Secondary nucleation of monomers on fibril surface dominates \(\alpha\)-synuclein aggregation and provides autocatalytic amyloid amplification

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Abstract. Parkinson’s disease (PD) is characterized by proteinaceous aggregates named Lewy Bodies and Lewy Neurites containing \(\alpha\)-synuclein fibrils. The underlying aggregation mechanism of this protein is dominated by a secondary process at mildly acidic pH, as in endosomes and other organelles. This effect manifests as a strong acceleration of the aggregation in the presence of seeds and a weak dependence of the aggregation rate on monomer concentration. The molecular mechanism underlying this process could be nucleation of monomers on fibril surfaces or fibril fragmentation. Here, we aim to distinguish between these mechanisms. The nature of the secondary processes was investigated using differential sedimentation analysis, trap and seed experiments, quartz crystal microbalance experiments and super-resolution microscopy. The results identify secondary nucleation of monomers on the fibril surface as the dominant secondary process leading to rapid generation of new aggregates, while no significant contribution from fragmentation was found. The newly generated oligomeric species quickly elongate to further serve as templates for secondary nucleation and this may have important implications in the spreading of PD.

1. Introduction

Protein misfolding and aberrant aggregation processes that elude cellular maintenance mechanisms can result in major disturbances of cellular processes. This may lead to protein aggregation diseases, for example Parkinson’s disease (PD), the prevalence of which is increasing (Dobson, 2003). In PD, the formation and deposition of amyloid fibrils by the protein \(\alpha\)-synuclein (\(\alpha\)-syn) is the pathological hallmark associated with degeneration of dopaminergic neurons in the substantia nigra (Fink, 2006), and other brain regions. Neurodegeneration is believed to initiate at the synapse, and once started, the disease spreads without remission until reaching a terminal phase (Danzer et al. 2009; Schulz-Schaeffer, 2010). Cell death appears to result from the aggregation process \textit{per se} or the presence of oligomeric aggregates that impair neurotransmission (Lesné et al. 2006; Shankar et al. 2008; Wakabayashi et al. 2007; Winner et al. 2011). Indeed, toxic forms may arise in a reaction involving both monomeric and fibrillar species (Jan et al. 2011), generating oligomers at the fibril surface (Cohen et al. 2013).

\(\alpha\)-Syn is a natively unfolded 140 amino acid protein that exists abundantly in neuronal cells, where it is located in the proximity of vesicles within the presynaptic terminals (Izawa et al. 2012). \(\alpha\)-Syn comprises 1% of total cytosolic
protein in the nervous system (Stefanis, 2012) with an estimated intracellular concentration ranging from 30 to 60 µM (Rabe et al. 2013). The physiological functions of α-syn are still unclear, but are likely related to vesicle trafficking and release (Bisaglia et al. 2009). The onset of PD is also unclear, but has been suggested to be related to α-syn levels above a critical aggregation concentration (Galvagnion et al. 2015; Pinotsi et al. 2016; Rabe et al. 2013). The amyloid fibrils formed from recombinant α-syn in vitro are highly similar to those extracted from PD patients in terms of morphology and size (Conway et al. 1998). In vitro experiments have shown that the aggregation of α-syn is very sensitive to solution conditions, such as temperature (Uversky et al. 2001), pH (Buell et al. 2014), salt concentration (Munishkina et al. 2004) and the presence of cofactors (Ashmad et al. 2012). In addition, the presence of surfaces, e.g. air–liquid interface for which α-syn has high affinity, has been shown to influence aggregation kinetics in vitro (Campioni et al. 2014). The primary nucleation of α-syn can be accelerated by the presence of lipid membranes (Galvagnion et al. 2015; Grey et al. 2015), surfactant micelles (Giehm & Otzen, 2010) and nanoparticles (Vácha et al. 2014). Mechanical agitation enhances fibril fragmentation and increases the air–water interfacial area, which may promote heterogeneous primary nucleation (Campioni et al. 2013; Giehm & Otzen, 2010). Quiescent conditions may therefore be preferred in mechanistic studies.

