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## Amyloids: Friend or Foe?

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### Abstract

Amyloidogenesis is the aggregation of soluble proteins into structurally conserved fibers. Amyloid fibers are distinguished by their resistance to proteinase K, tinctorial properties and  $\beta$ -sheet-rich secondary structure. Amyloid formation is a hallmark of many human diseases including Alzheimer's, Huntington's and the prion diseases. Therefore, understanding amyloidogenesis will provide insights into the development of therapeutics that target these debilitating diseases. A new class of 'functional' amyloids promises a unique glimpse at how nature has harnessed the amyloid fiber to accomplish important physiological tasks. Functional amyloids are produced by organisms spanning all aspects of cellular life. Herein we review amyloidogenesis, with special attention focused on the similarities and differences between the best characterized disease-associated amyloidogenic protein amyloid- $\beta$  and the formation of several functional amyloids. The implications of studying functional amyloidogenesis and the strategies organisms employ to limit exposure to toxic intermediates will also be discussed.

### INTRODUCTION

Amyloidogenesis is recognized as being the underlying cause of neurodegenerative diseases such as Alzheimer's (AD), Huntington's and Parkinson's disease. Amyloid fibrils have biochemical and biophysical properties that distinguish them from other biological polymers. Amyloid fibers are incredibly stable, detergent insoluble,  $\beta$ -sheet rich structures that many proteins can form [120]. Amyloid fibers associated with neurodegenerative diseases are considered the product of a protein misfolding event. The pathology of neurodegenerative diseases defined amyloid polymerization as an aberrant process where misfolded proteins aggregate and cause disease. However, there are a number of examples where organisms can utilize either the amyloid fiber itself or intermediates formed during the amyloid polymerization process to fulfill specific biological functions [21,25,30,40,41,64,115,132]. Unlike disease-associated amyloidogenic proteins, functional amyloid assembly is a regulated process that minimizes the cellular toxicity associated with disease-associated amyloids. There are, though, examples where organisms utilize the toxicity of the amyloid fold to carry out a function. Understanding mechanisms that promote functional amyloidogenesis will provide an unprecedented glimpse into amyloidogenic systems in general and will lead to new ideas for preventing disease-associated amyloidogenesis. Guided by this perspective we compare and contrast amyloid- $\beta$  ( $A\beta$ ) amyloidogenesis as it relates to AD to several systems where functional amyloidogenesis occurs presenting ideas about how these functional amyloid systems prevent the build up of amyloid associated toxicity.

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## ALZHEIMER'S DISEASE

AD is the most common neurodegenerative disease. More than 4 million people are afflicted with this neurodegenerative disease in the United States alone (<http://www.ahaf.org/alzdis/about/adabout.htm>). The clinical and neuropathological characteristics were first reported in 1906 by Alois Alzheimer. The abnormal deposits, described as both plaques and tangles, were found in the postmortem diseased brain and were later called amyloid plaques [2]. The plaques were found to be composed of long, unbranched 4–10 nanometer wide fibers when viewed with an electron microscope (Fig. 1A) [65,127]. These structures were discovered to be proteinaceous in nature and contained a uniquely stable cross-beta sheet quaternary structure. Fibers with similar structural characteristics have now been described in other neurodegenerative disorders including Parkinson's disease and Huntington's disease [48,112].

The A $\beta$  polypeptide was purified from AD associated plaques and was determined to be the major protein component of amyloid plaques [43,144]. A $\beta$  is formed when the amyloid- $\beta$  protein precursor (A $\beta$ PP) is sequentially cleaved by  $\beta$ - and  $\gamma$ -secretases [49]. It is proposed that A $\beta$ PP plays important physiological roles in cell adhesion, neurite outgrowth, synaptogenesis and synapse remodeling [148], however, the function of the A $\beta$  polypeptide is currently unknown. There are two major cleavage products, A $\beta$ 40 and A $\beta$ 42 [57]. The primary sequences of A $\beta$ 40 and A $\beta$ 42 only differ in that A $\beta$ 42 has 2 additional C-terminal residues, Ile<sup>41</sup> and Ala<sup>42</sup>. Mutations in presenilins, a central component of  $\gamma$ -secretase, account for most cases of familial AD. These mutations increase the production of A $\beta$ 42 in both transfected cells and transgenic mice [24]. In sporadic AD cases the apolipoprotein E (APOE)  $\epsilon$ 4 allele is the genetic risk factor most often linked to disease onset [106]. In cultured neuronal cells APOE4 enhances A $\beta$  production by modulating A $\beta$ PP processing [146]. In addition, it was reported that APOE4 also modulates the degradation and clearance of deposited A $\beta$  [5,42,69,147].

Several lines of evidence link A $\beta$ PP and misfolded A $\beta$  to AD (for review see [13,45,50]). However, the molecular mechanism behind A $\beta$  misfolding and how this leads to AD remains unclear. Hardy and Selkoe proposed the "Amyloid Cascade Hypothesis" in which the central event in AD development is an imbalance between A $\beta$  production and clearance [55]. The biochemical species of A $\beta$  that induces pathogenesis is still a hotly debated topic. Experimental evidence suggests two models: (1) the final amyloid fiber product causes neuronal damage or (2) neuronal cells are exposed to a toxic intermediates formed as A $\beta$  polymerizes into the amyloid fiber.

