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A spectroscopic characterization of a monomeric analog of copper, zinc superoxide dismutase

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Received: 28 February 1994 / Accepted: 12 May 1994

Abstract. A mutated protein of human Cu(II)₂Zn(II)₂ SOD in which residues Phe50 and Gly51 at the dimer interface were substituted by Glu's, thus producing a monomeric species, has been characterized by electronic absorption spectroscopy, EPR, relaxivity and ¹H NMR techniques. Such substitutions and/or accompanying remodeling and exposure of the dimer interface to solvent, alter the geometry of the active site: increases in the axiality of the copper chromophore and the Cu-OH₂ distance have been observed. The affinity of both metal binding sites for Co(II) is also altered. The observed NMR parameters of the Co(II) substituted derivative have been interpreted as a function of the decrease of rotational correlation time as a consequence of the lower molecular weight of the mutated protein. Sharper NMR signals are also obtained for the reduced diamagnetic enzyme. Results are consistent with an active site structure similar to that observed for the dimeric analog Thr137Ile characterized elsewhere. An observed proportional decrease in enzymatic activity and affinity for the N₃-anion suggests the importance of electrostatic forces during substrate docking and catalysis.

Key words: Cu, Zn, Superoxide Dismutase – ¹H NMR – Monomeric analog

Introduction

Superoxide Dismutase (SOD or WT-Cu(II)₂Zn(II)₂-SOD) is a homo-dimeric enzyme of 16,000 MW per subunit, containing a copper and zinc ion per subunit whose physiological role is the dismutation of the superoxide radical to hydrogen peroxide and molecular oxygen (Fridovich 1974; Valentine and Pantoliano 1982; Tainer et al. 1982; Fridovich 1987; Banci et al. 1990 a). The enzy-

matic reaction occurs through a two step mechanism involving the reduction of copper(II) to copper(I) by a first moiety of superoxide and the reoxidation of copper(I) with a second moiety. The copper(II) ion is located at the bottom of a cavity about 1 nm deep (Tainer et al. 1982). The role of aminoacids constituting the catalytic cavity of SOD has been extensively investigated through site directed mutagenesis techniques. Various mutated proteins have been characterized using several spectroscopic techniques (Beyer et al. 1987; Banci et al. 1988, 1990 b, 1991 a; Bertini et al. 1989) and the functional roles of various residues in catalysis have been deduced accordingly. For example, Arg143 and Thr 137 face each other at the entrance to the active site cavity where the cationic Arg143 is apparently positioned to guide the superoxide anion to the active site. Accordingly, replacement with neutral or negative residues produces dramatic decreases in enzymatic activity (Beyer et al. 1987; Banci et al. 1988). Furthermore, it has been observed that Thr137 is involved in hydrogen-bonding with Glu133 and Lys136 and contributes to the hydrophilicity of the cavity (Bertini et al. 1989; Banci et al. 1990b). Indeed, the substitution of Thr with a hydrophobic residue such as Ile causes a water molecule to be expelled (Bertini et al. 1989) which is otherwise weakly coordinated to copper (Banci et al. 1990a). The copper and zinc ions are bridged by an imidazole group of a histidine in each subunit. Copper(II) is also coordinated to three other histidines and semi-coordinated to a water molecule in a distorted square pyramidal geometry. Zinc(II) is also bound to two other histidines and to an aspartate residue in a distorted tetrahedral coordination geometry. A schematic drawing of the active site is shown in Fig. 1. Both metal binding sites can also accommodate other metal ions [e.g. cobalt(II) and nickel(II)]. The protein maintains its enzymatic activity, however, only in those derivatives where copper(II) occupies its native site (Valentine and Pantoliano 1982). Cobalt(II) has proven to be a useful spectroscopic probe because it gives rise to well shaped and informative electronic spectra (Bertini et al. 1986). Furthermore, high spin cobalt(II) can be used to detect hyperfine-shifted NMR signals of

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Fig. 1. Schematic drawing of the metal sites of human WT-Cu(II)₂Zn(II)₂SOD

ligands coordinated to the paramagnetic Co(II) ion (Bertini and Luchinat 1986). The native wild type oxidized enzyme (WT-Cu(II)₂Zn(II)₂-SOD) is not suitable for NMR investigation of structure around copper(II) since signals are too broad to detect. Substitution of Zn(II) with Co(II), however, has allowed ¹H NMR characterization of the Cu(II) site (Bertini et al. 1985 a; Banci et al. 1987, 1989 a). Indeed, magnetic coupling between cobalt(II) and copper(II) has permitted the observation as well as the assignment of those ¹H NMR signals arising from ligand-associated protons.

The dimeric nature of the protein originates from hydrophobic interactions at the interface. Specifically residues Phe50 and Gly51 provide intersubunit hydrophobic and hydrogen bonding interactions respectively, that stabilize quaternary structure. Since SOD can be expressed efficiently in yeast (Beyer et al. 1987) and in *E. coli* (Banci et al. 1991a; Getzoff et al. 1992), a series of analogs were prepared where hydrophobic residues were substituted with charged residues (Mullenbach et al., unpublished results).

