Formation of compound I in heme bound Aβ-peptides relevant to Alzheimer's disease†

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Proteolysis of Amyloid Precursor Protein, APP, results in the formation of amyloid β (Aβ) peptides, which have been associated with Alzheimer's disease (AD). Recently the failure of therapeutic agents that prohibit Aβ aggregation and sequester Cu/Zn in providing symptomatic relief to AD patients has questioned the amyloid and metal ion hypothesis. Alternatively, abnormal heme homeostasis and reduced levels of neurotransmitters in the brain are hallmark features of AD. Heme can bind Aβ peptides forming a peroxidase type active site which can oxidatively degrade neurotransmitters like serotonin. To date the reactive species responsible for this activity has not been identified. Using rapid kinetics and freeze quenching, we show that heme bound Aβ forms a highly reactive intermediate, compound I. Thus, compound I provides a basis for elucidating the oxidative degradation of neurotransmitters like serotonin, resulting in abnormal neurotransmission, a key pathological feature of AD. Site directed mutants indicate that the Arg5 and Tyr10 residues, unique to human Aβ, affect the rates of formation and decay of compound I providing insight into their roles in the oxidative degradation of neurotransmitters. Tyr10 can potentially play a natural protective role against the highly reactive oxidant, compound I, in AD.

Introduction

Alzheimer's disease (AD) is a terminal neurodegenerative disease that is likely to affect around 115.4 million people by 2050.1 Generally, amyloidogenic plaques formed by the aggregation of small amyloid β (Aβ) peptides resulting from the hydrolysis of amyloid precursor protein (APP) by the action of secretases are observed in the hippocampal cortex of the brain of an AD affected patient.2–4 Co-localization of Zn and Cu metals in these Aβ plaques has led the community to invoke a potential role of these metals in aggregation.5 Specifically for Cu, neurotoxicity can be derived from oxidative stress owing to the generation of reactive oxygen species by the reaction of Aβ peptide/aggregate bound cuprous ions with oxygen.6,7 Over the last few decades several small molecule inhibitors of aggregation and Cu/Zn chelators in these Aβ plaques have been tested as potential drug candidates.8 Unfortunately, to date, molecules that dissolve such aggregates and/or chelate Cu/Zn have failed to provide credible symptomatic relief during clinical trials.9–41

This has prompted investigation of other likely origins of the disease. Heme, the chromophore present in proteins like hae moglobin and myoglobin is ubiquitous in the mammalian body (~60 g of heme in a grown adult) and has been detected in the Aβ plaques.12,13 While the takers of the heme hypothesis are few, the role of heme in the important cytopathologies of AD cannot be ignored.14,15 AD pathology includes disruption in heme homeostasis, enhanced heme oxygenase activity, reduced levels of heme proteins like NO synthase, increase in iron uptake, dysfunction in mitochondrial complex IV, etc., all indicating a potential association of heme with AD.16–37 Heme has been established to bind to Aβ peptide via a histidine residue in the hydrophilic segment (1–16) of Aβ peptide.17–26 The three residues deemed relevant to the reactivity of heme–Aβ complexes, namely His13, Arg5 and Tyr10, are unique to human Aβ peptides and are absent in rodents who do not have AD.28 The heme–Aβ complexes show peroxidase activity owing to the presence of a distal Arg5 residue28 and can catalyze the oxidation of the neurotransmitter, serotonin (5-HT).21 Serotonin, an essential neurotransmitter for cognitive functions and formation of new memories,22 is catalytically oxidized by heme–Aβ and H$_2$O$_2$ primarily to its dimer dihydroxybenzylamine.23 Significant reduction of the serotonin level and its oxidation leading to neurotoxicity are common phenomena in the pathology of AD.24,25 Since the peroxidase activity of heme–Aβ is unregulated, such reactivity of heme–Aβ can account for the abnormal neurotransmission observed in AD (Scheme 1).21,26 In the absence of the substrate, heme–Aβ can oxidize the Tyr10 residue to form dityrosine linkages between Aβ peptides leading to their aggregation.14,27 Apart from its peroxidase activity with H$_2$O$_2$, reduced heme–Aβ is known to generate H$_2$O$_2$ following
Results and discussion

