

USING STEFIN B AS A MODEL AMYLOIDOGENIC PROTEIN – OVERVIEW

STEFIN B KOT MODEL ZA AMILOIDOGENE PROTEINE – PREGLED

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Abstract

Our in vitro studies of human stefin B are described. Human stefin B (cystatin B) gene was reported as the first gene of the two known genes, whose mutations cause progressive myoclonus epilepsy of type 1 (EPM1), also known under the name Unverricht-Lundborg disease. The product of the gene, stefin B, is a globular protein of 98 amino acids and no disulphide bonds. We have characterized this protein thoroughly: from structure, to folding, stability and aggregation. The main focus of this review is on the protein's ability to undergo amyloid fibril formation. This is not something special to stefin B (any protein can under certain circumstances transform into amyloid-fibrils) yet this protein proved as a very suitable model system showing all the characteristics of other more well known systems. It may have some advantages over amyloid-beta or prion peptide studies, for example, it is easier to isolate its oligomers and its aggregates are not infectious. In the Introduction, connection of the process of amyloid-fibril formation to neurodegenerative disease is discussed. Relevance of the molecular, in vitro studies to understand the molecular basis of neurodegenerative pathology is explained. What is known about the structure and function of cystatins and what has been learnt from studies of amyloid-fibril formation of stefin B, is described next. The final chapter is devoted to EPM1. An observation was made that some of the EPM1 mutants have changed aggregation properties, which may have implications for pathology.

Keywords

stefin B; protein aggregation; amyloid; progressive myoclonus epilepsy; human

Izvleček

V tem preglednem članku so opisane naše in vitro študije človeškega stefina B. Človeški stefin B (cistatin B) je prvi raziskani gen, izmed dveh znanih, katerega mutacije povzročajo EPM1 (progresivno mioklonsko epilepsijo tipa 1), poznano kot Unverricht-Lundborg bolezen. Produkt gena, stefin B, je globularni protein iz 98 amino kislin in brez disulfidov. Ta protein smo podrobno proučili: od strukture, do zvijanja, stabilnosti in agregacije. Glavni poudarek tega prispevka je na opisu procesa amiloidne fibrilacije. Sicer je znano, da se večina proteinov ob izbranih okoliščinah (T, pH, topilo) lahko pretvori v amiloidne fibrile, a se je stefin B izkazal kot zelo primeren modelni sistem, ki ima vse značilnosti drugih, bolj znanih sistemov. Lahko bi rekli, da ima delo s stefinom B celo nekatere prednosti pred delom s prioni ali amiloidom beta, ker 1) lažje ločujemo posamezne oligomere in, ker 2) mislimo, da agregati stefina B niso infektivni. V Uvodu je predstavljena povezava med procesom nastajanja amiloidnih fibril in neurodegenerativnimi boleznimi. Razložimo pomen molekularnih, in vitro študij za razumevanje molekularnih osnov neurodegenerativne patologije. Zatim, kaj je znano o strukturi in funkciji cistatinov in kaj povedo študije amiloidne fibrilacije stefina B. Zadnje poglavje je posvečeno EPM1. Poročali smo, da imajo nekatere EPM1 mutante drugačne lastnosti agregacije, kar bi se morda lahko odražalo v patologiji.

Ključne besede *stefin B; agregacija proteinov; amiloid; progresivna mioklonska epilepsija; človek*

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Introduction

Amyloid¹ plaques or filamentous cellular inclusions are hallmark of neurodegenerative diseases.² There is no doubt that aberrant protein folding and aggregation take place in neurodegenerative diseases.³⁻⁶ In Alzheimer's disease (AD) amyloid plaques, made predominantly of the cleavage peptide A-beta, accumulate extracellularly in the brain, whereas the paired helical filaments made of hyperphosphorylated protein Tau accumulate intraneuronally. In Huntington's disease huntingtin's aggregates cause slowing of the axonal transport along microtubules.^{7,8} and in Parkinson's disease Lewy bodies are found in the affected neurons. Familial cases and animal models demonstrate, that certain protein mutants, which lead to more heavy aggregation also lead to early outburst of disease,^{9,10} therefore, they must be the primary cause. It is not straightforward, whether the inclusions of the aggregated proteins are harmful or beneficial for neurons (at least initially) as they may sequester the toxic protein aggregates.⁶ More and more evidence has been gained that smaller, soluble protein oligomers are toxic and not so much the mature fibrils.^{11,12}