We report here a biophysical characterization of a mutated protein in which Phe50 and Gly51 were both substituted with Glu (i.e. M-Cu(II)Zn(II)SOD, hereafter). The protein is monomeric. The catalytic cavity has been investigated through NMR, EPR and electronic absorption spectroscopy. The spectroscopic parameters have been related to the functional properties. The rationale for substitutions of Phe50 and Gly51, as proposed by John Tainer and Elizabeth Getzoff is discussed in a joint manuscript in preparation (Mullenbach et al., unpublished results).

Material and methods

Preparation of the protein

The M-Cu(II)Zn(II)SOD mutated protein was expressed and isolated from E. coli cultures (strain MC1061) using a procedure previously reported (Banci et al. 1991 a). The mutated protein was purified by ion exchange chromatography on DEAE Sepharose CL-6B (Pharmacia). The molecular weight of the protein sample was checked through gel filtration experiments using a column packed with Sephadex G75 and equilibrated with 50 mm Tris-HCl, 100 mm NaCl, pH 7.0. In order to obtain a calibration line, different mixtures of standards (myoglobin, carbonic anhydrase, wild type SOD) were loaded on the column. Transferrin was used in all the mixtures to determine the void volume. Protein concentration was calculated from dry weight for a solution of the mutated protein and an extinction coefficient at 265 nm of 7400 cm⁻¹ M⁻¹ was calculated from the electronic spectrum of this solution in the ultraviolet region. This extinction coefficient was then used to determine protein concentrations of different samples of M-Cu(II)Zn(II)SOD. Atomic absorption analysis was performed on GBC 903 instrument. Activity measurements were performed using the method by Fridovich (McCord and Fridovich 1969).

Metal substitution

The apoprotein was obtained by dialysis against 10 mm EDTA in 50 mm acetate buffer, pH 3.8 (McCord and Fridovich 1969). EDTA was removed by dialysis against 100 mm NaCl in 50 mm acetate buffer, pH 3.8 and then against acetate buffer alone, gradually increasing the pH from 3.8 to 5.5 (Forman et al. 1973). The WT- $E_2Co(II)_2SOD$ (E = empty) and the M-ECo(II)SOD derivatives were obtained by adding a CoCl₂ solution to the apoprotein at pH 5.5 (Rotilio et al. 1972 a; Fee 1973; Pantoliano et al. 1979). The metal uptake was followed spectrophotometrically up to the complete development of the electronic spectrum. The WT-Cu(II)₂Co(II)₂SOD and M-Cu(II)Co(II)SOD derivatives were obtained by slow addition over 12 h of a stoichiometric amount of a CuCl₂ solution with gentle stirring at room temperature. The samples were concentrated by ultrafiltration using an Amicon cell equipped with a 500 Da cut off membrane.

Reduced analogs

The WT-Cu(I)₂Zn(II)₂-SOD and the M-Cu(II)Zn(II)-SOD derivatives were prepared by addition of a few crystals of solid sodium dithionite to the solution of the oxidized species (Cass et al. 1977 a; Lippard et al. 1987; Bertini et al. 1991 a).

Spectroscopic measurements

All spectroscopic measurements with the exception of ¹H NMR spectra were performed in unbuffered water solution, pH 5.5. Electronic spectra were recorded on a Cary 17D spectrophotometer. CD spectra were recorded on JASCO 500 C instrument. EPR spectra were recorded at room temperature on a Bruker ER 200 operating at 9.8 GHz. Water proton NMRD measurements were performed on a Koenig-Brown relaxometer, installed at the University of Florence thanks to an agreement between the latter and the IBM Watson Research Center of Yorktown Heights, New York. All NMR experiments were recorded on a Bruker AMX 600 spectrometer at the magnetic field of 14 T or on a Bruker MSL 200, operating at 4.7 T. They were performed at 298 K, on ca. 4 mm samples, 10 mm phosphate buffer. Experiments were performed at pH 5.1 for WT-Cu(I)₂Zn(II)₂SOD and M-Cu(I)Zn(II)SOD and at pH 7.0 for WT-Cu(II)₂Co(II)₂-SOD and M-Cu(II)Co(II)SOD. Chemical shift values were obtained by calibrating the H₂O signal at 4.8 ppm from DSS. The NOESY spectra were recorded in aqueous 10% D₂O solution. In the case of WT-Cu(I), Zn(II), SOD and M-Cu(I)Zn(II)SOD, the usual $(90^{\circ}-t_1-90^{\circ}-t_m-90^{\circ}-AQ)$ pulse sequence was modified by replacing the observation 90° pulse with a spin-echo pulse sequence and combining a four-step Exorcycle to the usual receiver phase list for recording NOESY spectra (Sklenar and Bax 1987). This allows the suppression of the intense solvent peak without using a presaturation pulse. We have observed that, when a presaturation pulse is applied on the solvent peak, the intensity of the signals of the NH of histidines dramatically decreases. The NOESY spectra on the Cu(II)Co(II) derivatives were recorded by using a standard presaturation pulse. All the NOESY spectra were collected in phase sensitive absorption mode (TPPI) (Marion and Wuthrich 1983). 2K × 512 data points were acquired. Square sine shifted functions were applied to acquired data prior to Fourier transformation. A standard software package provided by Bruker was used for data processing. One-dimensional NOE experiments were recorded at 200 MHz using the previously reported methodology (Banci et al. 1989 a; Lecomte et al. 1991). T_1 values were obtained using the inversion recovery methodology (Inubushi and Becker 1983). Titration with sodium azide was performed at 200 MHz essentially as reported elsewhere (Bertini et al. 1985a; Banci et al. 1987).