*In vitro* self assembly of A $\beta$  polypeptides is characterized by nucleation-dependent polymerization kinetics (Fig. 1B blue line) [61,78]. Before mature fiber aggregates are detectable, there is a time period where the A $\beta$  polypeptide polymerization appears to be stagnant. However, during this lag phase trace amounts of dimer, trimer, and eventually, nucleus (oligomer) are formed (Fig. 1C) [104,105,137]. Nucleus formation is the rate-limiting step of fibril assembly. Once a nucleus has formed, monomer addition to the growing fiber becomes thermodynamically favorable and occurs quickly (Fig. 1B and C) [61]. As with any dynamic polymerization process where different folding intermediates are present at any one time, A $\beta$  monomer, oligomer, protofibrils (short fibrillar aggregates) and fibrils have been observed using different techniques including atomic force microscopy [108,137]. Amyloid formation inhibitors such as Congo red and curcumin potentially reduce neurotoxicity by stabilizing the monomeric state of A $\beta$ , thus reducing the amount of oligomer intermediates formed [79,104,105,145]. Therefore neurotoxicity seems to be linked to aggregation of monomers to higher ordered structures [16,101,102].

Amyloid laden plaques are often found in postmortem AD brains, which led to the suggestion that mature insoluble fiber aggregates of the causative agent for AD. However, statistical analyses have found only a weak correlation between the number of amyloid aggregates and the severity of AD [80,128]. In addition, high molecular weight A $\beta$ 42 aggregates do not correlate with toxicity in the *Caenorhabditis elegans* AD model [27]. The formation of high molecular weight protein aggregates may be a mechanism to protect cells from cytotoxicity by sequestering the toxic intermediates present formed during A $\beta$  misregulation [3,119]. A wide range of nonfibrillar A $\beta$  forms including dimer, trimer, oligomer, spherical aggregates and protofibrils have been reported to be cytotoxic and support this idea [26,56,60,71,75,92,108,130,138]. Different A $\beta$  forms, including the small diffusible A $\beta$  oligomer, high molecular weight oligomer, and fibers effect cortical neurons differently [37]. Collectively, this data suggest nonfibrillar intermediates trigger neuropathologies. Therefore, the development of neurodegeneration could be induced by a complicated combinatory effect of several toxic A $\beta$  conformers including the fibers themselves.

Despite evidence that prefibrillar aggregates may be the causative agents AD toxicity, many researchers have reported that mature A $\beta$  fibers to be toxic to cultured neuronal cells [17,37,56,100,133]. How can this apparently conflicting data be reconciled? Recent study has demonstrated that the amyloid fiber is not a static structure. For instance, amyloid fibers formed from an SH3 domain showed very dynamic properties, in which molecules can be recycled by a dissociation and re-association mechanism within the fibril population [19]. Therefore amyloid fibrils could provide a reservoir for toxic soluble oligomers, which could trigger the pathology [50]. Under different experimental conditions amyloid fibrils may have different potentials to liberate soluble oligomers, which may be cytotoxic to the cultured neurons. Nevertheless, the ability to effectively develop therapeutics that will deter AD development is difficult due to the lack of experimental evidence defining a toxic species. Moreover, the molecular mechanism behind the initial misfolding events that convert soluble A $\beta$  into an amyloid fiber *in vivo* has not been forthcoming. Perhaps exploring systems where amyloid formation occurs as a natural functional process will provide answers to these questions.

## AMYLOID AS A FUNCTIONAL FOLD

### Functional bacterial amyloids

**Curli**—The first example of a functional amyloid fiber was demonstrated in the common laboratory bacterium *Escherichia coli*. *E. coli* and other Gram-negative enteric bacteria produce a functional amyloid fiber called curli (Fig. 2A). These fibers mediate many important physiological functions for the cell. Curli fibers are the major proteinaceous component of the extracellular matrix produced by bacteria during growth in biofilms. Curli also induce a potent host inflammatory response, initiate binding to host cells, and increase the ability of the bacteria to persist within the environment and the host [10,11,73,134,135,139,142]. The genetic and biochemical tools afforded by *E. coli* have provided an in depth look at how bacteria control the assembly of amyloid fibers [21].

Biosynthesis of curli fibers is dependent on two divergently transcribed operons, *csgDEFG* and *csgBA*, both of which are under the control of a complex regulatory network [6,51,109,110]. The *csgBA* operon encodes the minor and major curli subunit proteins, CsgB and CsgA, respectively. The stability and secretion of both CsgA and CsgB is dependent on the outer-membrane localized CsgG protein [21,53,77,107]. The functions of CsgF and CsgE have not been elucidated, but it is clear that CsgE plays an important role in the stability of both CsgB and CsgA, while CsgF is required for efficient curli biogenesis [21].