The formation of amyloid fibrils occurs through a nucleation-dependent polymerization reaction. Underlying the macroscopically observable sigmoidal growth curves are several possible microscopic steps occurring simultaneously: primary nucleation of monomers in solution or on surfaces, elongation of fibrils through the addition of monomers to fibril ends, secondary nucleation of monomers on the surface of already existing fibrils and fibril breakage (Arosio et al. 2014; Pinotsi et al. 2014). In each case, detailed kinetic studies are needed to reveal the relative importance of these steps. For α-syn, mechanistic studies under quiescent conditions are difficult because homogeneous primary nucleation in bulk solution is undetectably slow, a behavior very different from that observed for many other aggregating proteins, including Aβ42 (Arosio et al. 2015; Cohen et al. 2013), Aβ40 (Meisl et al. 2014), actin (Oosawa & Asakura, 1975) and some prions (Collins et al. 2004; Tanaka et al. 2006). Therefore, the initiation of in vitro aggregation requires the presence of seeds or other surfaces that enhance nucleation; here we have used pre-formed α-syn fibrils.

2. Outline of the problem

The formation of amyloid fibrils by the intrinsically disordered protein α-syn is a hallmark of PD. There is a correlation between spreading of amyloid and neuronal death. It is therefore of utmost importance to characterize the underlying microscopic steps of the assembly reaction that lead to the conversion of soluble α-syn into its insoluble amyloid fibrils. At mildly acidic pH, mimicking specific cellular environments, such as endosomes and lysosomes, the aggregation of α-syn is greatly accelerated compared with neutral pH, and this effect has been attributed to a strongly pH-dependent autocatalytic process. The molecular mechanism of this process could be nucleation of monomers on fibril surfaces or fibril fragmentation as outlined in Fig. 1. Here, we address the problem of elucidating the α-syn aggregation mechanism, with an aim to distinguish between nucleation on fibril surfaces or fibril fragmentation. We have used seeded aggregation kinetics together with a filter trap assay, differential sedimentation analysis, quartz crystal microbalance studies and two-color super-resolution microscopy using dSTORM to distinguish between these two possibilities. Our data imply that the secondary process consists of nucleation of monomers on the surfaces of existing fibrils, hence rationalizing the autocatalytic nature of the aggregation process.

3. Results

3.1. Non-seeded aggregation kinetic experiments

α-Syn aggregation is strongly influenced by intrinsic and extrinsic factors. In order to obtain a well-controlled system, all kinetic studies were here performed under quiescent conditions at mildly acidic pH (10 mM MES buffer pH 5.5). To investigate the role of surfaces, reactions starting from monomeric α-syn were monitored in untreated polystyrene (PS) plates as well as non-binding PS plates coated with...
polyethylene glycol (PEG). Interestingly, no aggregation of \( \alpha \)-syn was detected during the time frame of the experiment (up to 100 h) in the PEGylated plates, whereas reproducible kinetic traces with typical sigmoidal curves were observed in PS plates (S3A). This highlights the importance of heterogeneous nucleation of \( \alpha \)-syn on the PS surface as previously found when adding PS nanoparticles to \( \alpha \)-syn in the PEGylated plates (Vácha et al. 2014). Another striking observation from the current experiments in PS plates is that \( \alpha \)-syn aggregation kinetics appear independent of the peptide concentration at high monomer concentrations (above ca. 30 \( \mu \)M, S3B). To characterize the aggregation mechanism of \( \alpha \)-syn in the absence of catalyzing foreign surfaces, all further experiments presented here were conducted in non-binding PEGylated plates in the presence of seeds.

