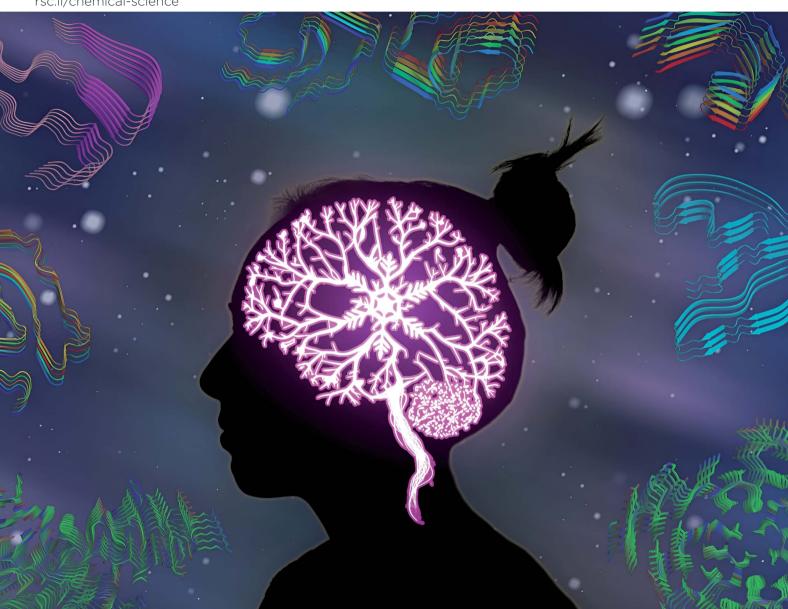
Volume 15 Number 1 7 January 2024 Pages 1-400

Chemical Science

rsc.li/chemical-science



ISSN 2041-6539



Chemical Science



PERSPECTIVE

View Article Online



Cite this: Chem. Sci., 2024, 15, 46

d All publication charges for this article have been paid for by the Royal Society of Chemistry

Received 31st July 2023 Accepted 27th September 2023

DOI: 10.1039/d3sc03981a

rsc.li/chemical-science

The supersaturation perspective on the amyloid hypothesis

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Development of therapeutic interventions for Alzheimer's over the past three decades has been guided by the amyloid hypothesis, which puts AB deposition as the initiating event of a pathogenic cascade leading to dementia. In the current form, the amyloid hypothesis lacks a comprehensive framework that considers the complex nature of A β aggregation. The explanation of how A β deposition leads to downstream pathology, and how reducing AB plaque load via anti-amyloid therapy can lead to improvement in cognition remains insufficient. In this perspective we integrate the concept of Aβ supersaturation into the amyloid hypothesis, laying out a framework for the mechanistic understanding and therapeutic intervention of Alzheimer's disease. We discuss the important distinction between in vitro and in vivo patterns of AB aggregation, the impact of different aggregation stages on therapeutic strategies, and how future investigations could integrate this concept in order to produce a more thorough understanding and better treatment for Alzheimer's and other amyloid-related disorders.

The amyloid hypothesis

Protein aggregation is associated with a wide range of human disorders such as Alzheimer's disease and type 2 diabetes. 1,2 The end-product of protein aggregation in these disorders is called amyloid,3 and the amyloids formed by different proteins share

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Molecular Biology at UCLA, studying protein structures with electron paramagnetic resonance techniques under the supervision of Dr Wayne Hubbell. After doing postdoctoral research on amyloid structures with Dr David Eisenberg, he joined the faculty at UCLA Department of Neurology in 2008. His research group is interested in the mechanistic and structural studies of protein aggregation involved in neurodegenerative diseases, with an emphasis on Alzheimer's disease. His long-term goal is to develop preventive and therapeutic interventions that target protein aggregation in these debilitating disorders.

some common properties such as binding to thioflavin T4,5 or cross-β structures.^{6,7} Recent breakthroughs in cryo-EM have led to the elucidation of the structures of many amyloid proteins, showing a diverse structural landscape.7,8