CsgA and CsgB are the crux of curli fibers. When incorporated into curli fibers, both CsgA and CsgB are detergent insoluble. Cells that do not express CsgB secrete CsgA into the

extracellular milieu as a soluble, unpolymerized protein (Fig. 2B). Therefore, *in vivo* both CsgA and CsgB are required for curli biogenesis. However, CsgA and CsgB do not have to be expressed by the same cell for curli assembly to occur. In a process called interbacterial complementation, CsgA secreted from a *csgB* mutant, or donating cell, can be polymerized by CsgB produced on the surface of a *csgA* mutant or accepting cell (Fig. 2B and C) [21,52,53, 77]. The ability of CsgB to convert CsgA into an insoluble fiber led it to be designated the curli nucleator protein.

CsgA and CsgB are 30% identical and 40% similar at the amino acid level, and each protein has a domain composed of five glutamine-asparagine rich oligopeptide repeats (Fig. 2D) [28, 52,141]. Each glutamine-asparagine rich repeating unit is composed of roughly 20 amino acids and is predicted to form consecutive  $\beta$ -strand loop  $\beta$ -strand motifs that stack perpendicular to the axis of fiber growth (Fig. 2D). Peptides composed of the first, third and fifth oligopeptide repeats of CsgA are amyloidogenic [140]. Mature CsgA protein has been purified, and can self-assemble into curli-like amyloid fibers [21]. *In vitro*, purified CsgA can form amyloid in the absence of CsgB, whereas *in vivo*, CsgA amyloid formation is CsgB-dependent.

CsgA and  $A\beta$  *in vitro* polymerization share common features. First, *in vitro* polymerization of both proteins contains three distinct phases: a lag phase, a growth phase, and a stationary phase (Fig. 1B blue line). Second, in a process called seeding, the lag phase associated with the polymerization of CsgA and  $A\beta$  can be abrogated by the addition of preformed fibers composed of CsgA and  $A\beta$  respectively (Fig. 1B red line) [78,140]. Lastly, a conformation specific antibody recognizes a folding intermediate formed during the lag phase of both protein's self assembly process [63,140]. These polymerization features are characteristic of an assembly mechanism that is dependent on nucleus formation. Nucleus formation is the rate limiting step and must occur before the protein can begin self-assembly into an amyloid fiber (Fig. 1C). While the roles of nucleus formation as it relates to  $A\beta$  polymerization and AD has yet to be elucidated, the curli system is unique in that CsgB's function is to serve as a nucleus for CsgA *in vivo*.

A truncated version of CsgB containing the repeating units most similar to those found in CsgA (R1–R4) was recently purified and also demonstrated the ability to self-assemble into an amyloid fiber (Fig. 2D) [53]. Similar to CsgA and  $A\beta$  polymerization, the polymerization of the truncated CsgB resembled nucleus dependent kinetics displaying a lag phase followed by a polymerization phase, followed by a stationary phase. Fibers composed of the truncated version of CsgB abrogate the CsgA's polymerization lag phase, thus recapitulating *in vivo* curli biogenesis [53]. These results demonstrate that CsgB acts as a template for CsgA polymerization.

The culmination of the experimental evidence suggests *E. coli* has evolved an elegant strategy to control amyloid fiber biogenesis. Curli biogenesis begins when CsgB is secreted and anchored to the outer membrane where it acts as a template for newly secreted CsgA. In a process called nucleation CsgB converts soluble monomeric CsgA into a  $\beta$ -sheet-rich, detergent insoluble protein. Then, in a process called seeding, the growing fiber tip can act as a folding template for additional soluble CsgA monomers. By strictly regulating the *csg* operons and by separating the nucleation process and seeding process into two separate proteins, the cell ensures amyloid fiber biogenesis occurs at the right place and at the right time. This strategy decreases exposure to potentially cytotoxic folding intermediates by promoting mature amyloid fiber formation. Therefore, understanding the molecular basis of curli nucleation and polymerization may provide new insights into how the toxicity of disease-associated amyloids can be reduced.

**Chaplins**—The chaplins are extracellular structures produced by the Gram-positive bacterium *Streptomyces coelicolor*. *In vivo*, these amyloid fibers reduce the surface tension at the media/air interface and allow for the development of aerial hyphae [25,38]. Without the chaplins development of aerial hyphae is impaired [25,38]. Chaplin biogenesis is dependent upon the translational products of the *chpA-H* operon. Like A $\beta$  and CsgA, the chaplins can assemble into  $\beta$ -rich insoluble fibers that bind the amyloid specific dye thioflavin T *in vitro* [25].

Like curli, chaplin amyloid biogenesis is temporally and positionally coordinated. Chaplin expression is dependent on the *bldN* developmental sigma factor, ensuring that fiber formation occurs at the proper time [38]. Furthermore, chaplin amyloid formation is localized to the extracellular space, which may limit exposure to cytotoxic intermediates [25,38].

**Microcin E492 and the harpins**—Two examples of bacteria utilizing the cytotoxic properties of amyloid to deter the growth of neighboring cells have been identified. Microcin E492 (also called Mcc), produced by *Klebsiella pneumoniae*, is a potent antibacterial bacteriocin. Mcc is most active during logarithmic growth, losing most of its cytotoxic properties in stationary phase [34,35]. Bieler and colleagues found that Mcc polymerizes into amyloid fibrils biochemically identical to A $\beta$  and CsgA fibers. Remarkably, the polymerization of Mcc into a mature amyloid fiber coincides with a loss of Mcc antibacterial activity [12]. Thus, a pre-fiber intermediate is proposed to be the cytotoxic species of Mcc [12]. It is also interesting to note that lower concentrations of Mcc are able to induce apoptosis in some human cell lines although the mechanism of Mcc induced apoptosis is currently unknown [59].