### 3.2. Seeded kinetic experiments

It is well established that by using preformed fibrils as seeds, the primary nucleation reaction can be bypassed (Buell et al. 2014; Giehm & Otzen, 2010). Therefore, the reaction was here monitored in the presence of controlled amounts of \( \alpha \)-syn seeds. As the reaction is very sensitive to the concentration and size of the seeds, it is vital to handle all seed solutions in the same manner, as described in the materials and methods section. Initial seeded kinetic experiments were conducted by systematically varying monomer (1–50 \( \mu \)M) and seed (0.3–3 \( \mu \)M) concentrations (Figs 2 and 3). The monomer concentrations fall within the physiologically relevant range (Rabe et al. 2013). Strikingly, for each seed concentration, the \( \alpha \)-syn aggregation rate appears to be independent of the initial monomer concentration above ca. 10 \( \mu \)M, as evident from the overlapping curves at early times in Fig. 2a–c. This implies that the processes contributing to the aggregation reaction under these conditions, elongation and secondary nucleation are saturated.

Comparing the kinetic curves at a fixed monomer concentration and varied amount of preformed seeds (Fig. 3), it is clear that increasing concentration of seed fibrils leads to a decrease in lag time, and that no aggregation is observed in the absence of seed fibrils. This behavior is observed at all monomer concentrations studied. The formation of new fibrils is thus strongly enhanced by the presence of seed fibrils, which is the definition of a secondary process (Cohen et al. 2012). In addition, most of the aggregation curves have concave shapes, i.e. an accelerating rate of aggregation at early times, indicating the existence of a process that significantly increases the number of growth competent ends (i.e. aggregates) (S5).

A number of kinetic models were globally fitted to the experimental data (Meisl et al. 2016a) and only models that include secondary processes were found to produce reasonable fits. There are some remaining deviations that may be due to higher-order assembly events (Buell et al. 2014) not included in the existing model. Simulated macroscopic traces for the case of monomer concentration variation in the presence of 1 \( \mu \)M seed concentration (experimental data shown in Fig. 2b), for the different kinetic models tested are shown in Fig. 2d–f (Meisl et al. 2016a). Two models were most consistent with the data: having either fragmentation or saturated secondary nucleation as the dominant processes of fibril multiplication (Fig. 2e, f). This is manifested in the very weak dependence of the overall aggregation rate on the monomer concentration observed in our seeded kinetic data. We next designed experiments to distinguish between fragmentation and nucleation of monomers on fibril surface as the dominant secondary process.

### 3.3. Sedimentation analysis of fibril size development

The fragmentation of fibrils would lead to a change in fibril size distribution, even after the monomer concentration has reached the solubility limit (Michaels et al. 2015). \( \alpha \)-Syn aggregates at different times after the aggregation process was completed were investigated using differential sedimentation analysis (Arosio et al. 2016). The method relies on the fact that aggregates of different sizes travel through a sucrose gradient at different speeds. The results show that the retention time profile of the samples remains unaltered over up to 20 days (Fig. 4a), implying that the fragmentation rate is undetectably low under quiescent conditions.

### 3.4. Trap and seed kinetic experiment

As a further test as to whether fragmentation or surface catalysis are the major sources of new aggregates, a set of experiments, referred to as the trap and seed kinetic approach (Arosio et al. 2014) was performed at 37 °C under quiescent conditions (Fig. 4b). Mature fibrils were trapped in low-binding GHP membrane filter plates (Nasir et al. 2015) with 200 nm cutoff (retentate), and the flow through was collected in non-binding PEGylated plates (filtrate 1). Purified \( \alpha \)-syn monomer at different concentrations or buffer alone was added and incubated with the trapped fibrils for 2 h and again filtered (filtrates 2 and 3, respectively). The aggregation kinetics of filtrates 1, 2 and 3 were followed by ThT fluorescence (Fig. 4b). For filtrate 1, no enhanced fluorescence was detected within the time frame of the experiment (90 h), which indicates that seeds were trapped in the GHP membrane filter, and that any monomer or smaller species in the filtrate are present at too low concentration to give rise to any significant aggregation (Fig. 4B1). This control is relevant to show that the system has reached equilibrium. When 16 \( \mu \)M of monomeric \( \alpha \)-syn was added to wells with filtrate 1, aggregation was detected. This implies that some catalyzing species are present in filtrate 1 (Fig. 4B1). For filtrate 2, sigmoidal ThT fluorescence curves are seen within ca. 15 h at all monomer concentrations (Fig. 4B2). In contrast, no fluorescence increase is observed for filtrated monomer that has been
incubated in the filter plate without seeds (negative control) (Fig. 4B2). Together, this indicates that during incubation of monomer with trapped fibrils, a fibril-catalyzed reaction generates a significant concentration of aggregates that are small enough to pass through the filter together with the remaining monomer. We conclude that the trapped fibrils present catalytic surfaces promoting aggregation of the added monomeric α-syn. ThT was added to filtrate 3 and the fluorescence was monitored for approximately 70 h (Fig. 4B3). The ThT intensity was close to background suggesting either that fibril fragmentation did not occur to any significant extent, or that fragments were larger than the membrane cutoff. After ca. 70 h, 16 µM monomer was added to filtrate 3, but no fluorescence increase was detected over the following 80 h, confirming the absence of small catalyzing species that could have been present as a result of fibril fragmentation (Fig. 4B3).