Results and discussion

The molecular weight of the protein was checked to be $16,000\pm3,000$. The content of copper(II) and zinc(II) measured using atomic absorption analysis has revealed that the copper content is 99% and the zinc content is 100%. The activity of the M-Cu(II)Zn(II)SOD, measured with the method of Fridovich (McCord and Fridovich 1969) and expressed as a function of copper(II) content, was found to be $10\pm5\%$ of that found for the wild type Cu(II)₂Zn(II)₂SOD. Since the copper content is

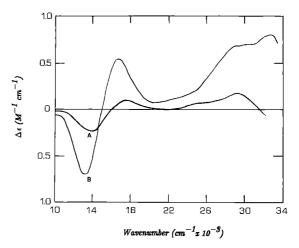


Fig. 2. Circular dichroism spectra of M-Cu(II)Zn(II)SOD A and WT-Cu(II)₂Zn(II)₂SOD B. Samples were in unbuffered water, at pH 5.5. $\Delta\varepsilon$ is expressed per mol of copper

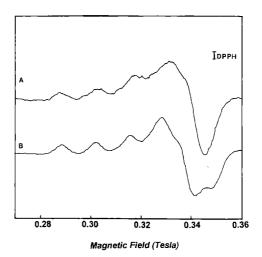


Fig. 3. Room temperature EPR spectra of M-Cu(II)Zn(II)SOD A and WT-Cu(II)₂Zn(II)₂SOD B

comparable with the wild type protein and constant with time, we cannot ascribed the decreased activity to alteration in the affinity for copper.

CD and electronic spectra

The electronic spectrum of M-Cu(II)Zn(II)SOD is nearly indistinguishable from that of the wild type enzyme (Pantoliano et al. 1982; Banci et al. 1990c). However, the CD spectrum (Fig. 2) shows d-d transitions at 13 800 and 17 400 cm⁻¹ which compare with 13 300 and 16 700 cm⁻¹ in the wild type enzyme, whereas the charge transfer band remain unchanged. Ipsochromic shift of the d-d transitions of copper(II) has been interpreted as a geometric change towards planarity of the coordinated histidines (Lever 1984; Banci et al. 1990 c, d).

EPR spectra

EPR spectra of wild type SOD and the monomeric analog are shown in Fig. 3. The spectrum of M-

Cu(II)Zn(II)SOD indicates a rather axial geometry whereas, in WT-Cu(II)₂Zn(II)₂SOD a rhombic component is apparent as extensively discussed (Rotilio et al. 1972 b; Bertini and Scozzafava 1981). The g_{\perp} value of 2.26 is the same as for the wild type enzyme; the g_{\parallel} value is 2.06 which compares with 2.09 in the wild type (the latter value represents the reading of the $g_x + g_y$ feature in the first derivative spectrum) (Banci et al. 1990 a, 1991 b). The A_{\parallel} value is 151×10^{-4} cm⁻¹, whereas it is 138×10^{-4} cm⁻¹ in the wild type. Such an increase in A_{\parallel} as well as an axial geometry indicated by the spectrum has been observed in the anion derivatives of the wild type enzyme (Banci et al. 1990 d) and in some mutated proteins (Banci et al. 1990 d).

Relaxivity measurements

The water ¹H NMRD profiles (Bertini et al. 1985 b; Koenig and Brown 1987; Koenig and Brown 1990) of M-Cu(II)Zn(II)SOD mutated protein and WT-Cu(II)₂Zn(II)₂SOD, recorded between 0.01 and 50 MHz (Fig. 4) have similar shapes, indicating that the correlation time τ_c is unchanged in the mutated protein. The correlation time is given by the electronic relaxation time (Bertini and Luchinat 1986). However the monomer has 20% lower relaxivity than the wild type, which may be ascribed to a slightly longer Cu-OH₂ distance. In the WT-Cu(II)₂Zn(II)₂SOD the Cu-O distance has been estimated to be around 0.27 nm (Tainer et al. 1982), a value in accordance with EXAFS data (Blackburn et al. 1984). A 20% decrease in T_1^{-1} corresponds to about a 5% increase in the Cu-O distance.

¹H NMR spectroscopy

Cobalt derivative. Addition of Co(II) ion to the monomeric metal-deprived M-SOD in a ratio metal: protein of 1:1 gives rise to a derivative whose ¹H NMR spectrum resembles that of the dimeric WT-Co(II)₂Co(II)₂SOD (Banci et al. 1986) (Fig. 5). We propose that the affinity for metal ions of the two metal sites in the monomeric analog is altered and that Co(II) also binds at the copper site even at pH 5.5 (whereas the wild type enzyme at pH 5.5 binds Co(II) only in the zinc site) (Valentine and Pantoliano 1982). This proposal is in agreement with the spectrophotometric titration of the apo M-SOD with Co(II) (data not shown). From the electronic spectrum we calculate an average maximum extinction coefficient of 300 M⁻¹ cm⁻¹ (the value is related to the Co(II) concentration); this value is lower than the value typical of WT-E₂Co(II)₂SOD (400 M⁻¹ cm⁻¹) and could be explained by taking into account a mixture of Co(II) in a tetrahedral site (the zinc site) and in a five-coordinated site (the copper site).