The harpins are a second class of bacterial proteins that capitalize on the cytotoxic features of amyloid biogenesis. Produced by plant pathogens, harpins are type-III secreted proteins that induce the hypersensitive response in plants [93]. The hypersensitive response is a plant defense mechanism that slows intracellular pathogen growth by eliciting plant cell death. The hypersensitive response is similar to apoptosis in animal cells [46,47,99]. Oh *et al.* discovered that HpaG, a harpin produced by *Xanthomonas axonopodis* pv. *glycines* 8ra, self assembles into amyloid-like fibers. Unlike Mcc, injection of HpaG protofibrils and mature amyloid fibers into plant cells is toxic and results in cell death. Oh *et al.* also demonstrated that a harpin from *E. amylovora*, HrpN, and a harpin from *Pseudomonas syringae* pv. *syringae*, HrpZ, form amyloid fibers [93]. Both of these harpins elicit the hypersensitive response. A harpin unable to induce the hypersensitive response, XopA from *Xanthomonas campestris* pv. *vesicatoria*, did not form amyloid fibers [93]. However, a gain-of-function mutant form of XopA (F48L/M52L) which does induce the hypersensitive response polymerizes into an amyloid fiber, correlating the ability to induce the hypersensitive response to the ability to form amyloid [93]. The harpins are an example of a functional amyloid fiber that is designed to be lethal.

**Potential bacterial amyloids**—Two recently discovered bacterial structures may be composed of amyloid fibers. *M. tuberculosis* produces a structure that resembles *E. coli* curli fibers. Like curli and other amyloid fibers, the *M. tuberculosis* pili (MTP) are stable and non-branching fibers [1]. Also like curli, MTP bind host extracellular matrix proteins [1]. Structural and biochemical tests including circular dichroism, the ability to bind the amyloid specific dyes Congo red and thioflavin T, and resistance to proteinase K treatment will determine if these pili are in fact amyloid.

The second potential bacterial structure that might be an amyloid is the bacterial endospore. When confronted with environments limited for nutrients some species of bacteria such as *Bacillus* and *Clostridium* initiate the formation of an endospore, a unique structure that is highly resistant to heat, radiation, pH extremes, and toxic chemicals. High resolution atomic force microscopy has revealed that the spore coat of *Bacillus atrophaeus* is composed of fibrils similar

to amyloid [103]. The inner and outer spore coats are composed of over 50 proteins and it is currently unknown which proteins form the fibril species observed and how this structure is assembled [66]. Thus further biochemical characterization of the proteins that form the spore coat, and their amyloidogenicity has not been elucidated. But it makes sense that sporulating bacteria would use the incredibly stable amyloid fiber as protective coat.

### Eukaryotic functional amyloids

**The yeast prion proteins: Eukaryotic functional amyloid domains**—The [*PSI*<sup>+</sup>], [URE3], and [*PIN*<sup>+</sup>] phenotypes of the yeast *Saccharomyces cerevisiae* are defined by non-Mendelian inheritance. These phenotypes are transmitted to daughter cells via a conformationally altered amyloid version of the yeast proteins Sup35p, Ure2p, and Rnq1p, respectively [15,36,68,96,124,143]. Sup35p, Ure2p and Rnq1p all undergo a conversion to an aggregative state that can incorporate soluble protein into an insoluble amyloid aggregate [44,67,68,70,85,97,98,116,121,122,125]. These proteins all contain a glutamine/asparagine (Q/N) rich domain that is essential for [*PSI*<sup>+</sup>] and [URE3] prion propagation [44,85,121,125,126]. In both [*PSI*<sup>+</sup>] and [URE3] this conversion leads to the loss of wild type Sup35p and Ure2p function. The ability to confer a phenotype by converting normally soluble wild type protein into an infectious amyloid aggregate defines these proteins as prions.

**[URE3]/Ure2p**—Ure2p represses the genetic network needed to utilize poor nitrogen sources [29]. When yeast are provided with good nitrogen sources such as ammonia or glutamine, Ure2p binds to the positive transcriptional regulators Gln3p and Gat1p and prevents their translocation into the nucleus [7,14,18,33,54,83]. Yeast carrying the [URE3] prion have little Ure2p activity, and no phenotypic advantages have been demonstrated to correlate with the [URE3] prion. In addition, Nakayashiki et al. noted that 70 natural isolates of yeast do not carry [URE3], suggesting that the Ure2p prion state is not advantageous in a natural setting [90]. However, recent work by Shewmaker et al. demonstrated that Ure2p missing the Q/N domain had substantially reduced stability and activity [113]. Ure2p missing the Q/N domain had reduced steady state levels compared to the wild type protein suggesting the Q/N domain can act to increase Ure2p stability. These data along with the prevalence of the Q/N domain in the yeast proteome, suggest that the Q/N domain, a domain known to promote amyloidogenesis, may also function as a modular protein-stabilizing domain that also initiates protein-protein interactions.