Alzheimer's disease has two main pathological hallmarks, the senile plaques consisting of the AB protein and the neurofibrillary tangles that are composed of tau.9-12 Aβ protein is produced from the sequential cleavage of amyloid precursor protein by β- and γ-secretases. The γ-secretase cleavage generates two main types of AB proteins: the 40-residue AB40 and the 42-residue Aβ42, with Aβ42 having two extra amino acids at the C-terminus. Although the overall concentration of Aβ40 is several fold more than that of Aβ42,14,15 the main component of the senile plaques is Aβ42.16,17

In 1992, Hardy and Higgins¹⁸ presented the amyloid hypothesis, which states that Aβ, "the main component of the plaques, is the causative agent of Alzheimer's pathology, and that the neurofibrillary tangles, cell loss, vascular damage, and dementia follow as a direct result of this deposition." Over the years, the amyloid hypothesis has been constantly re-evaluated in light of new experimental discoveries, 19-21 and has remained as the prevailing theory guiding therapeutic development for Alzheimer's disease.22,23 One notable development is the inclusion of Aβ oligomers in the amyloid hypothesis.²⁴ Mechanistic understanding of AB aggregation in terms of primary and secondary nucleation suggests that amyloid fibrils catalyze the formation of oligomers,25 linking oligomers to the overall process of Aβ aggregation.

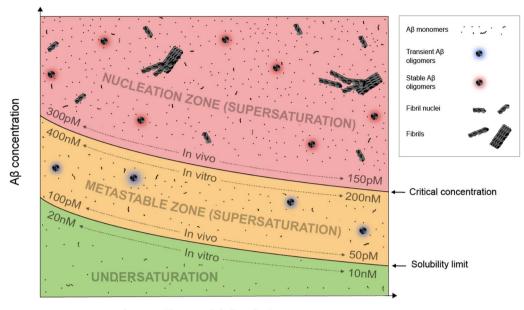
While earlier failures of anti-Aß clinical trials have led to criticism of the amyloid hypothesis, the full FDA approval of anti-Aß antibody lecanemab (marketed as Legembi) in July 2023 was a turning point in Alzheimer's research.26 Unlike the controversial aducanumab (Aduhelm),27,28 the findings of lecanemab are straightforward and robust. In the phase 3 trial, lecanemab slowed cognitive decline by 27% on the primary endpoint and also met all key secondary endpoints.29 The data from the lecanemab trial are widely considered as a validation of targeting Aβ aggregates as a disease-modifying therapy.^{30,31} The phase 3 trial data of donanemab, an antibody targeting pyroglutamated AB, show that donanemab treatment slowed clinical decline by 35% and met all secondary endpoints, further demonstrating the clinical benefits of anti-amyloid therapy.32

Basic concepts of supersaturation in the context of Aβ aggregation

Supersaturation is a well-known concept in the field of protein crystallization, which, like protein aggregation,33 is a nucleation-dependent polymerization process.34,35 Supersaturation is a non-equilibrium state in which protein concentration exceeds the solubility limit. Equilibrium is restored when aggregates or crystals are formed and the protein concentration reaches the solubility limit. Through a series of elegantly designed experiments, Goto and colleagues have demonstrated that protein aggregation is driven by the same principle of supersaturation.36,37 Vendruscolo and colleagues88,39 examined cellular protein concentrations relative to their solubility limit and found that neurodegeneration-related pathways are enriched in proteins at supersaturated concentrations.

Fig. 1 depicts an AB phase diagram in the context of aggregation. The Aß solubility curve divides the phase diagram into two regions: undersaturation and supersaturation. The supersaturation region is further divided into two zones: metastable zone and nucleation zone. The boundary between the nucleation and metastable zones corresponds to the "critical concentration" for Aβ aggregation. 40,41 Below we describe seven key points of AB aggregation in the framework of supersaturation.