Copper-Cobalt derivative. Figure 6 compares the ¹H NMR spectra of WT-Cu(II)₂Co(II)₂SOD and M-Cu(II)Co(II)SOD at 600 MHz. The latter was obtained by adding a stoichiometric amount of copper(II) to M-ECo(II)SOD. The NMR spectrum shows that copper(II)

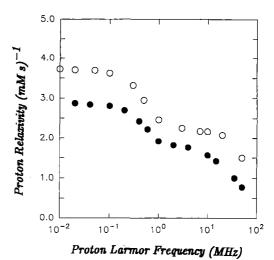


Fig. 4. Water proton NMRD profiles at 298 K, of WT-Cu(II)₂Zn(II)₂SOD (o) and M-Cu(II)Zn(II)SOD (•). Samples were in 10 mm Hepes, pH 7.5. The values have been subtracted of the water and the diamagnetic protein contribution and normalized to

water and the diamagnetic protein contribution and normalized to 1 mm copper concentration according to the standard procedure of relaxivity data treatment

B

BO 60 40 20 0 -20 -40 -60 δ (ppm)

Fig. 5. ¹H NMR spectrum of M-ECo(II)SOD A, recorded at 200 MHz in H₂O solutions at pH 5.5. For comparison purposes the spectrum of bovine WT-Co(II)₂Co(II)₂SOD B, recorded at 90 MHz, is also shown

binds at the copper center in a quantitative fashion. The assignment follows that already reported for WT-Cu(II)₂Co(II)₂SOD. It is apparent that signal linewidths are decreased by about a factor of two for the monomer. This is due to the decrease of the Curie relaxation contribution (Bertini and Luchinat 1986). The contribution to T_2^{-1} (transverse relaxation rate) provided by this mechanism is given by:

$$\begin{split} T_{\rm 2M}^{-1} &= \frac{1}{5} \bigg(\frac{\mu_0}{4 \, \pi} \bigg)^2 \, \frac{\omega_I^2 \, g_e^4 \, \mu_B^4 (S \, (S+1))^2}{(3 \, k \, T)^2} \\ &\cdot r^{-6} \left(4 \, \tau_r + \frac{3 \, \tau_r}{1 + \omega_I^2 \, \tau_r^2} \right) \end{split}$$

where τ_r is the rotational correlation time, ω_t is the proton Larmoer frequency of the proton, r is the metal to proton distance and the other symbols have their usual meanings.

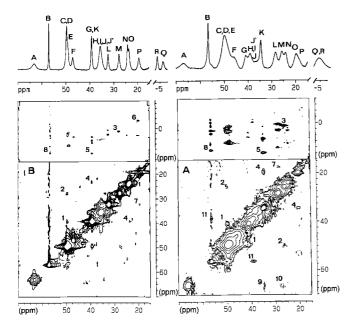


Fig. 6. 600 MHz ¹H NMR NOESY spectra of A WT-Cu(II)₂ Co(II)₂SOD and **B** M-Cu(II)Co(II)SOD. The monodimensional spectra of the two derivatives are also reported. Shaded signals disappear in D₂O. Cross peaks are numbered as follows: 1 (C-G), 2 (C-M), 3 (M-CH₃ Ala140), 4 (K-O), 5 (K-His48 H β_2), 6 (P-R), 7 (L-P), 8 (B-His120 H β_2), 9 (A-K), 10 (A-L), 11 (B-H). Cross peaks 9 to 11 are observed in the dimer derivative; cross peak 6 is observed only in the monomer derivative. Conditions: mixing time 4 ms, relaxation delay 150 ms

At 600 MHz, the Curie relaxation mechanism is expected to be the dominant contribution to the T_2^{-1} in the wild type protein. An inspection of the linewidths of the hyperfine shifted signals as a function of the magnetic field (Bertini et al. 1994), indicates that the contribution to T_2^{-1} due to Curie relaxation mechanism at 600 MHz ranges, in the case of the native dimeric protein, from 70% to 90%, depending on the signal. Therefore, since τ_{\star} is linearly dependent on the molecular size, the Curie contribution to T_2^{-1} is expected to decrease by a factor of two for M-SOD, if the investigated derivative is really a monomeric analog of WT-Cu(II)₂Co(II)₂SOD. The NMR data provide a nice example of the relevance of the Curie relaxation mechanism in macromolecules at high field and further substantiate the absence of quaternary structure of this analog. The ¹H NMR spectrum of copper-cobalt SOD is therefore a very effective tool for monitoring the monomeric nature of Phe 50Glu, Gly 51Glu mutated protein (M-SOD). Moreover, the decrease of signal linewidths enhances resolution and con-

sequently affords added structural information.