**[PSI<sup>+</sup>]/Sup35p**—The Sup35p protein is an essential component of the translation termination machinery. In [*psi*<sup>-</sup>] yeast, Sup35p recognizes stop codons and terminates protein synthesis [123]. In [*PSI*<sup>+</sup>] cells wild type Sup35p is sequestered in self-assembled amyloid aggregates. Aggregated Sup35p is unable to participate in translational termination, resulting in translational read-through at wild type stop codons and C-terminally elongated proteins. As with [URE3], the [*PSI*<sup>+</sup>] phenotype is propagated through the community as dividing cells transmit the [*PSI*<sup>+</sup>] phenotype to daughter cells [31,32]. Novel work done by True and Lindquist demonstrated that the [*PSI*<sup>+</sup>] prion is advantageous under several growth conditions and may provide an alternative mechanism for phenotypic plasticity during environmental insult by altering the yeast proteome [131]. In addition, the Q/N domain itself has been estimated to be conserved for several hundred million years [23,62,89]. This suggests a strong selection to retain this amyloidogenic domain despite the possible detrimental effects of decreased translational termination fidelity or amyloid associated toxicity. Because some natural isolates of *S. cerevisiae* do not carry [*PSI*<sup>+</sup>], it has been proposed that the [*PSI*<sup>+</sup>] phenotype is not under selective pressure [90]. However, these studies are ongoing and the evolutionary impact of the [*PSI*<sup>+</sup>] phenotype is difficult to assess.

**[PIN<sup>+</sup>]/Rnq1p**—The [PIN<sup>+</sup>] phenotype is defined by the ability to induce the [PSI<sup>+</sup>] phenotype. The Rnq1p protein was discovered to induce [PSI<sup>+</sup>] [121]. Interestingly, the only known function of the Rnq1p protein is to induce the [PSI<sup>+</sup>] phenotype *de novo*. In addition to Rnq1p, Ure2p and New1p can also induce [PSI<sup>+</sup>] when over-expressed [36,94]. Having a protein dedicated to the induction [PSI<sup>+</sup>] suggests that [PSI<sup>+</sup>] maybe advantageous in growth conditions where *rnl1* is expressed. The study determining the prevalence of prions in natural yeast isolates found that the [PIN<sup>+</sup>] prion is present in some yeast found within the environment [90].

**Regulation and coordination of yeast amyloid formation**—Like A $\beta$  and CsgA, Sup35p and Ure2p self assemble into amyloid fibers *in vitro* [39,116,129]. Also like CsgA and A $\beta$  the self assembly process amyloid fiber polymerization contains a distinct lag phase that can be eliminated by the addition of preformed fibers composed of the respective protein [39,116,129,140]. Moreover, like A $\beta$  and CsgA a conformational specific antibody reacts to an intermediate formed during Sup35 polymerization [114,116]. The curli proteins, CsgB and CsgA, are also similar to the yeast prion proteins, Sup35p, Ure2p, and Rnq1p, in that they all contain the Q/N rich domains [76,94]. In fact, the GNNQQNY peptide found within the Q/N rich domain of Sup35p forms biochemical distinct amyloid fibers [4]. This peptide has been used to examine the cross-beta structure of amyloids at high resolution using X-ray crystallography [91]. Also like CsgA and CsgB, oligopeptide repeats are found within the Q/N domain of Sup35p that aid the propagation and amyloidogenicity of the [PSI<sup>+</sup>] phenotype [76,95]. The Q/N domain of Rnq1p also contains several imperfect oligopeptide repeat sequences that are important for the propagation of [PIN<sup>+</sup>] [136]. In addition to Sup35p, Ure2p, and Rnq1p, 104 other polypeptides in the *S. cerevisiae* proteome contain Q/N rich domains [87]. However, their ability to form amyloid has not been demonstrated.

The conversion to the prion state for each of [PSI<sup>+</sup>], [URE3] and [PIN<sup>+</sup>] occurs at a low rate [81,143]. Even though the conversion rate to the prion state is low, yeast employ molecular chaperones called heat shock proteins to limit exposure to any toxic intermediates formed during prion propagation. Heat shock proteins, such as heat shock protein 104 (Hsp104), play an essential role in modulating the prion state. Propagation of [PSI<sup>+</sup>], [URE3], and [PIN<sup>+</sup>] all require Hsp104p as deletion of Hsp104 ‘cures’ (i.e. the prion phenotype no longer propagates to daughter cells) cells from [PSI<sup>+</sup>], [URE3] and [PIN<sup>+</sup>]. However, overexpression of Hsp104p also cures [PSI<sup>+</sup>] and overexpression of Ydj1p, a member of the Hsp40 family of proteins, cures cells of the [URE3] prion [22,88,121]. Shorter and Lindquist reconciled these seemingly contradictory findings by demonstrating that *in vitro* low concentrations Hsp104 catalyzed the formation of intermediates critical for Sup35p and Ure2p fiber formation, while high concentrations of Hsp104 completely abrogated the ability of both proteins to form an amyloid [114,116]. These data suggest that Hsp104 may sequester toxic intermediates as well as decrease the time cells are exposed to such intermediates. These findings also suggests that another mechanism heat shock proteins employ to limit exposure to toxic folding intermediates is to speed the formation of an amyloid fiber to the fiber final product.