3.5. Surface affinity of monomers is pH dependent

The interaction between monomeric and fibrillar α-syn as a function of pH was studied by means of quartz crystal microbalance with dissipation (QCM-D) to monitor the association and dissociation of monomers to and from surface-attached fibrils. This experimental strategy relies on the observation that fibril elongation occurs at significant rates over a much larger pH range than secondary nucleation (Buell et al. 2014). The QCM-D measurements provide information on the total amount of adsorbed material (including the coupled solvent) from the change in frequency (ΔF), as well as the viscoelastic properties of the attached layer from the dissipation (ΔD). Figure 5a shows typical QCM-D data where the decrease in frequency is due to added mass, albeit the relation between frequency and mass addition can be non-linear for viscoelastic layers. Gold coated sensor crystals with covalently immobilized and elongated α-syn fibrils were exposed to 20 µM α-syn monomer in 10 mM MES buffer at pH 5·5, 5·7, 5·9, 6·1 and 6·5 to allow for monomer adsorption and fibril elongation in different proportions. After a certain frequency shift (∼420 Hz) was obtained for each pH condition, each sensor was washed with 10 mM MES buffer pH 6·5 to monitor dissociation. We observe a strong pH dependence of monomer association with the fibrils. A sharp decrease in frequency was observed during incubation with monomer at pH < 6·0, followed by a rapid increase during washing at pH 6·5 (Fig. 5a). This indicates that the majority of mass that was added at pH < 6·0 is reversibly associated. A less sharp decrease in frequency was observed during incubation with monomer at pH > 6·0, followed by a smaller increase during washing, indicating that the majority of the mass added is unaffected by washing at pH 6·5 (Fig. 5a). We interpret this behavior as evidence for two types of mass addition, the relative importance of which depends on the pH. At pH > 6·0 mostly elongation occurs, and monomers are very slowly dissociating upon washing. At pH < 6·0, surface binding becomes significant, and the mass addition is reversible upon washing at pH > 6·0. Therefore, reversible
surface binding has a similar pH dependence as the secondary process (Buell et al. 2014), providing additional support for the hypothesis that the secondary process consists of nucleation of monomers on the surface of existing fibrils.

