

Contribution of a Peroxide Adduct of Copper(II)-Peptide Complex to Modify the Secondary Structure of Albumin

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Copper(II)-peroxide Adduct, Modification of Protein, Copper(II)-peptide Complex

We have found that copper(II) compounds containing a peptide group in the chelate exhibit high activity for modification or degradation of albumin in the presence of hydrogen peroxide, whereas no activity was detected for the copper(II) compounds without an amide-group. It is suggested that presence of the amide-group in the ligand may play an important role in the formation of a peroxide adduct and in activation of the peroxide ion, leading to cleavage of the peptide bond of a neighboring protein. It is implied that conversion of normal cellular prion protein PrP^C into a disease-causing isoform, PrP^{Sc} is attributed to the activated peroxide ion coordinated to a copper(II) captured in the NH₂-terminal domain of the PrP^C.

In general, the neurons in human substantia nigra deteriorate during normal aging, and loss of these neurons is prominent in Parkinson's disease (Floor and Wetzel, 1998). These degenerative processes are hypothesized to involve oxidative stress (Stadtman, 1992; Sohal and Weindruch, 1996), and the oxidative stress hypothesis predicts that endogenous oxidants may cause greater cellular damage, which results in several neurodegenerations. In previous papers, we have proposed that among the species to induce oxidative stress, hydrogen peroxide is the most important one (Nishida and Ito, 1995). Very recently, Brown *et al.* (1997) have shown that the NH₂-terminal domain of PrP^C (the normal cellular prion protein) exhibits five to six sites that bind copper(II) presented as a glycine chelate, indicating that PrP^C can exist in a Cu-metalloprotein form *in vivo*. This finding suggests that formation of a copper(II) within the octapeptide may be closely related with the conversion of PrP^C into PrP^{Sc} (the abnormal disease-causing isoform) (Prusiner, 1997). Thus in this study the effect of a copper(II)-peroxide adduct on the modification of albumin was investigated,

attempting to elucidate the possible contribution of a copper(II)-peroxide adduct to induce the modification of the NH₂-terminal region of PrP^C.

Experimental

Materials

The copper(II) compounds used in this study are of general form, Cu(L)ClY, where (L) are illustrated in Fig. 1. The structures of these compounds are similar to each other (Okuno *et al.*, 1997; Kobayashi *et al.*, 1996; Kobayashi *et al.*, 1998, in press), and as a representative one, the ORTEP drawing of Cu(tfpy)Cl⁺ is illustrated in Fig. 2, which was determined in this study, where (tfpy) denotes N,N-bis(2-pyridylmethyl)-2-aminomethyl-tetrahydrofuran (see Fig. 1). Crystal data of Cu(tfpy)ClClO₄·H₂O: triclinic P $\bar{1}$, $a = 10.673(6)$, $b = 12.325(4)$, $c = 8.999(4)$ Å, $\alpha = 96.78(4)$, $\beta = 114.44(4)$, $\gamma = 69.93(4)^\circ$, $V = 1011.8(9)$ Å³, $Z = 2$, $D_x = 1.62$ Mg m⁻³; $R = 0.093$ for 3250 observed

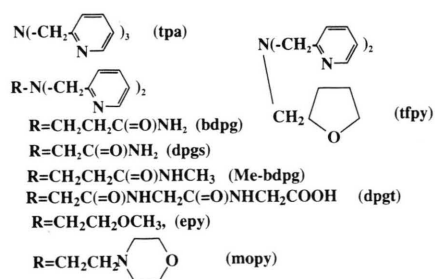


Fig. 1. Chemical structures of the ligands cited in this paper.