- (i) Aβ aggregation requires a supersaturated solution. Protein aggregation involves two distinct steps: fibril nucleation and growth. Fibril nucleation requires overcoming of a kinetic or energy barrier to form structurally ordered fibril nuclei and is thus the rate-limiting step. Fibril growth is an energetically favorable reaction. Both fibril nucleation and growth require supersaturation. Changes in solution pH and addition of salts, ions, or polymers are often used to alter the properties of proteins, the chemical potential of the solution, or interactions between proteins to achieve supersaturation. In a typical in vitro aggregation experiment, AB stock solutions in denaturing buffers such as urea or organic solvents such as dimethyl sulfoxide are mixed with a native buffer to immediately create a supersaturated solution. Depending on the concentration, AB would aggregate immediately or after a lag time.33
- (ii) To spontaneously aggregate, Aβ concentration needs to be in the nucleation zone of supersaturation. When AB concentration exceeds the solubility limit, it does not immediately form the stable fibril nucleus. The energy barrier for nucleation allows Aβ concentrations to increase further from the solubility limit and into the zone of supersaturation. The supersaturation zone that results in spontaneous nucleation of Aβ fibrils is referred to as the nucleation zone. For in vitro aggregation, Hellstrand et al.40 reported that there was no spontaneous Aβ42 aggregation when Aβ concentration was between 10 and 200 nM. Aβ42 aggregation was observed at Aβ42 concentrations higher than 260 nM, which defines the boundary between the nucleation zone and metastable zone under their aggregation conditions.40
- (iii) Within the nucleation zone, higher Aβ concentrations lead to faster nucleation rates. The further away from the solubility limit, the higher energy Aβ accumulates. As a result, Aβ at higher concentrations aggregate at a faster rate. Hellstrand et al.40 studied the aggregation of Aβ42 at a wide range of concentrations, and found that AB concentration has a linear relationship with the logarithmic value of the aggregation lag time. A β 42 at 0.26 μ M has a lag time of \sim 24 h, whereas A β 42 concentrations at $>5 \mu M$ observe almost no lag time.
- (iv) AB in the metastable zone of supersaturation does not spontaneously initiate aggregation, but can aggregate in the presence of pre-formed aggregates, often referred to as "fibril seeds". While spontaneous fibril nucleation needs to overcome an energy barrier, fibril-seeded aggregation is a much more energetically favorable reaction. Cohen et al.25 showed that Aβ



Aggregation modulating factors

Fig. 1 A phase diagram of Aβ supersaturation. Both Aβ concentration and environmental factors affect the phase diagram. In the undersaturation zone, A β exists mostly as monomers. The area of supersaturation consists of a metastable zone and a nucleation zone. In the metastable zone, A β exists as monomers and transient oligomers, and does not spontaneously aggregate but can aggregate in the presence of aggregate seeds. In the nucleation zone, Aß can aggregate spontaneously and exists as a mixture of soluble Aß monomers, stable oligomers, fibril nuclei, and fibrils.

aggregation in the presence of even small amounts of amyloid fibrils is dominated by fibril-catalyzed secondary nucleation reactions, rather than the classical mechanism of primary nucleation.

(v) Once aggregation starts, it will continue until the protein concentration reaches the solubility limit. Because the supersaturation is a non-equilibrium state, initiation of protein aggregation will restore the equilibrium state of saturation, where solubilization of AB from fibrils and fibrillization of AB from monomers reach equilibrium. Hellstrand et al.40 found that, with starting concentrations ranging from 0.2 to 10 µM, the soluble Aβ concentration at the end of aggregation converge to approximately 15 nM, suggesting that Aβ42 solubility is approximately 10-20 nM for the specific aggregation conditions of their study. For in vivo Aβ concentrations, Portelius et al.⁴² found that the Aβ42 concentrations in the cerebrospinal fluid of familial Alzheimer's patients are similar to the sporadic Alzheimer's patients, even though this familial mutation has been shown to increase plasma Aβ42 levels at preclinical stage. 43 The implications of these studies are that even though familial mutations of Alzheimer's disease changed the AB concentrations and thus result in increased aggregation propensity, the Aβ aggregation in the post-amyloid stage is similar to that in sporadic Alzheimer's patients because the AB solubility for these patients are similar.