Even though under stress conditions (such as infection, fever, oxidative damage) some proteins may aggregate in the cell, there are regulatory mechanisms to correct this burden. Under normal conditions, a vital role is played by the two degradation systems of the cell: the ubiquitin proteasome system (UPS) and the autophagy.^{13,14} With aging both systems get less efficient and a sporadic neurodegenerative disease may break out. Autophagy has been shown of particular importance in aggregates clearance.¹⁵

Several attempts to improve prospects for therapy of neurodegenerative diseases are in progress. The pre-clinical and clinical studies comprise stem cells producing nerve growth factors, which fight against neural death,¹⁶ anti-amyloid antibodies, which clear amyloid plaques¹⁷ and so on. Unfortunately, they all face severe side-effects in human trials. One of the most promising trials seems to be gene therapy (at least for Huntington's, familial Parkinson's and Lafora diseases). Therefore, understanding the primary cause of pathology and directing therapies to the route of the problem may be among the most efficient solutions for the future.

In order to arrive at the molecular understanding of the process of protein ordered aggregation, we study amyloid-fibril formation of stefin B - as a model system.

Cystatins and stefins: structure and function

To introduce our model protein, some facts about its structure and function are described. Three-dimensional structures of a number of members of the cystatin family have been determined. Crystal structure of stefin B monomer has been solved in complex with the protease papain.¹⁸ Solution structure of stefin A monomer and dimer^{19,20} have been solved by heteronuclear NMR. Structures of cystatin C monomer in

solution and that of cystatin C domain-swapped dimer in crystal²¹ have also been determined.

The best known function of stefin B is inhibition of the cysteine proteinases.^{22,23} Inhibition of cathepsins, in particular, cathepsin B, could partially explain its regulatory role in apoptosis^{24,25} and in cancer.²⁶ However, more and more evidence points to some alternative function of this small protein. Stefin B (sometimes called - cystatin B) has been shown as part of a multi-protein complex specific to the cerebellum.²⁷ By gene-expression studies it was shown to be overexpressed in amyotrophic lateral sclerosis - ALS²⁸ and in innate immunity response.²⁹

Pathologies observed in stefin B deficient mice are cerebellar apoptosis, ataxia and myoclonus²⁴ as well as glial cells activation.³⁰ The protein gets overexpressed post-seizures,³¹ implying its neuroprotective role. Cystatin C was similarly found over-expressed in status epilepticus.³² In double knock-out mice of stefin B and cathepsin B genes²⁵ apoptosis was reduced maximally by 40 %, whereas ataxia and myoclonus remained, suggesting that stefin B may have other functions than protease inhibition. Of interest is a recent report that tryptophane metabolism (linked to serotonin neurotransmission) is affected in stefin B (cystatin B) deficient mice, making this protein of potential interest in psychiatric diseases.³³ In EPM1, which will be discussed separately, first trials to replace the protein in affected brain regions by the »protein replacement therapy« have been made.³⁴

Searching for amyloid pathology, cystatin C is a well known amyloidogenic protein causing cerebral amyloid angiopathy (CAA). A rare hereditary cerebral hemorrhage with amyloid angiopathy of Islandic type (HCHWA-I), also termed hereditary cystatin C amyloid angiopathy (HCCAA), occurs upon L68Q mutation.³⁵ Cystatin C was found co-precipitated with A-beta in amyloid plaques³⁶ and inhibited A-beta fibrillation in *in vitro* studies.³⁷ Stefins A and B (cystatins A and B) together with some cathepsins were found in amyloid plaques of different pathologies,³⁸ possibly as a means of unsuccessful clearance by autophagy. That ubiquitin proteasome system (UPS) components are often co-precipitated with amyloid plaques is well known.

Amyloid-fibrillation by stefin B

Amyloid fibrils form *in vitro* in a process governed by external and internal forces. Among the external forces are temperature, solvent components, pH, salt and metal ions. Internal factors arise from protein sequence and structure but no final clue has been obtained, which is the main determinant. Some predictions of the propensity to form amyloid-fibrils were generated from data on known amyloidogenic proteins,^{39,40} which, however, do not hold for all proteins.⁴¹ The question remains whether hydrophobicity, non-fulfilled H-bonds at the edges of the β -strands, aromatic and charged residues, structurally important residues such as prolines and glycines, which render rigidity or mobility to loops, or a combination of all these contribute? Protein structural class seems im-

portant.⁴² It was predicted that proteins of α/β type have to undergo a transition through an α -helical intermediate in the lag phase⁴³ before they enter the fibril growth. It is possible that amyloid-fibril formation under physiological conditions has been avoided by evolution.⁴⁴ This is contradicted by several cases of »functional« amyloids.⁴⁵