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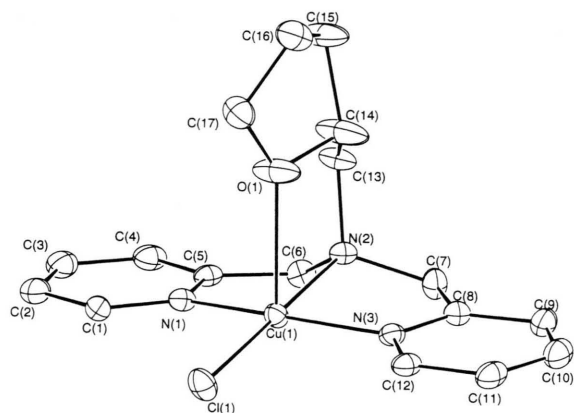


Fig. 2. ORTEP drawing of Cu(tpfy)Cl⁺ cation. Cu(1)–Cl(1), 2.226(3); Cu(1)–N(2), 2.031(8); Cu(1)–N(1), 2.000(9); Cu(1)–N(3), 1.994(8); Cu(1)–O(1), 2.456(10) Å.

reflections ($F_o \geq 3\sigma(F_o)$). Supplementary data on atomic positions, bond lengths, bond angles, and F_o - F_c tables are not documented. The crystal structures of other compounds ((L) = (bdpg) and (dpgs), (Okuno *et al.*, 1997); (mopy), (Kobayashi *et al.*, 1996); (dpgt) and (Me-bdpg) (Kobayashi *et al.*, 1998, in press) were already reported. Human carbonic anhydrase (HCA), albumin (bovine, BSA), and cytochrome c were purchased from Sigma (USA).

Degradation of albumin by copper(II)/H₂O₂ systems

To the reaction mixture containing a copper(II) compound (5 μ l, 0.15–0.6 mM solution), Tris = tris (hydroxymethyl)aminomethane)-HCl buffer (5 μ l, 0.1 M pH = 7.8), hydrogen peroxide (5 μ l, 6.25–100 mM solution), was added a protein solution (5 μ l, 0.11 mM), and one hour after the mixing the solution was mixed with a solution containing 2-mercaptoethanol, and then electrophoresed (Rana and Meares, 1991); denatured samples were analyzed on 12.5% sodium dodecylsulfate-polyacrylamide gel electrophoresis. Products were visualized by Coomassie blue and the band intensities were quantified on an ATTO densitograph model AE-6920-M/W/V.

ESR spectral measurements

ESR spectra of the solutions containing copper(II) complex (1–10 mM in water/acetonitrile (1/1, v/v) solution), hydrogen peroxide (100 mM in

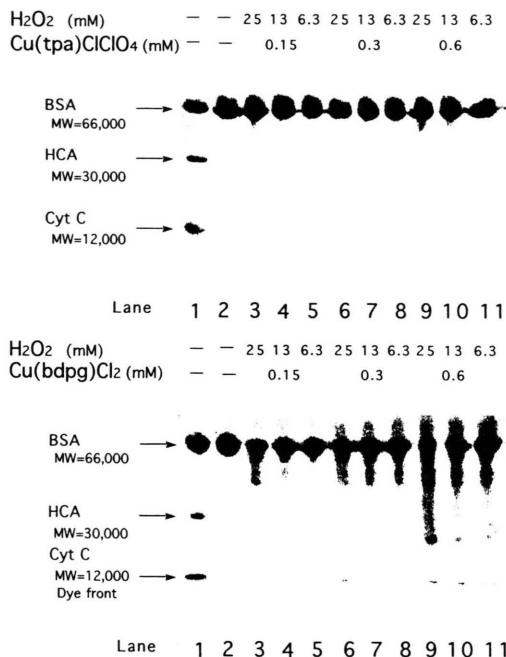


Fig. 3. Separation of the cleaved products by Na-DodSO₄/acrylamide gel electrophoresis. BSA, HCA, Cyt c denote bovine serum albumin, human carbonic anhydrase, and cytochrome c, respectively. Lanes 1 and 2, proteins in the absence of copper(II) and hydrogen peroxide; lanes 3–11, albumin, hydrogen peroxide and copper(II) complex (in the upper (A), Cu(tpa)Cl⁺, and the lower, (B), Cu(bdpg)Cl⁺). The concentrations of hydrogen peroxide and copper(II) complex are written in the figure; concentrations of the copper(II) complex in the lanes 3–5, 6–8, and 9–11, are 0.15, 0.30, and 0.60 mM, respectively.

water/acetonitrile (1/4, v/v) solution), PBN (α -phenyl-N-*t*-butylnitrone), one of the spin-trapping reagents for OH· radical (Janzen *et al.*, 1978) (100 mM in water/acetonitrile (1/4, v/v) solution) were measured with a JEOL ESR apparatus, model RE-2X using an X-band at 298 K.