(vi) An Aβ solution in the presence of aggregates can no longer maintain supersaturation. Due to the presence of seeded aggregation, an increase in Aβ concentration above the solubility limit will lead to aggregation. As a result, Aβ concentration can no longer maintain supersaturation. A direct in vivo

implication of this point is that AB concentrations in amyloidpositive individuals cannot reach the same level as amyloidnegative individuals. After injecting isotopically-labeled $\ensuremath{\mathsf{A}\beta}$ into the interstitial fluid, Hong et al.44 found that the recovered Aβ from plaque-rich mice is only 45% of that from plaque-free mice, supporting the notion that most of the newly produced Aβ proteins deposit to amyloid plaques.

(vii) In the presence of a large amount of aggregates, Aβ concentration cannot become undersaturated, because the aggregates can be solubilized when protein concentration reaches below the solubility limit. For individuals that are amyloidpositive, this means that the AB clearance pathway will not be able to lower Aβ concentrations as much as in amyloid-negative individuals. It has been shown that, in plaque-free mice, acute inhibition of γ -secretase activity led to rapid decline of A β 42 concentration.44 In contrast, plaque-rich mice showed significantly less concentration reduction, supporting the role of amyloid plaques as a reservoir of soluble Aβ.44

Difference in the Aβ phase diagram for in vitro and in vivo conditions

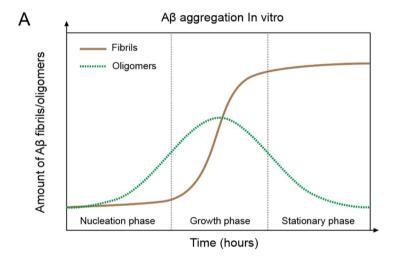
The exact parameters that define the A β phase diagram under *in* vitro and in vivo conditions are vastly different. The extensive study by Hellstrand et al. 40 of Aβ42 aggregation in vitro at a wide range of Aβ42 concentrations put Aβ42 solubility at approximately 10-20 nM and Aβ42 critical aggregation concentrations at approximately 200-400 nM. For in vivo conditions, it is not possible to perform any controlled aggregation studies.

However, some parameters of the phase diagram can be implicated from biomarker studies in Alzheimer's patients. Because $A\beta$ solubility is defined as the $A\beta$ concentration in the presence of amyloid plaques, we used the cerebrospinal fluid (CSF) Aβ42 concentrations in the amyloid-positive individuals as an approximation of Aβ42 solubility and CSF Aβ42 concentrations in the amyloid-negative individuals as an approximation of Aβ42 critical concentrations. With these assumptions, the Aβ42 solubility in vivo was estimated to be 50-100 pM and Aβ critical concentration was estimated to be 150-300 pM. 15,45,46 The Aβ42 concentration for in vitro aggregation differs from in vivo aggregation by approximately three orders of magnitude. Part of the reason for the extremely low critical concentration of in vivo Aβ42 aggregation may be the presence of aggregationpromoting factors such as lipids, membrane surfaces, and interacting proteins.

We note that each individual may have a distinct *in vivo* phase diagram that determines their individualized $A\beta$ aggregation behavior. The $A\beta$ solubility and the boundary of the

nucleation zone are determined by the local concentrations of proteins, lipids, and metabolites. A wide range of A β concentrations have been observed in amyloid-positive individuals. ^{15,45} Based on the supersaturation theory, A β concentrations in the presence of amyloid plaques correspond to the solubility limit, and thus these results suggest a wide range of A β *in vivo* solubility in different individuals.

Aβ40 modifies the phase diagram of Aβ42 aggregation by interacting with Aβ42. As a result, Aβ42/Aβ40 ratio is a more reliable descriptor of Aβ42 aggregation propensity than the absolute Aβ42 concentration alone. The interaction alone accomprehensive study of 138 pathogenic present mutations, Sun et al. The found that a quarter of the present producing lower levels of Aβ42 exhibited a compromised ability to produce Aβ40, leading to a higher Aβ42/Aβ40 ratio. The work of Sun et al. Suggests that familial Alzheimer's disease mutations modulate the phase diagram of Aβ42 aggregation through not only Aβ42 concentrations, but also Aβ42/Aβ40 ratio.