Structure and Morphology as a function of solvent and time

Already in 2002, we first reported that this protein forms amyloid-like fibrils *in vitro*.^{46, 47} It was shown that the process of fibrillation starts with a lag phase during which granular aggregate accumulates, composed of globular oligomers (Figure 1A). Further characterization of the mature amyloid fibrils formed by stefin B (Figure 1B) and comparison to stefin A, which is less prone to fibrillise, followed.⁴⁸ In order to gain insight into differences in sequence, which determine the propensity of stefin B to fibrillise, studies of the mutants, among them the chimeras between the two stefins, were performed.⁴¹

In the initial stages of amyloid-fibril formation oligomers are often detected. Soluble oligomers, which accumulate in the lag phase, are believed to be more toxic than the mature fibrils.^{11, 12} In order to design oligomerization inhibitors, which could prevent toxicity, it would be of utmost importance to solve three-dimensional structure of such a pre-fibrillar oligomer.

Stefin B forms well defined oligomers, which appear upon several freeze-thaw cycles, already at neutral pH and can be isolated by gel-filtration. By solving three-dimensional structure of stefin B tetramer⁴⁹ it was shown that oligomerization is strongly coupled to cis-trans proline isomerization. It was revealed that stefin B tetramer is made from two domain-swapped dimers, which swap loops.⁴⁹ Thus, domain swapping has an important role in amyloid-fibril formation of cystatins and, likely, of a number of other proteins.

Morphology and size of the oligomeric particles during the lag phase and subsequent growth phases can be followed using time-resolved transmission electron microscopy (TEM), atomic force microscopy (AFM) and dynamic light scattering (DLS), (Čeru et al., 2008). With such studies we hope to decipher the mechanism of fibrillation. However, the sequence of events is not always clear-cut. There may be parallel routes, and the mechanism depends on the mutant studied and the conditions chosen. To see the influence of various solvent conditions, we have recorded morphology of amyloid-fibrils formed by stefin B at pH 3 and 5, with and without the organic solvent TFE.⁵⁰

Kinetics as a function of protein concentration and temperature

To come closer to the mechanism we decided to study the effects of protein concentration and temperature, respectively, on the fibrillation rates. We then used a set of differential mathematical equations to fit the data (Škerget et al., 2008, submitted). To fit the kine-

tics a model was proposed, taking into account previous studies (both, structural & morphological). The model, which fits kinetic data rather well, predicts a nucleus, in which a number $N_1 = 64$ of, presumably, domain swapped dimers accumulate and undergo a slow conformational change before the fibril growth continues. It also predicts that a side-pathway of trapped oligomers becomes important at higher temperatures than 35 °C and at higher protein concentrations.

From temperature dependence 2 high enthalpic barriers were calculated, consistent with findings in some other amyloidogenic proteins, including A-beta.

Morphology and size of the prefibrillar aggregates and fibrils

The prefibrillar aggregates accumulate in the lag phase of fibril formation, which is either 48 hours at pH 3.3 (high ionic strength) or 170 hours at pH 4.8, 10 % TFE, both at room temperature. Fibrils eventually grow even at pH 4.8, with no TFE added.⁴⁶ The size of the globular oligomers (Figure 1A) is around 12 nm in

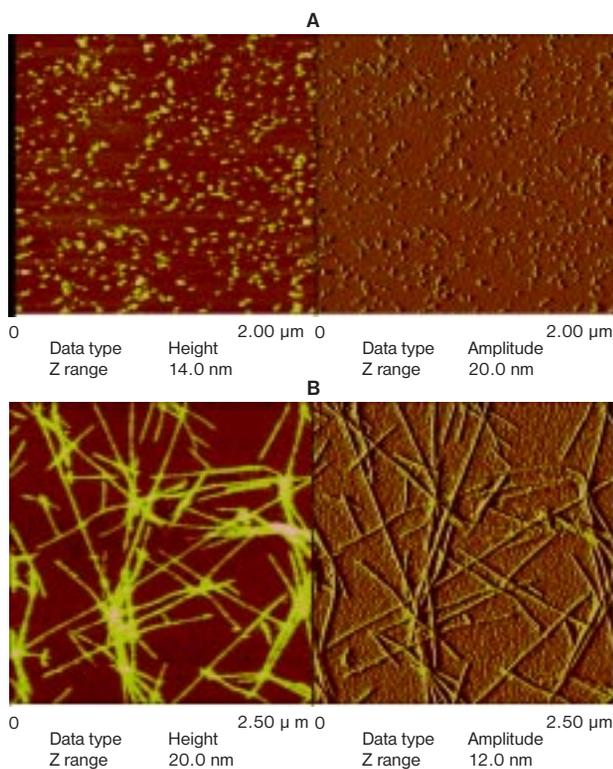


Figure 1. *Atomic force microscopy images. Images were obtained in tapping mode and they represent height variation (left) and the amplitude of the tip (right). We thank Miha Škarabot (IJS, Dept. Condensed Matter Physics), who contributed these data. (A) Globular oligomers making the prefibrillar aggregate. The sample of stefin B aggregates was taken within the lag time of fibrillation and was absorbed on a mica surface for at least 30 s, after which the solvent was blown away by dry air. (B) Mature fibrils. A sample of stefin B fibrils was taken at the end of the fibrillation reaction.*