Formation of reactive intermediates in the reaction of heme–Ab with m-CPBA

The heme–Ab complex reacts with m-CPBA with an observed rapid decrease in the absorbance of the Soret band and a concomitant blue shift of the Soret band from 392 nm to 365 nm (Fig. S1a†). The Q-band at 606 nm corresponding to heme bound Ab red shifts to ~675 nm in ~27 ms (Fig. 1 and S1b†). Reaction of heme with peroxide/peracid can lead to a ferric peroxide which can either cleave the O–O bond homolytically to form compound II or heterolytically to form compound I. Heme peroxides are characterized by absorption at 526–540 nm and 556–575 nm while compound II is characterized by absorption at 525–551 and 556–586 nm.21,26–31 Alternatively, compound I is characterized by absorption at 645–690 nm.32–41 Absorption in this region results in a green colour and is characteristic of a ferryl porphyrin cation radical (FeIV=O Peroxy•) or compound I (Table S1†).42–44 The absorbance at ~675 nm is found to decrease within 4 s indicating the decay of compound I (Fig. 2a). As the reaction progresses, a new species is formed which is characterized by a red shift of the Soret band to 403 nm and new bands at ~565 nm and 595 nm indicating the decay of compound I to other intermediate species, such as ferryl heme (FeIV=O porphyrin) or compound II (Fig. 1 and S1b†).15,16,19 Note that we have not been able to accumulate a high enough amount of compound I with H2O2 because the rate of formation of compound I in H2O2 is slower than in m-CPBA as it is well documented for peroxidases.47 In contrast, the decay of compound I to compound II is independent of the source of peroxide. This is why compound I is barely observed in the reaction of heme–Ab with H2O2; rather compound II is observed (Fig. S2f).16

Kinetic assays

The kinetic trace of the reaction between heme–Ab and m-CPBA at 675 nm shows an exponential increase followed by a decay indicating the formation and decay of compound I, respectively (Fig. 2a). The rate constants for the formation and decay have been estimated to be 115 s−1 and 1.2 s−1 for heme–Ab(1–16). In the presence of serotonin, the decay of compound I is accelerated as the compound I formed oxidizes it to its dimer dihydroxybutyramine (Fig. 2b, and S4f), at a rate which is faster than that of its auto decay in the absence of the substrate (Table 1 and Scheme 2). Note that heme–Ab can oxidize serotonin to its
a slower rate of formation and a faster rate of decay of compound I relative to heme–Aβ[1–16] (Fig. 2a and Table 1), suggesting that the presence of the hydrophobic region hinders the formation of compound I and marginally accelerates its decay. The decay of compound I is faster in the presence of serotonin (Fig. 2b and S6†), similar to that of heme–Aβ[1–16].

The reactions of heme–Aβ[1–40] and heme–Aβ[1–16] with m-CPBA have been monitored at 675 nm in D2O (Fig. 2c and S7b, Table S2†). Both complexes exhibit a slower rate of formation of compound I in D2O relative to H2O suggesting protonation is involved in the rate determining step (r.d.s). The Kp/KD was found to be ~2 (Table 1) which compares very well with the Kp/KD reported for the O–O bond heterolysis in peroxidases.48 However, no isotope effect was observed in the case of decay of compound I (Fig. S7a and c†) consistent with reports on peroxidases as compound I decays by outer sphere electron transfer. These data are consistent with protonation assisted O–O bond heterolysis as the rate determining step in the formation of compound I.49,50

Role of second sphere residues in controlling the rate of formation and decay of compound I

The Arg5 and Tyr10 residues are involved in peroxidase activity and reactive oxygen species generation, respectively, by heme–Aβ complexes.18 In naturally occurring heme peroxidases a distal Arg residue plays a key role in the heterolytic cleavage of the O–O bond as well as stabilizing the FeIV=O intermediate.31 The Arg5Asn mutant of heme–Aβ[1–16], i.e. heme–Aβ[1–16, Arg5Asn], reacts with m-CPBA and shows a slower rate of formation and a comparable rate of decay of the band at 675 nm suggesting that the Arg5 residue assists in the formation of compound I (Table 1, Fig. 3a) akin to natural peroxidases. Thus, the role of the Arg5 residue, which was proposed to induce a pull effect assisting in O–O bond heterolysis and help the heme–Aβ complex function as a peroxidase, is confirmed. Similar results are obtained with the Arg5Asn mutant of heme–Aβ[1–40] (Fig. S8a†).

The Tyr10Phe mutant of heme–Aβ[1–16], i.e. the heme–Aβ[1–16, Tyr10Phe] complex, shows a slower rate of formation of compound I followed by a slower rate of decay relative to the native heme–Aβ[1–16] complex (Scheme 2, Fig. 3b). In fact the decay of compound I from heme–Aβ[1–16, Tyr10Phe] is almost three times slower compared to that for native Aβ[1–16].