**Filamentous fungi Het-S amyloid**—Vegetative cell fusions occur within and between individual cells of the filamentous fungi *Podospora anserina*. These fusion events lead to cytoplasmic mixing and the production of a vegetative heterokaryon or multinucleated cells. The *het* locus controls the viability of the fused fungi, whereby heterokaryons that differ at the *het* locus are destroyed. This process is called heterokaryon incompatibility (For review see [111]). The *het* locus has two alleles, *het-s* and *het-S*. Het-S is the soluble protein product of the *het-S* loci while the protein product of the *het-s* loci, Het-s, has the ability to convert to an aggregated prion state. When fusion between a *het-S* cell and a *het-s* cell occurs the aggregated Het-s interacts with soluble Het-S and this interaction induces the incompatibility reaction. This leads to death of the heterokaryon and prevents any fusion from occurring between the

two cells [30]. Maddelein et al. demonstrated that the heterokaryon incompatibility reaction is induced when cells are transformed with amyloid fibers composed of recombinant Het-s. The incompatibility reaction is not induced when a soluble version of Het-s was transformed into cells. This result provided direct experimental evidence that strengthened the protein only prion hypothesis [82]. The molecular mechanisms of Het-s-induced cell death are currently unknown.

**CPEB**—CPEBs are highly conserved RNA-binding proteins localized at neuronal synapses that stabilize messenger RNA molecules [86]. CPEBs have been found to be important for memory retention due to their ability to activate dormant messenger RNA transcripts near neuronal synapses. These activated messages can then be translated into proteins that stabilize neuronal synapses or help create synaptic connections necessary for long term memory [117]. The CPEB protein of the sea hare, *Aplysia californica* (ApCPEB), contains a Q/N rich domain. Si et al. demonstrated that ApCPEB acts as a prion in yeast and that the aggregative amyloid state of CPEB is the functional, RNA-binding, form of the protein [118]. Thus, ApCPEB is functionally active when polymerized into amyloid aggregates, whereas, the wild type functions of Ure2p and Sup35p are impaired when the proteins are aggregated. It has yet to be elucidated if CPEB folds into an amyloid in neuronal cells, but the ability of the protein to do so in yeast suggests it has the capability to do so in other cell types.

**Pmel17**—Melanocytes and retinal pigment epithelium are specialized cell types responsible for the production of melanin, a tyrosine based polymer that protects the mammalian eyes and epidermis from ultra-violet damage and other environmental insults. These cells types synthesize melanin within specialized membrane enclosed vesicles called melanosomes [58, 72,84]. Melanosome maturation and polymerization of melanin are dependent on insoluble fibers composed of the PMEL17 protein [8,9,20,64,74]. Fowler and colleagues demonstrated that fibers composed of PMEL17 contain the biochemical hallmarks of amyloid [40]. PMEL17 amyloid fibers function by kinetically enhancing the polymerization of melanin, presumably by acting as a scaffold for reactive melanin precursors [40]. Mammalian cells have evolved several mechanisms to reduce exposure to toxic folding intermediates produced by PMEL17 amyloid polymerization: (1) polymerizing the amyloid fiber in a membrane enclosed vesicle sequestering folding intermediates from the cytoplasm, (2) regulating the start of polymerization via proteolysis, and (3) using reaction kinetics that skew towards the stability of the mature amyloid fiber [40,41].

## CONCLUDING REMARKS

Despite over twenty years of AD research the nature of the toxic species of  $A\beta$  has yet to be conclusively identified and little is known about how  $A\beta$  polypeptide aggregation begins *in vivo*. Insights into these two critical phenomena will undoubtedly lead to advances in AD treatments. The functional amyloids may hold the key to understanding the molecular mechanisms of amyloid fiber toxicity and initiation of amyloid fiber polymerization because they are naturally occurring directed polymerization processes. Not only are the amyloid fiber end products in both AD and the functional amyloid systems biochemically similar, but a common intermediate has been identified for CsgA, Sup35p, and  $A\beta$  polymerization. This suggests that amyloid biogenesis occurs via a conserved mechanism. Interestingly, most of the directed amyloid synthesis pathways discussed herein polymerize to higher order aggregates/fibers *in vivo* and these fibers have physiological nontoxic roles in most cases. A folding intermediate of Mcc amyloid fibers is cytotoxic but not the mature amyloid fiber itself. Thus, it seems likely that the functional amyloids lend credence to the hypothesis that the fiber end product may not be toxic. The role of the chaperone Hsp104 in yeast prion propagation also supports this idea. At high concentrations the chaperone abrogates amyloid fiber polymerization, but at low concentrations Hsp104 kinetically accelerates fiber formation.