Besides changes in signal linewidths, marked changes in chemical shifts are observed in the ¹H NMR spectra of M-Cu(II)Co(II)SOD. Because of those spectral changes, a straightforward assignment of the hyperfine shifted signals by comparison of the WT-Cu(II)₂Co(II)₂SOD and M-Cu(II)Co(II)SOD cannot be performed. Hence, in order to assign the hyperfine shifted signals, NOESY experiments (Fig. 6) and a titration with sodium azide have

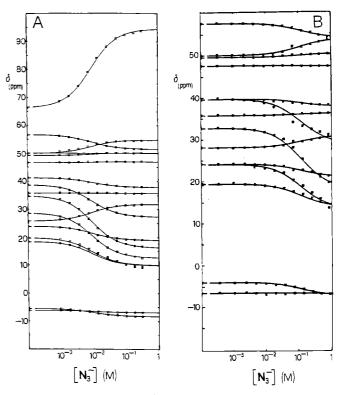


Fig. 7. Chemical shifts of the ¹H NMR hyperfine shifted signals of WT-Cu(II)₂Co(II)₂SOD A and M-Cu(II)Co(II)SOD B as a function of azide concentration. Experiments were performed at 200 MHz, in H₂O solutions, pH 5.5

been performed (Fig. 7). Figure 6 presents NOESY experiments on M-Cu(II)Co(II)SOD (B) and on WT-Cu(II)₂Co(II)₂SOD (A). In the NOESY spectrum the advantage of narrower lines for the mutated protein is lost by the lower τ , which decreases cross relaxation and, as a consequence, the intensities of cross peaks (Ernst et al. 1987; Dugad et al. 1990; Banci et al. 1991 c). Several connectivities can be observed among hyperfine shifted signals on the M-Cu(II)Co(II)SOD derivative. The exchangeable signal at 49.7 ppm is connected to two hyperfine shifted signals at 39.3 ppm and 27.7 ppm (cross peaks 1 and 2, respectively). This pattern has been observed in the dimeric WT-Cu(II)₂Co(II)₂SOD. In such a case it originated exclusively from His46 NHε2, which has two vicinal protons on the imidazole ring. On this basis signals at 49.7, 39.3 and 27.7 ppm have been assigned to His46 NH ε_2 , H δ_2 and H ε_1 , respectively. They are labeled C, G and M according to WT-Cu(II)₂Co(II)₂SOD assignment. Signals G and M can be distinguished by their NOEs in the diamagnetic region. As discussed for the WT-Cu(II)₂Co(II)₂SOD (Banci et al. 1989 a, 1993) the strong connectivity (cross peak 3) observed between the signal at 27.7 ppm and a signal at about 1.0 ppm allows assignment of the signal at 27.7 ppm to signal M (Banci et al. 1993). In Fig. 6A the spectrum of WT-Cu(II)₂Co(II)₂SOD is reported for comparison purposes. Table 1 reports the observed chemical shifts for the two derivatives. In M-Cu(II)Co(II)SOD the chemical shift of signal C differs from the WT-Cu(II), Co(II), SOD by less than 1 ppm, while a more remarkable difference is experienced by signals G and M, i.e. -1.6 and +2.3 ppm, respectively.

Titration experiments of monomer and dimer with azide (Fig. 7) indicate that three hyperfine shifted signals of monomer (one exchangeable and two non exchangeable) undergo dramatic decreases in their chemical shifts. This is similar to what has been observed in the native protein (Bertini et al. 1985a; Banci et al. 1987) and previously interpreted as related to the increase of the Cu-N His48 bond distances when azide binds to the enzyme (Banci et al. 1989 a). This allows us to assign the three signals at 39.4, 32.4 and 23.6 ppm, labeled K, L and O, respectively, to His48 imidazole ring protons. The observed connectivity between signals at 39.4 ppm (overlapping signal G) and 23.6 ppm (cross peak 4, Fig. 6) is consistent with the assignment of K and O as two vicinal protons of the same histidine. Because His48 NH δ_1 (signal K) is 0.24 nm and 0.42 nm apart from His48 H ε_1 and His 48 H δ_2 , respectively, the observed connectivity between K and O discriminate between signal O and L which can be assigned to His48 H ε_1 and His48 H δ_2 , respectively. We observe an increase in the hyperfine shift of 4.7 ppm for signal K and 4.0 ppm for signal O and L occurs in the M-Cu(II)Co(II)SOD with respect to the WT-Cu(II)₂Co(II)₂SOD (see Table 1), corresponding to an increase of 21%, 36% and 19%, respectively, in their hyperfine shifts. The upper part of the two-dimensional spectra of Fig. 6 shows the region of connectivities between the hyperfine shifted signals and the diamagnetic (or slightly hyperfine shifted) signals. In both derivatives signal K experiences a strong cross peak at 12.5 ppm with a signal assigned to His48 H β_2 (Banci et al. 1993) (cross peak 5, Fig. 6). Hence, no difference in chemical shift is observed on His 48 H β_2 , which is at variance with what is observed for His48 imidazole ring protons.