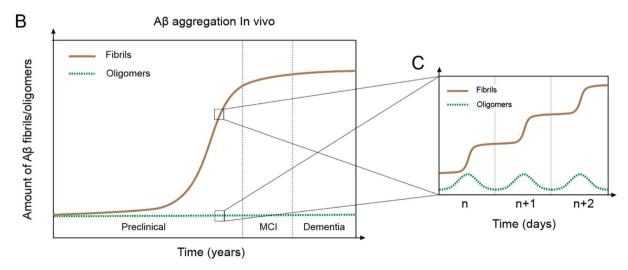


Fig. 2 In vivo and in vitro $A\beta$ aggregation curves. (A) $A\beta$ aggregation in vitro leading to fibril formation (brown line) shows a typical sigmoidal curve with three phases: nucleation, growth, and stationary. Oligomers (green line) first appear in the nucleation phase but disappear towards the end of the aggregation process. (B) $A\beta$ aggregation in vivo displays a similar sigmoidal curve of fibril formation as the *in vitro* system, but with fundamentally different features. (C) In vivo day-to-day $A\beta$ aggregation shows a sigmoidal curve and oligomer formation.

Comparison between *in vivo* and *in vitro* Aβ aggregation

In vitro Aβ aggregation kinetics are typically represented by a sigmoidal curve, ^{33,50} which consists of three phases: nucleation, growth, and stationary (Fig. 2A). The rate of *in vitro* aggregation can be measured by the length of the nucleation phase, also called "lag time". Using chemical kinetics and mathematical modeling, Dear *et al.*⁵¹ show that oligomers are transiently formed during the process of fibrillization and disappear towards the end of the aggregation reaction. The secondary nucleation process⁵⁰ also leads to the formation of toxic oligomers, suggesting that oligomer formation may be an integral part of the overall Aβ aggregation process.⁵² Cryo-EM studies have revealed mechanistic insights into the fibril-catalyzed secondary nucleation.⁵³

Accumulation of A β plaques *in vivo* appears to show a similar sigmoidal curve^{21,54} (Fig. 2B), but the nature of the *in vivo* A β aggregation curve is fundamentally different from the *in vitro* aggregation curve. *In vitro* A β aggregation is a closed system, transitioning from a non-equilibrium state consisting of a supersaturated solution to a final equilibrium state consisting of A β fibrils and a saturated A β solution. *In vivo* A β aggregation, on the other hand, is an open system, constantly replenishing and

removing A β through production and clearance pathways. Because A β production and clearance is under the control of the 24-hour circadian clock, A β aggregation *in vivo* likely also has a circadian rhythm, with a daily sigmoidal aggregation curve (Fig. 2C). A β oligomers, due to their association with the A β aggregation process, are also produced as part of the daily aggregation process.

In vivo A β concentration dynamics in the framework of A β supersaturation

Based on the framework of A β supersaturation, the A β concentrations of two imaginary individuals are plotted in Fig. 3A. One is an amyloid-negative individual, who never develops amyloid and dies amyloid-free. This amyloid-negative individual's A β concentration is simplified as a linear line, showing the overall increase in A β concentration over this person's adult lifetime. The A β concentration of this amyloid-negative individual stays in the metastable zone. The other imaginary person is an amyloid-positive individual who develops amyloid deposition later in life. The age-dependent changes of A β concentration over the amyloid-positive individual's adult lifetime can be divided into four phases: soluble phase, burst phase, reduction phase, and stationary phase (Fig. 3A). The burst phase is a prediction based on the framework of supersaturation because spontaneous A β