3.6. Imaging of amyloid growth from seed fibrils

In order to investigate amyloid growth from seed fibrils at mildly acidic pH conditions, we imaged samples with super-resolution microscopy. The approach employed was a two-color dSTORM strategy previously reported (Pinotsi et al. 2014). This technique relies on labeling two samples of an α-syn cysteine variant (N122C) with two different Alexa Fluor dyes, namely Alexa Fluor 647 (AF647) and Alexa Fluor 568 (AF568). Preformed seeds of α-syn-AF647 (purple) were incubated with α-syn-AF568 (green) monomer at pH 5.5 (Fig. 6). Comparing with images taken at neutral pH (Pinotsi et al. 2014), it is again clear that the aggregation mechanism is pH dependent. Two scenarios were discerned from these images: at mildly acidic pH monomer showed affinity for the surface along the sides of the existing seeds (co-localization of purple and green in Fig. 6), while for neutral pH conditions elongation dominated and monomer showed greater affinity for the growth-competent fibril ends (Pinotsi et al. 2014). It should be noted here that, irrespective of the conditions during sample preparation, the dSTORM imaging was performed in a dedicated imaging buffer at pH 8.2. As the majority of the mass added at mildly acidic pH is reversibly associated, as inferred from the QCM-D data (Fig. 5), it is likely that the majority of the mass added to the fibril seeds at pH 5.5 detach from the fibrils when they are placed in buffer of higher pH due to repulsive electrostatic interactions. This might then lead to an underestimation of the amount of associated α-syn-AF568 species at the fibril surface. Still, it is evident that the surfaces along the α-syn-AF647 fibrils contain along their length α-syn-AF568 species.

4. Discussion

Alterations in the balance of protein synthesis and clearance may lead to the formation of toxic oligomers and trigger a neurodegenerative cascade (Lee et al. 2012). No clear correlation has been found between the amount of α-syn inclusions and the stage of PD (Chaudhary et al. 2014), although larger areas of the brain contain aggregated α-syn as the disease progresses (Braak et al. 2002). In a previous study, we have shown that the α-syn aggregation is dominated by secondary processes under mildly acidic conditions (pH < 6.0) (Buell et al. 2014). It was also shown that at neutral pH, there is a linear relation between the elongation rate and monomer concentration at low monomer concentrations, and that the elongation rate

Fig. 3. Seeding efficiency in α-syn aggregation. (a–c) Representative seeded aggregation kinetic traces in the presence of fixed (3, 1, 0.3 and 0 µM) seed concentrations incubated with (a) 50 µM, (b) 10 µM and (c) 5 µM α-syn monomer. For each condition three traces are shown in bold circles. (d) Aggregation with systematic variation of α-syn seed concentration from 0 to 20% in the presence of a fixed α-syn monomer concentration (20 µM). Averages of three traces are shown as solid lines. All figures show ThT intensity as a function of time (non-normalized raw data). Therefore, experiments in the presence of seeds show elevated ThT intensity at time zero. All experiments were performed in 10 mM MES pH 5.5 in non-binding PEGylated plates at 37 °C and under quiescent conditions.
Fig. 4. Experiments designed to identify the dominant secondary process of α-syn aggregation at mildly acidic pH conditions. (a) Time-dependent differential sedimentation analysis performed on fibrils incubated at 37 °C under quiescent conditions in 10 mM MES buffer pH 5.5 for 1–20 days. Aggregates sediment within a sucrose gradient on a rotating disc where longer retention times correspond to smaller size aggregates. The raw data is shown to the left and processed data to the right. The calculations of relative weight and size are made under the assumption of spherical particles, which leads to an underestimation of the size and relative weight for a fibrillar particle. Nevertheless, changes in size distribution can be detected, which was the purpose of this experiment. The figures show representative traces of each condition that was repeated at least two times. (b) Trap and seed kinetic experiment. Fibrils made from 20 µM α-syn monomer supplemented with 3 µM seed fibrils in 10 mM MES pH 5.5 were trapped by filtration in filter plates and the flow-through (filtrate 1) was collected in non-binding PEGylated plates, supplemented with ThT and monitored in a plate reader (B1). The trapped fibrils were then incubated for 2 h with concentrations ranging from 10 to 50 µM α-syn monomer or 10 mM MES buffer pH 5.5 and newly filtered (filtrates 2 and 3, respectively). Again, the flow-through was collected in non-binding PEGylated plates, supplemented with ThT and monitored (B2 and B3). The figures show averages of at least four traces that are shown in bold with individual traces dotted below and are plotted as ThT intensity as a function of time (non-normalized data).
becomes saturated at high monomer concentrations (Buell et al. 2014). Similar overall behavior has been observed for other amyloid proteins, including Sup35 yeast protein (Collins et al. 2004), S6 (Lorenzen et al. 2012), insulin (Buell et al. 2010a) and α-lactalbumin (Buell et al. 2010a).