A signal at 19.3 ppm (signal P) yields a small cross peak with the signal at 32.4 ppm (signal L) (cross peak 7) already assigned as His48 H δ_2 . Comparison with NOE data on the WT-Cu(II)₂Co(II)₂SOD allows the assignment of signal P at 19.3 ppm to His46 H β_1 . The cross peak observed between signals at 19.3 ppm and -3.9 ppm (signal R) (cross peak 6, Fig. 6A) allows the observation of both His46 β -CH₂ protons (signals P and R, respectively).

At variance with what is observed in WT-Cu(II)₂Co(II)₂SOD, in which a cross peak is observed between signals B and H (cross peak 11, Fig. 6A), no clear connectivities are observed from signal B (His120 NH δ_1) in the NOESY spectrum of M-Cu(II)Co(II)SOD in the region 70-15 ppm. The assignment of signal B of M-Cu(II)Co(II)SOD to His20 NH δ_1 is straightforward because of its T_1 and T_2 values and because it exchanges in D₂O solution. A one-dimensional NOE experiment (data not shown) has allowed the observation of connectivity between signal B and a signal at about 36 ppm, a region where the monodimensional spectrum indicates the occurrence of four signals. Among these, the signals I, J and J' are almost unaffected by titration with sodium azide (Fig. 7) and therefore can be assigned to cobalt-coordinated proton resonances. The fourth signal, overlapping

Table 1. Chemical shifts of the hyperfine shifted signals of M-Cu(II)Co(II)SOD, recorded at 298 K, and compared with WT-Cu(II)₂Co(II)₂SOD and IIe137-Cu(II)₂Co(II)₂SOD. Signals are labelled according to the usually reported labelling of WT-Cu(II)₂Co(II)₂SOD hyperfine shifted signals

Signal	$_{\delta}^{\mathrm{M}}$	$_{\delta}^{\mathrm{WT}}$	Ile137 δ	Assignment
	(ppm)	(ppm)	(ppm)	
A	63.3	66.0	63.3	His 63 H δ_2
В	57.1	56.4	57.3	His120 NH δ_2
C	49.7	50.3	48.4	His 46 NH ε2
D	49.7	49.4	49.6	His 71 H δ_3
E	49.2	48.8	47.3	$\text{His } 80 \text{ H } \delta_{2}^{2}$
\mathbf{F}	47.1	46.2	47.3	His 80 HN_{ϵ_2}
G	39.3	40.9	47.3	His 46 H δ_3
K	39.3	34.6	38.6	$His 48 NH\delta_1$
I	35.6	36.3	36.1	Asp 83 H β_1
H	35.6	38.5	43.8	$His120 H\epsilon_1$
J′	35.6	35.8	36.1	Asp83 H β_2
J	35.6	35.6	36.1	His 71 HNε ₂
L	32.4	28.4	38.0	His 48 H δ_2
M	27.7	25.5	20.1	$His 46 H \varepsilon_1^2$
N	24.2	23.6	23.7	His 120 H δ_2
0	23.6	19.6	22.5	$His 48 H \varepsilon_1^2$
P	19.3	18.3	16.8	$His 46 H \beta_1$
R	-3.9	-5.6	-8.1	His 46 H β_2
Q	-6.3	-5.6	-6.5	His 71 H β_2

with I, J and J', is assigned to His120 H ε_1 (signal H) because of NOE experiments. In the diamagnetic region, signal B (His120 NH δ_1) is expected from X-ray data (Tainer et al. 1982) to give a strong connectivity with His120 H β_2 . In WT-Cu(II)₂Co(II)₂SOD, His120 H β_2 has been recently assigned at 11.1 ppm (cross peak 8, Fig. 6A), while in the monomer derivative the same connectivity is observed at 12.2 ppm. Hence, in the latter derivative His120 H β_2 is shifted downfield about 1 ppm more with respect to the dimer.

The NOESY spectrum of the monomer is of poorer quality than for WT-Cu(II)₂Co(II)₂SOD, though recorded with a slightly longer experimental time. This is indicated, in the spectrum of M-Cu(II)Co(II)SOD derivative, by the absence of cross peaks between signal A and signals K and L, previously observed in the WT-Cu(II)₂Co(II)₂SOD (i.e., cross peaks 9 and 10, Fig. 6A). The decrease by a factor of two in τ_r (rotational correlation time) causes a decrease by a factor of two in the NOE intensity. For example, the extent of the one-dimensional NOE observed on signal C, when signal M is saturated at 200 MHz, is $2.8 \pm 0.4\%$ in the dimer and $1.0 \pm 0.3\%$ in the monomer. Since the T_1 values of signal C in the two derivatives are basically similar, the NOEs are consistent with a 50% reduction of the rotational correlation time. Again this effect provide spectroscopic evidence of the monomeric nature of the presently investigated deriva-

The occurrence of a sizable increase of the hyperfine shift of His 48 imidazole ring protons is, perhaps, the most noteable feature of the ¹H NMR spectrum of M-Cu(II)Co(II)SOD. The same observation, though of different magnitude, was observed for the SOD analog