Fig. 2 (a) Comparison of formation and decay of compound I during the reaction of heme–Aβ[1–16] with m-CPBA, red, and heme–Aβ[1–40] with m-CPBA, blue. (b) Comparison of decay of compound I during the reaction of heme–Aβ[1–16] with m-CPBA, in the absence of the substrate, red; and in the presence of the substrate, green, and heme–Aβ[1–40] with m-CPBA, in the absence of the substrate, red; and in the presence of the substrate, green; in 50 mM PO42– buffer at pH 8. (c) Formation of compound I from heme–Aβ[1–16] in H2O, red, and in D2O, purple, in 50 mM PO43– buffer at pH/D 8. All kinetics were followed at 675 nm.

Table 1 The rate constants of formation and decay of compound I on reaction of heme–Aβ[1–16] and heme–Aβ[1–40] with m-CPBA in H2O and in D2O in presence and in the absence of the substrate (serotonin) as well as of the reaction of the heme–Aβ complexes of the site directed mutants with m-CPBA

| Heme–Aβ complexes | Formation rate (s–1) | Decay rate (s–1) |
|-------------------|----------------------|-----------------|
| Heme–Aβ[1–16]     | 115 ± 5              | 1.20 ± 0.10     |
| Heme–Aβ[1–16] + m-CPBA | 45 ± 2         | 1.10 ± 0.10     |
| Heme–Aβ[1–40]     | 47 ± 1              | 2.40 ± 0.20     |
| Heme–Aβ[1–16] + m-CPBA | 180 ± 5        | 2.05 ± 0.20     |
| serotonin         |                      |                 |
| Heme–Aβ[1–40] + serotonin | 70 ± 2       | 3.00 ± 0.15     |
| Heme–Aβ[1–16, Arg5Asn] | 40 ± 2         | 1.32 ± 0.20     |
| Heme–Aβ[1–16, Tyr10Phe] | 55 ± 3        | 0.40 ± 0.05     |
suggesting that Tyr10 is likely associated with the decay of compound I. Similar results are obtained with the Tyr10Phe mutant of heme–Ab(1–40) (Fig. S8b†). It can thereby possibly exhibit a protective role by mitigating the highly reactive oxidant, compound I.

Attempts to trap a tyrosine radical that would be produced upon its oxidation were not successful implying that the lifetime of such a radical is short. Note that the slower rate of decay of compound I in the Tyr10 mutant is consistent with the faster peroxidase activity exhibited by this mutant (Fig. S9†), since a slower self-decay rate allows compound I to oxidise more of the substrate.

Characterization of compound I by temperature dependent EPR

Compound I [Fe(IV)=O Por+] in heme proteins is characterized by an asymmetric signal ~15 gauss wide with \( g \approx 1.995 \), which results from the weak coupling between the \( S = 1 \) ferryl centre and \( S = \frac{1}{2} \) porphyrin radical.\(^{30,43,52}\) The broad EPR signal is temperature sensitive and almost disappears at temperatures \( \geq 30 \text{ K} \) due to spin relaxation, inflicted by the interaction between the porphyrin radical and heme centre.\(^{53}\) Since the Tyr10Phe and Arg5Asn mutants of Ab exhibit slower kinetics relative to native heme–Ab (Table 1), these mutants are used for the spectroscopic characterisation of compound I. EPR data of the green species formed by the reaction of heme–Ab(1–16, Tyr10-Phe) and heme–Ab(1–16, Arg5Asn) with m-CPBA frozen within their decay times, show an axial signal with a broad estimated \( g_\perp = 2.05 \) and \( g_\parallel = 1.97 \) at 11 K and 5 K, respectively. The data

![Fig. 3](image)

(a) Formation and decay of compound I during the reaction between heme–Ab(1–16) and m-CPBA, red; and between heme–Ab(1–16, Arg5Asn) and m-CPBA, cyan. (b) Formation and decay of compound I during the reaction between heme–Ab(1–16) and m-CPBA, red; and between heme–Ab(1–16, Tyr10Phe) and m-CPBA, black, followed at 675 nm in 50 mM PO\(_4\)\(^{-}\) buffer at pH 8.

![Fig. 4](image)

(a) EPR spectrum of the heme–Ab(1–16, Arg5Asn) complex on reaction with m-CPBA (mixing time 5 s), at 5 K, green, and (b) the heme–Ab(1–16, Tyr10Phe) complex on reaction with m-CPBA (mixing time 10 s), at 11 K, red. (c) Temperature dependent EPR spectra of the heme–Ab(1–16, Tyr10Phe) complex on reaction with m-CPBA (mixing time 10 s), at 11 K, red; at 13 K, purple, and at 77 K, blue; in 50 mM PO\(_4\)\(^{-}\) buffer at pH 8.