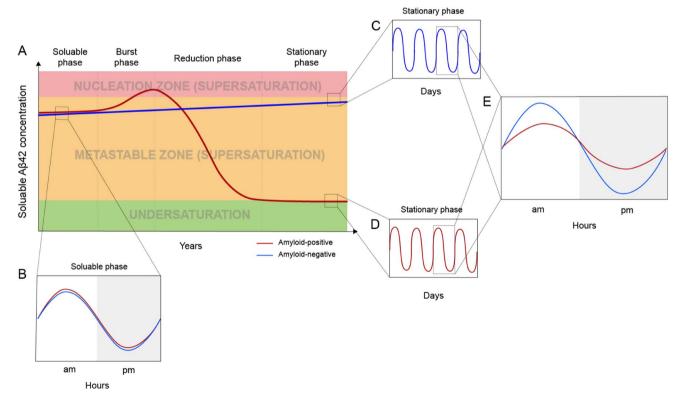


Fig. 3 In vivo Aβ dynamics in the framework of supersaturation. (A) Two imaginary individuals are considered here: one eventually becomes amyloid-positive (red line) and the other one remains amyloid-negative (blue line). The Aβ concentration in the amyloid-negative individual has a slow linear increase but never goes into the nucleation zone. For the amyloid-positive individual, Aβ concentration can be divided into four phases: soluble, burst, reduction, and stationary. (B) Before amyloid formation, the amyloid-positive individual and the amyloid-negative individual display highly similar circadian fluctuations. (C and D) Daily modulation of soluble Aβ42 in amyloid-negative (C) and amyloid-positive (D) individuals. (E) After amyloid formation, the amyloid-positive individual has a dramatically reduced circadian amplitude as a result of amyloid formation.

aggregation requires Aβ concentration to be in the nucleation zone. This can be achieved by an accelerated increase in AB concentration, a "burst", where AB concentration crosses the threshold into the nucleation zone (moving up along the Y-axis of Fig. 1). This could also be achieved by lowering the boundary of the nucleation zone because variations in in vivo environments can modulate the boundaries between the two zones of the supersaturation and even the solubility limit of Aβ (moving right along the X-axis of Fig. 1). The reduction phase is when spontaneous Aß aggregation starts and eventually leads to a lower Aß concentration. The stationary phase can be classified as the stage when the Aβ concentration reaches a steady-state. Mild cognitive impairment and dementia appear years or decades into the stationary phase.58 Studies have been performed to compare the amyloid-positive group and amyloid-negative group in the stationary phase, and show that the AB concentration in the amyloid-positive group is markedly lower than that in the amyloid-negative group. 15,59 In addition to lowered Aβ concentration, amyloid formation also leads to a reduction in the amplitude of AB circadian fluctuations (Fig. 3E).

Post-amyloid Aß dynamics and circadian rhythm

Aβ concentration has a circadian rhythm.⁵² Amyloid formation leads to reduced overall AB42 concentration and reduced amplitude of the Aβ42 circadian rhythm. Since Aβ can no longer maintain supersaturation in the presence of plaques, the postamyloid A β concentration is close to A β 's in vivo solubility. For the same individual, the post-amyloid Aβ concentration is likely lower than the pre-amyloid AB concentration. Bateman and colleagues¹⁵ studied the circadian dynamics of Aβ concentration and found that the circadian amplitude in amyloid-negative group is 15.6 pM, almost 3-fold higher than the circadian amplitude of the amyloid-positive group (6.3 pM).

Both the lowered Aβ42 concentration and diminished circadian rhythm over a long period of time may be pathogenic and contribute to cognitive decline and dementia. Aß is an evolutionarily conserved protein,60 although its precise physiological function has not been conclusively established.⁶¹ The reduced amplitude in AB circadian rhythm may underlie the sleep disturbances associated with amyloid deposition.⁶² In an analysis of 598 amyloid-positive individuals, Sturchio et al.63 found that normal cognition is associated with preservation of soluble Aβ42 concentrations, suggesting that sufficient Aβ42 concentrations are critical for cognition. In a cellular model, Zhou et al. 64 showed that restoring physiological amounts of AB in APP-deleted neurons elevated synapse number and synaptic transmission, supporting a positive role of $A\beta$ in synapse function.