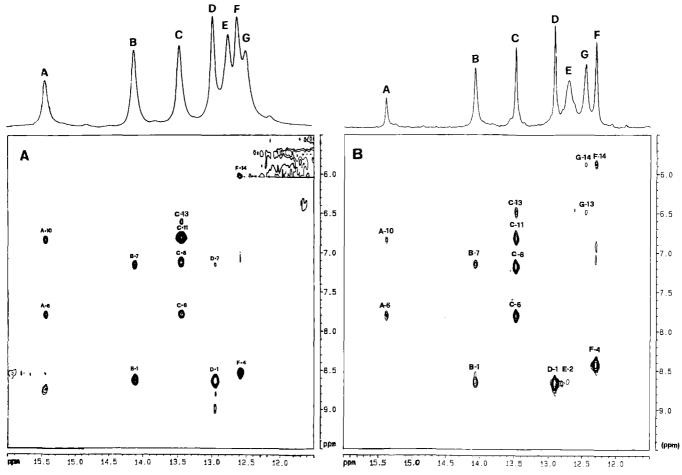


Fig. 8. 600 MHz ¹H NMR NOESY spectra of A WT-Cu(I)₂Zn(II)₂SOD and B M-Cu(I)Zn(II)SOD. Signals are labeled according to the labeling reported in Table 2. Conditions: mixing time 100 ms, relaxation delay 500 ms

Thr137 Ile and was related to the occurrence of an increase in the Cu-N48 bond strength which makes the chromophore more axial (Bertini et al. 1989). The effect observed on the monomer as well as on the Ile137 mutated protein is opposite to that observed upon addition of anions like azide or cyanide (Banci et al. 1990 d, 1989 b; Bertini et al. 1991 b) which cause a sizable decrease of the hyperfine shift of His48 proton resonances.

The assignments made here on the basis of the NOESY experiment in comparison with the NMR data on WT-Cu(II)₂Co(II)₂SOD is confirmed by the interaction of M-Cu(II)Co(II)SOD with sodium azide. The chemical shifts of the hyperfine shifted signals of M-Cu(II)Co(II)SOD with increasing amounts of sodium azide are displayed in Fig. 7. Because only signals of copper-coordinated residues are affected by interaction with azide, signals I, J, J', D, E are readily assigned to protons of cobalt-coordinated residues. Their shift is essentially unaltered with respect to WT-Cu(II)₂Co(II)₂SOD. With regard to signals of copper-coordinated residues, the well known chemical shift dependence of signals K, L, and O of WT-Cu(II)₂Co(II)₂SOD with azide concentration has been previously discussed. Signals deriving from His 48 protons move toward the diamagnetic region, indicating that the quenching of the hyperfine coupling of His 48 poton signals upon azide binding is observed in the case

of the monomer derivative as well. The shift of the signal of the bridging His63 (A), as well as that of two of the three imidazole ring protons of His46, should experience an opposite trend, i.e. a chemical shift increase.

The affinity constant of M-Cu(II)Co(II)SOD for azide is $10.6\pm1.5~{\rm M}^{-1}$. Interestingly this value is lower than that measured for WT-Cu(II)₂Co(II)₂SOD ($138\pm5~{\rm M}^{-1}$) and correlates with a decrease in activity observed for the monomer. A similar trend of azide affinity and enzymatic activity has been found in most SOD analogs investigated to date (Beyer et al. 1987; Banci et al. 1988). This correlation demonstrates the importance of electrostatic factors in the catalytic reaction. For M-SOD the introduction of two negative charges (i.e. Glu), even if on the surface and far from the metal size, directly or indirectly modifies the electrostatic field around the protein, thus affecting the entrance of negative ions into the catalytic channel.

Cu(I) Zn(II) SOD derivatives. The reduced form of native SOD has been characterized through ¹H NMR spectroscopy (Lippard et al. 1987; Bertini et al. 1991a; Cass et al. 1977b; Stoesz et al. 1979; Mota de Freitas et al. 1990; Paci et al. 1990). A previous reported investigation of WT-Cu(I)₂Zn(II)₂SOD (Bertini et al. 1991a) has allowed the assignment of imidazole ring resonances of the dimeric enzyme. NOESY experiments on the reduced

Table 2. Chemical shift values of imidazole ring proton resonances of M-Cu(I)Zn(II)SOD and WT-Cu(I)₂Zn(II)₂SOD, at 298 K and pH 5.5. Signals are labelled according to the previously reported labelling of the imidazole ring proton resonances of WT-Cu(I)₂Zn(II)₂SOD (Bertini et al. 1991a)