In the current work, we aim to understand the nature of the dominant secondary process at mildly acidic pH. As a first strategy we studied the monomer dependence of the aggregation kinetics in the presence of low concentrations of preformed seed fibrils. Two different scenarios are consistent with the observation that the aggregation kinetics is only weakly dependent on the concentration of monomeric α-syn: (a) fibrils multiply through fragmentation or (b) fibrils catalyze the formation of new aggregates from monomers on their surface, but this reaction is saturated at the monomer concentrations investigated. Secondary nucleation consists of an initial attachment of monomers to the surface, followed by nucleus formation and detachment. However, secondary nucleation may saturate at high enough monomer concentrations, where the initial attachment becomes very fast. The fibril is then fully covered in monomer and the second, monomer-independent (rearrangement or detachment) step, becomes more limiting (Meisl et al. 2014). The two models lead to the same overall scaling of the kinetic behavior with monomer and fibril concentration.

To distinguish the nature of the dominant secondary mechanism, additional and complementary experiments were performed including: (i) differential sedimentation, (ii) the trap and seed kinetic approach, (iii) QCM-D biosensing studies and (iv) two-color super-resolution microscopy using dSTORM.

Fragmentation and secondary nucleation mechanisms may lead to different final states. If fragmentation is the dominant mechanism, then the mature fibrils will keep fragmenting even after completion of the aggregation reaction. However, the differential sedimentation analysis shows that the mature fibrils do not become shorter over time, implying that spontaneous fragmentation occurs very slowly. This makes fragmentation of fibrils less likely to be the dominant secondary mechanism.

QCM-D experiments were set up with changes in pH between the association and dissociation phases to probe whether the added aggregate mass would be reduced at different rates upon washing with buffer at pH 6.5, depending on the pH value during mass association. The QCM-D results reveal that part of the mass associated with the surface-bound fibrils at low pH, dissociates upon pH increase, which is likely due to release of protein that is relatively weakly attached to the surface of the fibrils, i.e. monomeric protein or indeed already formed secondary nuclei. On the other hand, at pH > 6.0 mostly elongation occurs, and monomers dissociate very slowly upon washing due to the high thermodynamic stability.
of the fibrils (Baldwin et al. 2011). The QCM-D experiments, also support that nucleation of new fibrils from surface-bound monomers is the most likely secondary process at mildly acidic pH. The dependence on pH of α-syn monomer surface affinity was also evident in the two-color dSTORM images. Here, it was clearly shown that at mildly acidic pH conditions, a larger proportion of monomer is bound at the surface along the seed fibrils, opposing to neutral conditions, where monomer has higher affinity for the growth-competent fibril-free ends (Pinotsi et al. 2014).

In summary, the combination of experiments presented here very strongly suggests that the nucleation of monomers on fibril surfaces is the secondary process that dominates the aggregation mechanism for α-syn at pH < 6.0. Thus, at mildly acidic pH the aggregation of α-syn follows the same mechanism as previously found for insulin (Foderà et al. 2008), IAPP (Padrick & Miranker, 2002) and the amyloid β peptide, Aβ (Cohen et al. 2013; Meisl et al. 2014). Although surface catalyzed secondary nucleation dominates the aggregation process for Aβ also at basic pH, a reduction in pH lowers the electrostatic repulsion between monomers and fibrils leading to enhanced secondary nucleation (Meisl et al. 2016b). α-Syn has a pI of 4.7 (Uversky et al. 2001) and carries a net negative charge at neutral pH. The sequence is separated into three distinct regions, with a large number of charged residues in the N- and C-terminal regions and a higher fraction of hydrophobic residues in the central region. Interactions involving hydrophobic groups may play a significant role at all pH values, but at neutral pH, there is significant electrostatic repulsion between monomers, as well as, between monomers and fibrils. The charge of the residues in the termini is modulated by pH and therefore the electrostatic interactions between monomers and fibrils are likely to have strong pH dependence. This may underlie the observed pH dependence of secondary nucleation (Buell et al. 2014).