Implications for therapeutic development

In considering the daily production and clearance of AB proteins in vivo, therapeutic treatments must be designed so as to address the constant cycle of Aβ aggregation.

Non-linear effects of plaque removal

One important implication of the supersaturation framework is that the effect of plaque removal on AB aggregation and the subsequent effect on cognitive function is not linear. Due to the ability of the large aggregates to act as both fibril seeds for aggregation and reservoirs for soluble monomers, we expect that cognitive impairement would be mitigated only after a large proportion of the accumulated plaques have been cleared. Aβ aggregation in the presence of plaques versus in the absence of plaques is fundamentally different: one being spontaneous aggregation and the other seeded aggregation. In the framework of Aβ supersaturation, the success of the antiamyloid therapy depends on the removal of most seedingcompetent plaques so that aggregation is no longer driven by fibril seeds. By examining clinical trial data of four anti-AB antibodies, Karran and De Strooper23 reached a similar conclusion that amyloid plaque needs to be reduced to a low level to show significant clinical benefit.

Anti-Aβ treatment

Several anti-Aß monoclonal antibodies have advanced to late stage clinical trials or gained FDA approval as treatment options. The main mechanism of action for these antibodies is the reduction of plaque load. Surprisingly, an enormous amount of resources has been poured into developing antiamyloid therapies, but there are no well-explained biochemical pathways that would lead from plaque reduction to cognitive improvement. Likewise, there is no clear biochemical rationalization as to how plaque reduction would lead to reduced toxic oligomer production. The supersaturation framework points to the removal of seeded AB aggregation as the main benefit of plaque removal, which restores AB42 concentration to a higher level and reduces the daily toxic assault of Aß oligomer formation.

Modulation of Aβ concentration

Lowering monomer Aβ concentration has long been considered as a therapeutic strategy. This can be achieved using inhibitors or modulators of β-secrease⁶⁵ and γ-secretase.⁶⁶ Alternatively, antibodies that bind soluble AB can also be used to lower AB levels. Recent development in this area has been reviewed in Long and Holtzman.⁶⁷ As a standalone strategy, this approach is likely most effective in the burst phase (Fig. 3A), when an increase in Aβ concentration poses the greatest risk of initiating amyloid formation. Once amyloid is formed, the mechanism of aggregation shifts from spontaneous aggregation to seeded aggregation, and Aβ concentration plays a lesser role in the rate of aggregate formation. In the scenario where the majority of plaques and seeding-competent components have been removed, Aβ concentration will return to a supersaturated state, which can be monitored with CSF or plasma Aβ measurements.

Personalized AB biomarkers

Measurements of Aβ42 in human CSF show a wide range of concentrations. Although the amyloid-positive and amyloid**Chemical Science** Perspective

negative groups can be distinguished using a cutoff of Aβ42 concentration, a large number of individuals, for example, 8% of cases in Palmqvist et al.,59 do not show agreement between Aβ42 concentration and amyloid imaging. This is likely due to large inter-individual differences in Aβ42 concentrations. One solution to this problem is to establish Aβ concentration as a personalized biomarker. Then changes in Aβ concentration can be compared to the past levels of the same individual. It has been shown that the Aβ42 concentrations in amyloid-positive and amyloid-negative cohorts differ by 2-3 fold. 15,59 A change of this magnitude would be readily detected using the same individual's history of Aβ concentration. The personal history of Aβ concentration will be particularly useful to detect if Aβ supersaturation is restored after a therapeutic intervention that has cleared the amyloid plagues.

Aggregation inhibitors

An additional personalized treatment strategy would be tailored to the specific pattern of aggregation exhibited by the patient. Due to the difference between spontaneous and seeded aggregation, two types of aggregation inhibitors may be needed. Spontaneous aggregation inhibitors are most important in the burst phase before a significant amount of amyloids have built up. Once the seeded aggregation becomes the dominant mechanism, inhibitors for seeded aggregation will work more effectively.