Signal	M	WT	Assignment
	δ (ppm)	δ (ppm)	
A	15.38	15.40	His71 HNε,
В	14.06	14.06	His 43 HN ε_2
C	13.48	13.42	$His 46 HN \epsilon_2$
D	12.90	12.90	$\text{His 43 HN} \delta_1$
E	12.69	12.70	His 80 HN ε_2
F	12.29	12.54	$\text{His 48 HN} \delta_1$
G	12.44	12.44	$His 63 HN \epsilon_2$
1	8.64	8.64	His 43 H ε_1
2 3	8.63	8.57	$His 80 H \varepsilon_1$
	_	8.54	$His110 H\epsilon_1$
4	8.41	8.52	$His 48 H \varepsilon_1$
5	_	8.29	$His120 H_{\epsilon_1}$
6	7.79	7.78	His 71 H ε_1
7	7.14	7.14	His 43 H $\dot{\delta}_2$
8	7.11	7.11	$\text{His 46 H }\delta_2$
9	6.91	6.86	$\text{His 80 H }\delta_2^2$
10	6.84	6.82	$His 71 H \delta_2^2$
11	6.78	6.78	$His 46 H \epsilon_1^2$
12	_	6.64	$\text{His} 120 \text{H} \hat{\delta}_2$
13	6.48	6.57	$His 63 He_1^2$
14	5.86	6.05	$His 64 H \delta_2$

monomeric derivative (Fig. 8B) have been similarly performed and compared with the data obtained on the analogous dimeric wild type (Fig. 8A). As above a sizable reduction in signal linewidth of the monomer is observed. This effect is most apparent in the region between 17 and 12 ppm, where well resolved NH resonances of imidazole ring protons are observed. The obvious comparison of the two spectra of Fig. 8 allows the assignment of signals, as reported in Table 2. For comparison the signals have been labeled as in a previous reported investigation of WT-Cu(I)₂Zn(II)₂SOD (Bertini et al. 1991a). It is observed that while chemical shifts of the non-metal coordinated His 43 resonances are identical, for other metal-coordinated residues some variations are observed. In particular, the two assigned signals of His 48 (NH δ_1 and H ϵ_1) and two of the three imidazole ring resonance of His 63 $(H\varepsilon_1 \text{ and } H\delta_2)$ experience decreases in chemical shifts from 0.09 to 0.25 ppm in the monomer with respect to the dimer, suggesting that the performed mutations reflect slight changes in the active site. Nevertheless the NOESY spectrum does not show evidence of significant changes in the interproton distances: all the observed connectivities of spectrum 8A are confirmed in the monomer derivative, with relative intensities of cross peaks always conserved. The narrower signals afford additional interpretative information from bidimensional maps. For example, connectivities involving signals E and G in the monomer are visible in the NOESY spectrum, while in the dimer, connectivities G-13, G-14, E-2, could be detected only through monodimensional NOE difference spectra.

Concluding remarks

The spectroscopic characterization of a monomeric analog of SOD reveals some structural changes in the ligand arrangement around the metal ions: the increase in A_{\parallel} , the axial EPR spectrum, the increase in Cu-OH, distance, the ipsochromic shift of d-d transitions and some variations in the hyperfine shifts of the histidine protons in the axial EPR spectrum, the increase in Cu-OH₂ distance, the ipsochromic shift of d-d transitions and some variations in the hyperfine shifts of the histidine protons in M-Cu(II)Co(II)SOD indicate a structural change of the CuN₄ chromophore towards planarity. The above spectroscopic parameters are similar to those observed in the Thr137Ile SOD analog for which a slight distortion toward planarity (Banci et al. 1991b) and a 1.4-fold reduction in specific activity (Bertini et al. 1989) (probably originating from changes in hydrophilicity (Bertini et al. 1989) and altered arrangement of charged residues in the active site channel (Banci et al. 1992)) were observed. The observation that substitution so far from the metal ions provides structural changes substantially analogous to those determined by the replacement of a residue inside the active cavity may shed new light in the understanding of the factors affecting structure-function relationships in SOD. In the monomer, substitutions so far from the metal ions (1.3 and 1.4 nm from copper(II) to Phe 50 and Gly 51) and from the active site channel would probably not *directly* induce a significant change in the active site. It seems more likely that such structural changes derive indirectly via extensive solvation of the newly exposed dimer interface and/or its distortion. It is possible that the similar arrangement around copper of Thr137 Ile SOD and M-SOD is due to a balance of different contributions; the active channel is probably different since one is much more active than the other.

In M-SOD such changes presumably may also effect the active site channel which contributes to substrate docking and could be responsible for an approximately 10-fold reduction in specific activity observed in the monomer. In other mutated proteins such those in which the Arg143 (Beyer et al. 1987; Banci et al. 1988) has been substituted with a neutral or negative ligand or where Glu133 (Getzoff et al. 1992) has been replaced with a neutral residue, it has been shown that electrostatic forces are important in determining the dismutation rate under non saturating conditions. For monomeric SOD, reduced enzymatic activity may likely be ascribed to the introduction of two negative groups, though far from the active site, and/or to the restructuring of the exposed dimeric interface with concomitant shift of various unspecified charged residues. This hypothesis is consistent with the observed 15-fold reduction in affinity for azide.

Finally the monomerized protein, because of its reduced molecular weight, shows narrower NMR linewidths thus providing additional useful structural information. It would therefore also seem likely that larger proteins with higher quaternary structure (e.g., tetrameric human catalase) could be similarly "monomerized" by appropriate mutagenesis and thus permit for the first time NMR studies of large proteins not now accessible to this kind of analysis.

Acknowledgements. The Italian Council for Research (C.N.R.) is acknowledged for financial support to M.S.V. who prepared the mutated protein here described at Chiron Corporation, in 1990.

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