diameter, which also is the width of the fibrils (Figure 1B). Height of the oligomers and of the fibrils is 3 nm. There also are fibrils with a double height, of around 6 nm.⁴⁸

Interaction of the aggregates with membranes and their cytotoxicity

We have shown that stefin B prefibrillar aggregates composed of globular oligomers (such as those in Figure 1A) interact with predominantly acidic phospholipid membranes and exert cytotoxicity.⁵¹ The aggregates were introduced in the medium in which the cells were incubated over-night. To measure toxicity and co-localization of the aggregates when protein will be expressed in cells, is our next challenge.

EPM1 mutant studies

The majority of idiopathic epilepsies are caused by mutations in genes that code for ion channels (channelopathies). Among the idiopathic epilepsies very rare are purely monogenic, rather they are polygenic. In addition to the idiopathic epilepsies, about 200 single gene disorders are known, in which epilepsy is an important part of the phenotype; among them are the progressive myoclonus epilepsies.

Progressive myoclonus epilepsy of type 1 – EPM1, also known as Unverricht Lundborg disease,⁵² is a serious condition, which, however, does not deteriorate that fast as for example EPM2, also known as Lafora disease. The Unverricht-Lundborg disease occurs mainly in Baltic and Mediterranean regions. It is a progressive myoclonus epilepsy with autosomal recessive inheritance. The onset of disorder is between 6 and 18 years of age, the course is characterized by progressive myoclonic jerks and generalized tonic-clonic seizures. In later stages, the disorder is accompanied by mental deterioration, dysarthria and ataxia. Pathology has shown a marked loss in Purkinje cells in the cerebellum, neuronal loss in the spinal cord and medial thalamus and a proliferation of Bergmann glia.⁵³

Genetic studies have led to discovery of stefin B (cystatin B) as the responsible gene.^{54,55} Most common change reported is the dodecamer repeats expansion in the promoter region of the cystatin B gene (CSTB),⁵⁵ which leads to reduced mRNA and protein levels. New advances in studies of the responsible gene have been made.⁵⁶ There often is the case that one patient is heterozygous, possessing one mutant and one dodecamer repeats gene. In such cases 50–60 % expression of stefin B mutated protein still takes place.⁵⁷

After Suzuki et al., 2004:⁵⁸ »An emerging role appears for several epilepsy genes whose role is in the maintenance of normal neuronal structures, through cell-survival and cell-death pathways. A common epilepsy mechanism may involve abnormalities in functional connectivity that are due to small structural changes in the brain. Subtle increases in specific populations of neurons may be associated with juvenile myoclo-

nus epilepsies (JME), whereas extensive cell death is associated with more severe, progressive myoclonic epilepsies.«

We have determined stability and fibrillation rates of the G4R mutant and the fragment of stefin B to residue 68,⁵⁹ both occurring in some patients with EPM1. First of all, it should be understood that both mutated proteins lack activity as the protease inhibitors (loss of function). In the aggregation study⁵⁹ it was found that the G4R accumulated in a prefibrillar, aggregated state, whereas the fragment was immediately transformed into fibrils. Cellular consequences of the aggregation behavior of the G4R mutant (i. e., accumulation of the toxic prefibrillar aggregates) remains to be seen. Our hypothesis⁶⁰ is that those mutants, which accumulate in the form of prefibrillar aggregates, gain in toxic function, in addition to loss of normal function. In such a case, neurodegenerative changes of EPM1 could perhaps be halted by the same therapeutical approaches that are being introduced in AD or Parkinson's disease, where neuronal renewal, fighting oxidative stress, chelating toxic metals, clearance of cellular inclusions and replacement of damaged genes could be applicable one day.

The group of Melli and co-workers have shown that cystatin B, including the exonic EPM1 mutants, aggregates in the cells, especially under conditions of over-expression. They have observed oligomers in the cell and discovered a polymerizing factor, which promotes oligomer formation. Their thesis is that the oligomers might be functional.⁶¹

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