Toxicity blockers

Proteins or small molecules that bind directly to toxic species can serve as toxicity blockers. This class of therapeutic molecules would be effective throughout the course of Alzheimer's disease. It may be particularly helpful in combination with antiamyloid therapy, which by itself does not eliminate the toxicity of soluble Aβ. However, these types of potential drugs are also the most elusive due to a lack of understanding of both mechanisms of toxicity and the structures of the toxic Aβ species.

Different therapeutic windows call for different treatment strategies

Due to the high degree of variations in Aß aggregation behavior at different stages of pathogenesis, therapeutic strategies will need to be adjusted accordingly. In the soluble and burst phase, the most effective way to reduce the risk of Aβ aggregation is to keep Aβ levels away from the nucleation zone. This can be done either by reduction of soluble Aβ concentration (e.g., β - and γ -secretase inhibitors, Aβ immunization) or modulate the Aβ phase diagram by increasing the boundary concentration between metastable and nucleation zones. In the reduction phase, Aβ aggregation has started and the presence of small amounts of amyloid plaques provides the best opportunity for anti-amyloid therapy. Reduction of soluble Aβ concentration is likely not effective in the reduction phase because AB aggregation is driven by fibril-catalyzed secondary nucleation. Because oligomer formation is associated with the overall aggregation process, toxicity blockers will also be desired to limit damage to synaptic connections and neuronal cells. The stationary phase is the least desired treatment window

because the effect of treatment will only be felt after the vast majority of plagues have been removed.

Issues of interest for future investigations

In order to further our understanding of Alzheimer's disease and other amyloid-related disorders, in the light of the supersaturation framework, future investigation could expand on the following ideas. First, there is a wide range of Aβ42 concentrations in amyloid-negative individuals. It is important to distinguish whether a higher AB concentration means a higher risk of imminent aggregation or if it indicates that the individual has a higher tolerance to Aß aggregation, in other words, a higher boundary for the nucleation zone. It is conceivable that different individuals have their unique combination of aggregationpromoting and inhibiting factors and some may be more tolerant to higher AB concentrations than others. Identifying these aggregation-inhibiting factors may provide a new form of therapeutic intervention. Second, Aβ40 has been shown to be an important and likely the best-characterized inhibitor of in vivo Aβ42 aggregation. Mutations in familial Alzheimer's disease often lead to an increase in Aβ42/Aβ40 ratio, not simply increased Aβ42 concentrations. In sporadic Alzheimer's disease, Aβ42/Aβ40 ratio is a better predictor of Alzheimer's risk than the absolute A β 42 concentration. It is likely that this modulation of the A β 42 phase diagram is a result of a direct interaction with Aβ40. Therefore, exploring the potential use of Aβ40 or another Aβ variant as a modulator of Aβ42 aggregation deserves further investigation. Third, as a consequence of Aβ42 aggregation, the net concentration of Aβ42 is lowered as it is no longer able to maintain supersaturation. Although the exact physiological function of Aβ42 is not clear, the reduction in both absolute Aβ42 concentration and its circadian amplitude may have a negative effect on cognition, especially over a long period of time. While replenishment of Aβ42 is out of the question due to seeded aggregation, identification of a functionally equivalent and nonaggregating form of Aβ42 may provide another disease-modifying treatment.

Author contributions

ZG: conceptualization, analysis, funding acquisition, investigation, visualization, writing of original draft, manuscript editing and revision; DPB: analysis, investigation, visualization, manuscript editing and revision.

Conflicts of interest

Nothing declared.

Acknowledgements

We thank Dr Yuji Goto (Osaka University, Japan), Dr Sara Linse (Lund University, Sweden), and Dr Tuomas P. J. Knowles (University of Cambridge, United Kingdom) for their pioneering work on protein supersaturation and Aβ aggregation kinetics,

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which inspired the conceptualization of this work. We thank the members of the Guo group for insightful discussions. This work was supported by the National Institutes of Health (Grant number R01AG050687).

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