It can be postulated that changes in pH between different cellular environments may affect the rate of formation of potentially cytotoxic oligomeric species, as observed under the conditions studied here. Mildly acidic pH is found in many intracellular compartments, linked to the endocytic and exocytic pathways, making this set of conditions physiologically relevant. In vitro studies at mildly acidic pH can thus bring new insights into the microscopic steps underlying the aggregation mechanism of α-syn, and in particular, aggregate multiplication in the brain (Buell et al. 2014). The secondary nucleation process of α-syn monomers on fibril surfaces described here is an autocatalytic process, which constitutes a double threat; it increases rapidly both the total load of fibril mass and the amount of smaller oligomeric species that are thought to be the main responsible agents for cytotoxicity (Xue et al. 2009). Since secondary nucleation appears as the dominant route to α-syn aggregation at mildly acidic pH, this reaction can be considered a future therapeutic target for development of small molecular inhibitors or using certain chaperones that have been successfully shown to inhibit this specific microscopic process for the Aβ peptide (Cohen et al. 2015).
5. Material and method section

5.1. Recombinant α-syn peptide expression and purification

Human α-syn WT and α-syn cysteine variant (N122C) were expressed and purified using heat treatment, ion exchange and gel filtration chromatography as described previously (Grey et al. 2011) (S1). Labeling of α-syn cysteine variant (N122C) with Alexa Fluor 647 and Alexa Fluor 568 was performed as previously reported (Pinotsi et al. 2014) (S6).

5.2. ThT kinetic experiments

A key factor in achieving reproducible kinetics is to use pure monomeric α-syn as starting material. Prior to setting up any kinetic measurement, the frozen aliquots were purified with a final size exclusion chromatography run in 10 mM MES pH 5.5 (standard condition) were the central region of the peak is collected in order to assure the presence of only monomeric species (S1). The protein concentration was determined by measuring the UV absorbance at 280 nm and using the extinction coefficient $\varepsilon_{280} = 5800 \text{ M}^{-1} \cdot \text{cm}^{-1}$. Buffer solutions were filtered and degassed before each run. The isolated monomeric α-syn was always kept on ice to prevent aggregation.

To follow the fibrillation process, samples were aliquoted in 96-well plates with a non-binding surface (black PS plates treated with a PEGylated surface, half-area, 3881 Corning), supplemented with 20 µM of ThT and sealed with a plastic film to avoid evaporation. With the exception being for the experiment to investigate the role of surfaces on α-syn aggregation shown in S3, were also non-treated surface (black PS plates, full volumes, 3631 Costar) were used. The optimal concentration for ThT (20 µM) was accessed to have a linear relationship between fluorescence intensity and aggregate concentration (S2). Plates were incubated at 37°C up to 100 h in a plate reader (FluoStar Omega or FluoStar Galaxy, BMG Labtech, Offenburg, Germany) under quiescent conditions (excitation filter 440 nm and emission filter 480 nm).

5.3. Preparation of α-syn seed fibrils

α-syn seed fibrils were formed in Eppendorf tubes (Axygen low-bind tubes) at 37°C, with low stirring speed (300 rpm) with a teflon bar and left fibrillating for up to 48 h. Parallel kinetic ThT measurements were performed to assure that the plateau was reached during this time period. Before each kinetic experiment, seed fibrils were pre-treated by 1 min continuous sonication at maximum power in a sonicator bath (Struer, Copenhagen, DK) to disperse lumped fibrils. The concentration of seeds is counted as monomer equivalents.

5.4. Differential sedimentation method

In order to measure retentions times of the main populations of mature fibrils as a function of time a sedimentation analysis was performed using a CPS disc centrifuge instrument model DC24000. The instrument was operated at 13 782 rpm and a 4 to 12% sucrose gradient was cast in the spin fluid (Milli-Q water). Dodecane was added last to the gradient to extend its lifetime. Calibration was done with polyvinyl chloride particles with a weight-average diameter of 483 nm, and 100 µl samples were injected.

