein. Thus, from this initial conformation for molecular dynamics simulations in water, the energetically most favorable “docking” conformation was sought. It should be mentioned that during these calculations the starting configuration will not be the most sampled configuration if it is not energetically favorable, certainly if the simulation time is long enough. From these calculations it became apparent that, although both phenylalanines of the hybrid ligand adopt the same orientation as the phenylalanines of the Aβ42 protein, it is difficult to target the histidines in the Aβ42 protein with a non-peptide side-chain in the hybrid ligand. Rather, the side-chain bends away such that the sulfate groups interact with Lys15 of the Aβ42 protein backbone, rather than with His13 or His14 (Fig. S2). Interestingly, during further molecular modeling simulations it became apparent that the hybrid ligands could be fully incorporated into the β-sheet structure of aggregated Aβ (Fig. S3), explaining why our hybrid ligands exerted no effect on Aβ aggregation and toxicity.

It is thought that BSB peptides, such as Ac-LPFFD-NH2 (7), interfere with electrostatic interactions during aggregation or destabilize the Aβ-fibril internal hydrogen bond network, necessary to maintain the β-sheet structure, by forming strong hydrogen bonds with the Aβ subunits.60 During the calculations we were solely focused at the optimization of the affinity of the sulfonylated hybrid ligands to the Aβ protein. The disadvantage of these compounds, however, is that because of this high quality binding, it is very likely that we have designed compounds that incorporate into the β-sheet structure of Aβ42 aggregates, rather than inhibiting aggregation of the protein, due to restoring the Aβ fibril internal hydrogen bond network (Fig. S3). Thus, to be an effective BSB ligand, hybrid ligands should not only have a higher binding affinity to the Aβ42 protein, but should also disrupt the β-sheet structure. Therefore, to optimize the ligands, a “bulky” sidechain/group could be introduced to optimize our hybrid ligands, thereby preventing its incorporation into the β-sheet structure of Aβ42. An alternative strategy involves changing the amino acid sequence by replacing, for instance, one of the phenylalanines by a polar amino acid and/or reducing hydrogen bond interactions of the hybrid ligand with a next Aβ protein.

In conclusion, a hybrid ligand with improved characteristics with respect to inhibition of Aβ fibrillation and Aβ-mediated cytotoxicity compared to Ac-LPFFD-NH2 (7)10,14 was not found. However, as our molecular modeling experiments suggest, the designed hybrid ligands likely have a higher binding affinity for Aβ, but cannot avoid further aggregation of the Aβ protein. Changing the amino acid sequence by replacing, for instance, one of the phenylalanines by a polar amino acid and/or reducing hydrogen bond interactions of the hybrid ligand with a next Aβ protein could be a variable for optimization of the hybrid ligands in future studies to validate the hypothesis that hybrid ligands targeting Aβ fibrillization by a combination of peptide-peptide and sulfate-peptide interactions have enhanced properties.

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Reference list