![Fig. 5](image)

(a) High frequency region of the resonance Raman spectrum—experimental spectrum of heme–Ab(1–16, Tyr16Phe), purple; simulation spectrum, green. (b) Experimental spectrum of heme–Ab(1–16, Tyr16Phe) + m-CPBA, red; simulation spectrum, black; components of the rR spectrum were determined by simulating the spectra at the \( \nu_\alpha \) region. Data were obtained with an excitation wavelength of 413.1 nm (5 mW) at 77 K.
are similar to those reported for compound I of turnip peroxidase by Ivancich et al. and are thereby consistent with the formation of compound I. The intensity of the broad signal was found to decrease with increasing temperature and at 77 K there was hardly any signal, attributed to the spin relaxation phenomenon (Fig. 4 and S10).54,55

Characterization of compound I by resonance Raman spectroscopy

Resonance Raman (rR) spectroscopy is a unique technique for the characterization of structures of heme proteins.56,57 The rR spectra obtained from heme–Aβ complexes reacted with 5 times excess of m-CPBA clearly indicate a broadening of the oxidation state marker v4 band region due to the presence of compound I at 1368 cm−1 (Fig. 5b, blue) along with compound II at 1382 cm−1 (Fig. 5b, orange) in addition to the v4 band of resting ferric species at 1375 cm−1 (Fig. 5a and b, green).58,59 All these signals could be deconvoluted by fitting the v4 region of the spectrum. More importantly, in the low frequency region (600–900 cm−1) of rR spectra, we observe a weak feature at 843 cm−1 which shifted to 803 cm−1 when an isotope labelled solvent (H2O18) was employed. This corresponds to the v(Fe-O) of the oxyferryl fragment of compound I.60,61 Another less intense band at 817 cm−1 was observed corresponding to v(Fe-O) of compound II (Fig. S11f). We were unable to see convincing isotopic shifts of this band likely because of its weak intensity relative to the strong heme vibrations and due to low yields of these high valent intermediates, as expected due to the high reactivities of these species.

Conclusions

Heme–Aβ complexes have a peroxidase type active site. They react with m-CPBA to form a high valent iron–oxo species, which shows a characteristic absorption band at 675 nm and a broad axial EPR signal with effective g∥ = 2.05 and g⊥ = 1.97 at liquid helium temperatures, which disappeared almost completely at 77 K. In the rR spectra, the mixture of heme–Aβ and m-CPBA also shows appearance of new oxidation state marker (v4) bands at 1368 cm−1 in the high frequency region and at 843 cm−1 in the low frequency region. The low frequency band at 843 cm−1 shifts to about 803 cm−1 upon isotope incorporation (40 cm−1 shift). These features are characteristic of a reactive compound I type intermediate which can oxidize neurotransmitters like serotonin. This can potentially lead to abnormal neurotransmission, which is a key pathological feature of AD. A slower rate of formation of compound I in D2O than in H2O, but a comparable decay, is consistent with protonation assisted O–O bond heterolysis as the rate determining step for compound I formation. The effects of the second sphere residues Arg5 and Tyr10 on the formation and decay of this intermediate were probed using mutated Aβ peptides. In the absence of the Arg5 residue, the rate of formation of the 675 nm band was found to be slower while the decay was comparable to that of native heme–Aβ, indicating the role of Arg5 in assisting in compound I formation by inducing a pull effect helping in the O–O bond heterolysis and consequently in the peroxidase activity of the heme–Aβ complex. The Tyr10 mutant of the heme–Aβ complex shows a slower rate of formation of compound I and a slower decay of the same, relative to the native heme–Aβ complex suggesting a likely association of Tyr10 in the decay of compound I. Thus the Tyr10 residue might act as a natural defence against oxidation by compound I. Isolation and characterization of compound I in the oxidative degradation of neurotransmitters like serotonin provides a possible explanation and mechanism for the abnormal neurotransmission that is observed in AD. It must be noted that AD is a very slowly progressing disease. The catalytic oxidation of neurotransmitters like serotonin by heme–Aβ is expected to be slow, so that the deleterious effects of it would occur over a prolonged period of time, which also correlated with the relatively late onset of this disease. The relatively slow rate of serotonin oxidation is thus well in accordance with the established facts of AD.

Conflicts of interest

There are no conflicts to declare.

Acknowledgements

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