5.5. Trap and seed

Fibrils were made from 20 µM monomeric α-syn in the presence of 3 µM seeds under quiescent conditions at 37°C in non-binding PEGylated plates. The fibrils were trapped on the filter membranes (retentate) by filtration applying vacuum for 10 s on a low-binding AcroPrep 96-well filter plate (plate housing – Polypropylene) embedded with a Versatile GH Polypro membrane (GHP – hydrophilic Polypropylene membrane) ( Pall Life Sciences, Ann Arbor, MI). The flow through was collected in a 96-well non-binding PEGylated plate (filtrates). The filtration was done using a MultiScreenHTS vacuum (Millipore) manifold. Before loading the seed samples, the GHP filter membrane of the multi-well plate was washed with experimental buffer. The fluorescence intensity of ThT of each filtrate collected in the non-binding PEGylated plates was monitored in a plate reader at 37°C under quiescent conditions.

5.6. QCM-D measurements

The QCM-D measurements were performed with an E4 instrument (Q-Sense, Västra Frölunda, Sweden). α-Syn fibrils were produced and attached to the gold-coated surface of a quartz sensor (QSX 301) as previously described (Buell et al. 2010b, 2012) (S4). For the main experiments, the sensors were incubated with solutions of 20 µM monomeric α-syn in 10 mM MES buffer at the pH values of 5.5, 5.7, 5.9, 6.1 and 6.5. When the frequency shift had reached approximately 420 Hz in the frequency overtone $N = 3$, the sensor surface was washed with 10 mM MES buffer at pH 6.5.

5.7. Two-color super-resolution microscopy using dSTORM

Two-color super-resolution microscopy was performed on an inverted total internal reflectance fluorescence microscope which was custom-built for dSTORM imaging, as described previously (Kaminski Schierle et al. 2011; Pinotsi et al. 2014). Alexa Fluor 647 and 568 dyes were excited using a 640 nm diode laser (Toptica) and a 561 nm DPSS laser (Oxxius), respectively with an irradiance between 1 and 5 kW cm$^{-2}$, and a 405 nm laser diode was used as a reactivation source. The fluorescence was collected with a 100X/1-49 NA objective (Nikon) onto an EMCCD camera (iXon3 897, Andor). To induce photo-switching of the dye the fibrils were immersed in a switching buffer consisting of 100 mM mercaptoethylamine (Sigma) in PBS at pH 8.2 supplemented with an oxygen

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scavenger to reduce photobleaching (40 mg ml\(^{-1}\) glucose, 50 µg ml\(^{-1}\) glucose oxidase, 1 µg ml\(^{-1}\) catalase). The red and green channels were imaged sequentially, and for each field of view, a series of 10–15 000 frames was acquired with 15 ms exposure time. The acquired dSTORM datasets were analyzed using rapidSTORM 3-3 (Wolter et al. 2012) and super-resolution images were generated using a pixel size of 30 nm pixel\(^{-1}\) for both channels. Seeds with different labeling densities were tested for image optimization. Also, these dye labels were evaluated in terms of interfering with the aggregation process using ThT kinetics studies. It was shown that a 1:20 ratio of labeled α-syn to unlabeled peptide was the optimal in terms of labeling density and unperturbed aggregation kinetics (S7).

**Supplementary Material**

To view supplementary material for this article, please visit https://doi.org/10.1017/S0033583516000172

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**Author Contributions**

R.G., A.K.B, C.K., T.P.J.K., E.S. and S.L. designed the experiments. R.G., A.K.B and L.Y. performed the experiments. R.G., A.K.B, G.M., L.Y., T.P.J.K, E.S. and S.L. analyzed data. R.G., E.S. and S.L. wrote the paper. All authors contributed to the manuscript writing and revision.

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