These results demonstrate two mechanisms cells use to sequester the build up of toxic intermediates. Chaperones either bind the aberrant toxic intermediate, which allows the protein the opportunity to refold, or the chaperone binds to a fiber intermediate and facilitates the conversion to the amyloid form.

These functional amyloid synthesis pathways will continue to provide novel insights regarding amyloid biogenesis. The functional amyloid systems may even address pivotal questions that remain for AD progression such as, how does amyloid biogenesis begin *in vivo*, what is the most cytotoxic species produced during amyloid biogenesis, and what are the defining features of proteins that preclude the ability to fold into the amyloid conformation. The answers to these questions will in turn provide novel therapeutic strategies for treating disease associated amyloidosis such as AD.

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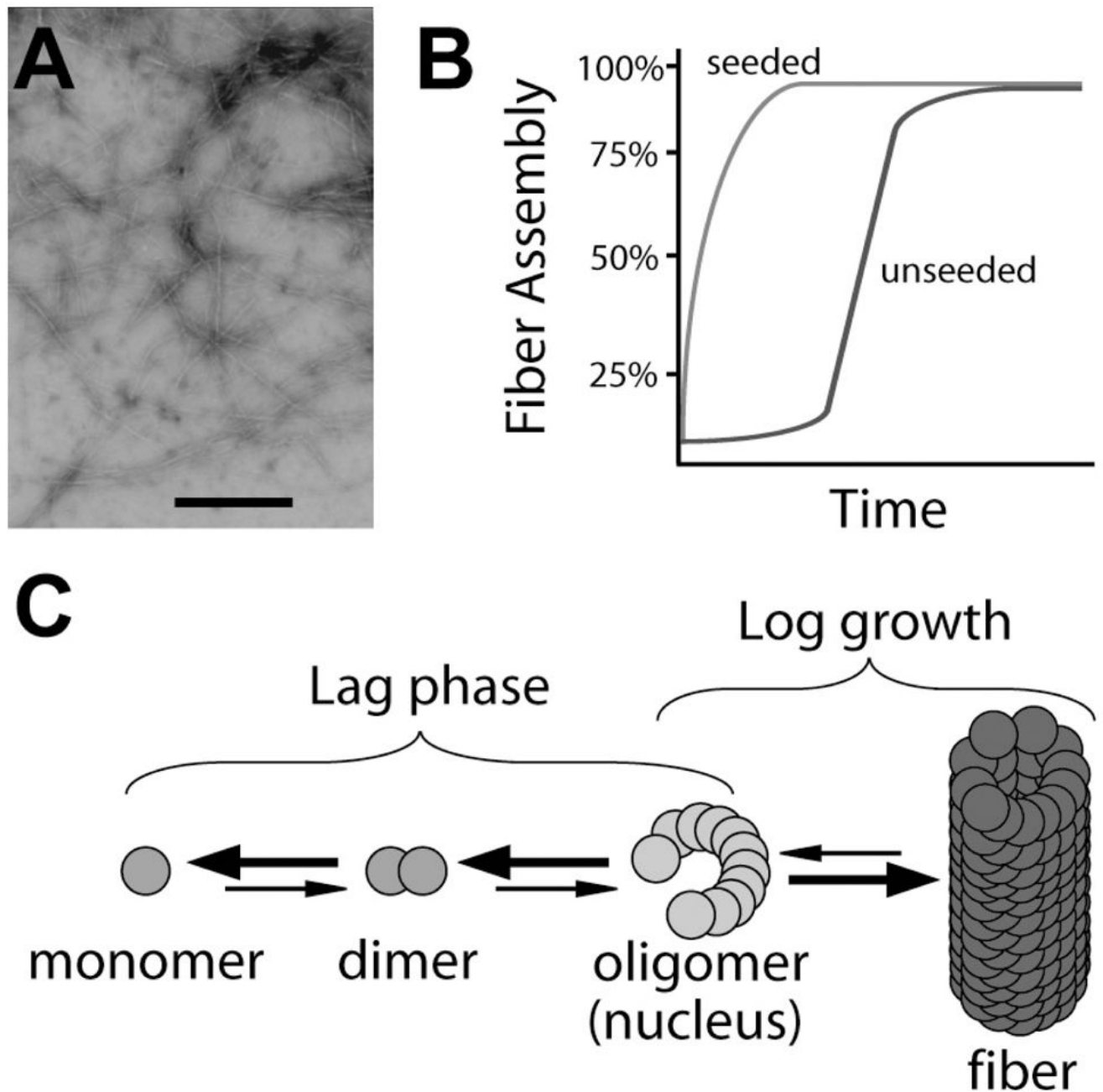
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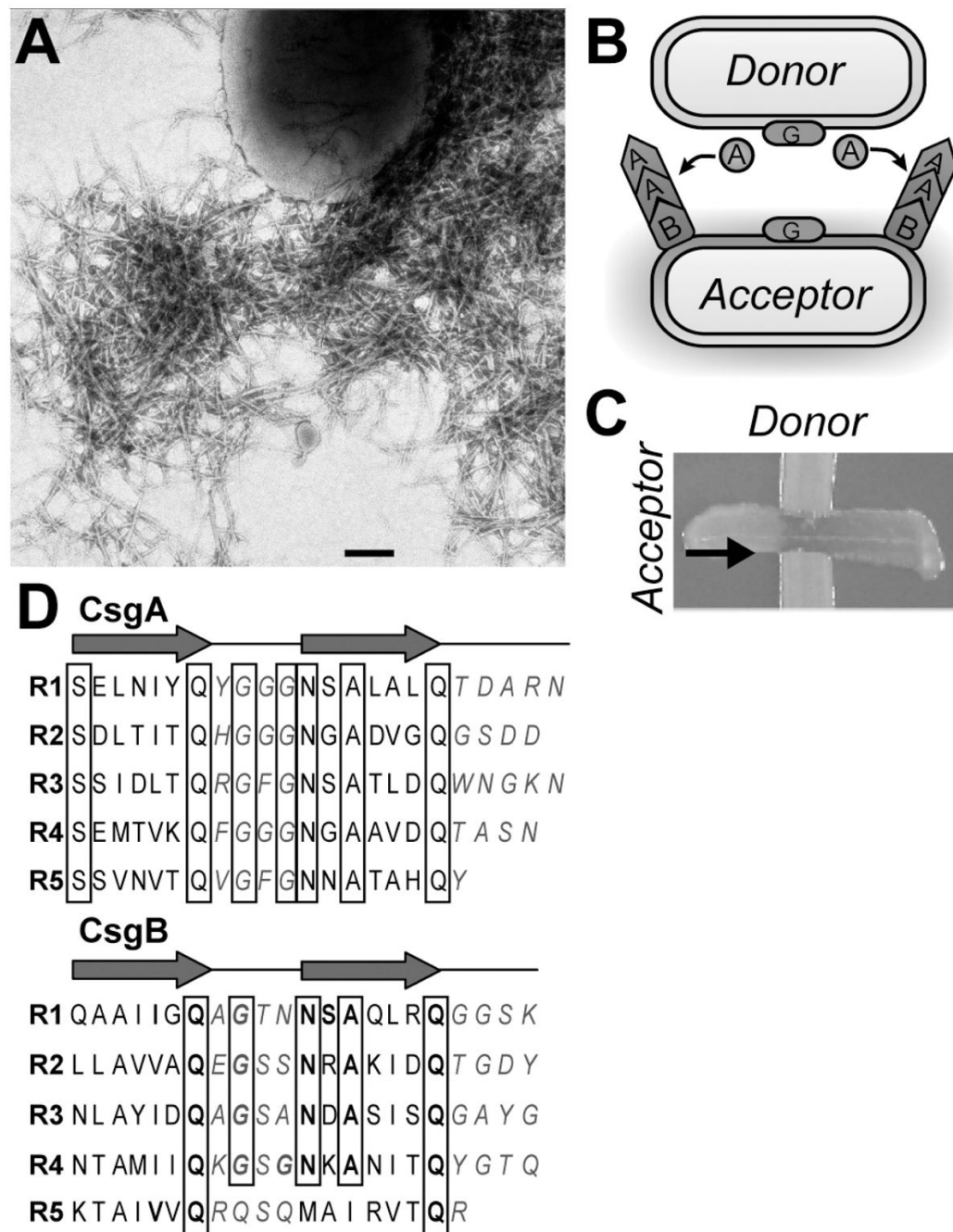
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**Fig. 1.** Properties of amyloid polymerization. (A) Negatively stained electron micrograph of polymerized  $A\beta$  fibers. The scale bar represents 500 nanometers. (B) A graphic representation of amyloid fiber polymerization displaying nucleus dependent kinetics (blue line). Preformed amyloid fibers can act as seeds to speed the kinetics of fiber polymerization (red line). This process eliminates the lag phase associated with nucleus formation. (C) Model of amyloid fiber