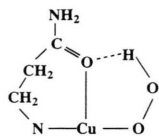
Results and Discussion

Degradation of albumin by copper(II)/H₂O₂ systems

As a representative example, the electrophoresis done for the systems containing Cu(tpa)ClO₄ and Cu(bdpg)ClO₄ are illustrated in Fig. 3. We have confirmed that the presence of a copper(II) complex or hydrogen peroxide only does not induce the degradation of albumin under the experimental conditions used in this study. As shown in

Complexes	Cu(bdpg)ClClO ₄	Cu(dpgs)ClClO ₄	Cu(tpa)ClClO ₄
Cu(II) complex; none H ₂ O ₂ none	100	100	100
Cu(II) complex; none H ₂ O ₂ (25 mM)	100	100	100
Cu(II) complex (0.3 mM) H ₂ O ₂ (1.6 mM)	100	100	100
Cu(II) complex (0.3 mM) H ₂ O ₂ (3.1 mM)	90	100	100
Cu(II) complex (0.3 mM) H ₂ O ₂ (6.3 mM)	62	83	100
Cu(II) complex (0.3 mM) H ₂ O ₂ (12.5 mM)	52	62	100
Cu(II) complex (0.3 mM) H ₂ O ₂ (25 mM)	30	46	100

the case of Cu(bdpg)Cl⁺, Cu(II)-O(amide oxygen) is 2.287(2) Å, Okuno *et al.*, 1997).



Since no formation of PBN-OH was detected in the solution containing a copper(II) complex, hydrogen peroxide, and PBN in the ESR spectra, it seems quite likely that OH-radical formation does not occur in the solution, because PBN is one of the famous spin-trapping reagents for OH-radical (Janzen *et al.*, 1978). Thus, we would like to propose that the degradation of albumin is caused oxidatively by the copper(II)-peroxide adduct shown above, which exhibits a high electrophilic nature (Okuno *et al.*, 1997). This assumption may be supported by several facts, for example, some cytochrome P-450 enzymes exhibit high activity for oxidation of organic compounds containing carbonyl group and amide groups (L.-Robichaud *et al.*, 1995; Peng *et al.*, 1995; Vaz *et al.*, 1996), peptidylglycine α -hydroxylating monooxygenase contains a copper(II) ion (Prigge *et al.*, 1997), and the iron(III)-peroxide adduct exhibits a protease-like function (Rana and Meares, 1991).

Protein modifications in the biological systems

Present results suggest that the presence of the peptide-group near the copper(II) ion may play

an important role in activating the peroxide ion, leading to modification or degradation of the neighboring peptide bonding. Thus, it seems most likely that the copper(II) ion coordinated by the peptide group in the octarepeat region in the PrP^C may contribute to the modification or degradation of the NH₂-terminal domain of PrP^C in the presence of hydrogen peroxide, and this may give a reasonable explanation for the formation of PrP^{Sc} reported in the previous papers (Prusiner, 1996, 1997).

It is known that the FALS (familial amyotrophic lateral sclerosis)-associated SOD1 (SOD = superoxide dismutase) mutations affect amino acid residues involved in enzymatic dimerization or β -barrel turns, rather than those corresponding to the active sites (Rabizadeh *et al.* 1995). Yim *et al.* (1993) have reported that in addition to its activity as a SOD, CuZnSOD catalyzes oxidation of substrates by hydrogen peroxide (Yim *et al.*, 1993; Pazos *et al.*, 1996). Based on these facts and the present results, it seems reasonable to assume that in the FALS-associated mutations in a copper(II) peroxide adduct, which is an intermediate formed in the decomposition of superoxide ion, can oxidize the protein nearby, and that this may be a main origin for the increased openness of the three dimensional structure of the SOD in FALS. (Deng *et al.*, 1993).