polymerization. A build up of monomer occurs which leads to the formation of multimers and finally the amyloid fiber end product. Large arrows represent processes that are energetically favorable while small arrows represent energetically unfavorable processes.



**Fig. 2.** Interaction between the curli subunit proteins CsgA and CsgB. (A) Negative stain electron micrograph of wild type cells producing curli. Scale bar represents 200 nanometers. (B) Model of Interbacterial Complementation. A donor cells secretes soluble CsgA that acts as a substrate for CsgB on an acceptor cells where curli biogenesis takes place. (C) A Congo red indicator plate demonstrating interbacterial complementation. The donor cells and the acceptor cells appear white until the two strains intersect. Once the two cell types intersect Congo red binding occurs demonstrating curli fiber polymerization as taken place. The arrow represents the direction in which the acceptor cells were streaked onto the plate. (D) The oligopeptide repeating units that compose the CsgA and CsgB proteins. The three dimensional structures

of CsgA and CsgB are predicted to be composed of five imperfect  $\beta$ -strand-loop- $\beta$ -strand oligopeptide repeats (R1–R5). Amino acids comprising the  $\beta$ -strand are located below the arrows, and amino acids predicted to comprise the loops are denoted with italicized blue letters. Bolded letters represent amino acids conserved in CsgB and CsgA at each position relative to the start of each repeating unit. Boxed letters represent amino acids conserved throughout the repeating units in both proteins.