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## Effects of Glyoxime and Dichloroglyoxime on Lysozyme: Kinetic and Structural Studies

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**Abstract:** Kinetic and structural studies have been made on the effect of glyoxime (GO) and dichloroglyoxime (DCGO) on the activity and the structure of lysozyme in 100 mM potassium phosphate buffer, pH 7.0, using UV spectrophotometry, circular dichroism (CD) and fluorescence spectroscopy techniques. GO and DCGO act as an uncompetitive inhibitors with  $K_i = 99$  and  $52 \mu\text{M}$ , respectively. Circular dichroism studies show that the secondary structure of the enzyme in the presence of different concentrations of GO and DCGO does not show considerable change. Kinetic results show that at low concentration of GO ( $0.12$ - $120 \mu\text{M}$ ) and DCGO ( $0.07$ - $64 \mu\text{M}$ ) considerable inhibition of enzyme could be seen, but the fluorescence data show that there is not noticeable change in the tertiary structure of lysozyme at low concentration of inhibitors. Also, these results indicate considerable decrease in the tertiary fold of the lysozyme at high concentrations of GO and DCGO especially dichloroglyoxime. Results show that, lysozyme in the presence of high concentration of GO ( $1200 \mu\text{M}$ ) and DCGO ( $640 \mu\text{M}$ ), presents structural characteristics of a molten globule like state.

**Key words:** Lysozyme,  $\alpha$ -dioxime, glyoxime, dichloroglyoxime, inhibition, molten globule state

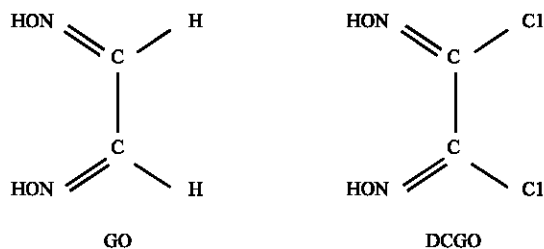
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### Introduction

$\alpha$ -dioxime derivations have many applications in the industry and agriculture, for example, for chemical sensors that are used for special elements and for pesticides, fungicides and bactericides. Remarkable activity against gram-positive and gram-negative bacteria as well as certain yeast was observed for dichloroglyoxime. In addition, these substances effect biological systems adversely. For example, dimethyl glyoxime causes irritation of the eye, skin, digestive and respiratory systems and moreover, proven dangerous if ingested. Experimental results show that these substances are mutagens (Khalili *et al.*, 1986; Bing *et al.*, 1999; Ayres *et al.*, 2002). Lysozyme (EC 3.2.1.17) is found in various animal and plant tissues, e.g., in tear liquid and chicken egg white. It functions as an antibacterial agent catalyzing the hydrolysis of a major cell-wall polysaccharide of

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Scheme 1

certain bacteria (Ovchinnikov, 1996). This enzyme hydrolyses  $\beta(1-4)$  glycosidic linkage from NAM (N-acetylmuramic acid) to NAG (N-acetylglucosamine) in the alternating NAM-NAG polysaccharide component of cell wall peptidoglycan of bacteria. Lysozyme is single domain protein and the active site is located just in the cleft (Ovchinnikov, 1996; Schomburg *et al.*, 1991; Smith *et al.*, 1993). Hen egg white lysozyme is one of the most studied and best characterized globular proteins. It was the first enzyme to have its structure determined by X-ray diffraction and has ever since been extensively used as a system in which the underlying principles of protein structure, function, dynamics and folding can be studied through both experimental theoretical approaches (Smith *et al.*, 1993; Matagne *et al.*, 1998; Alizadeh *et al.*, 2003; Godjaev *et al.*, 1998; Fujita *et al.*, 1995; Iwase *et al.*, 1999; Johannesson *et al.*, 1997; Schwalbe *et al.*, 2001; Kristiansen *et al.*, 1998).

Lysozyme binds to various small ligands which mimic the interaction of the acetamido group of its natural substrates within the active cleft of the enzyme (Johannesson *et al.*, 1997; Imoto *et al.*, 1972). Glyoxime (GO) and dichloroglyoxime (DCGO) were synthesized (Scheme 1) in our laboratory (Kakanejadifard *et al.*, 2003, 2004) and in the present research we describe the catalytic behavior and structural changes of lysozyme in the presence of GO and DCGO.

## Materials and Methods

### Materials

The hen egg white lysozyme and *Micrococcus lysodeikticus* were purchased from Sigma (St. Louis, Mo, USA). The enzyme was homogenous on SDS-PAGE. All other chemical reagents were from Merck (Darmstadt, Germany) and reagent grade. The solutions were prepared in double distilled water. Glyoxime was obtained by the condensation of glyoxal and hydroxylamine in water at 0°C and dichloroglyoxime were synthesized by chlorination of glyoxime in ethanol in our laboratory (Kakanejadifard *et al.*, 2003, 2004; Coburn, 1968; Willer *et al.*, 1985; Kanno *et al.*, 1995).

### Determination of Enzymatic Activity and Protein Concentration

Enzymatic activity was determined using *Micrococcus lysodeikticus* as substrate in 100 mM potassium phosphate buffer, pH 7.0. One enzymatic unit is equal to a decrease in turbidity of 0.001 per minute at 450 nm at pH 7.0 under specified conditions (Worthington, 1993). The protein concentration was determined by Lowry *et al.* (1951) method.

### Circular Dichroism (CD) Measurements

CD spectra were recorded on a JASCO J-715 spectropolarimeter (Japan) using solutions with protein concentrations varying from 0.15 (far-UV) to 2 mg mL<sup>-1</sup> (near-UV). The results were

expressed as molar ellipticity,  $[\theta]$  ( $\text{deg cm}^2 \text{dmol}^{-1}$ ), based on a mean amino acid residue weight (MRW) assuming its average weight for lysozyme to be equal to 111.5. The molar ellipticity was determined as  $[\theta] = (\theta \times 100 \text{MRW}) / (cl)$ , where  $c$  is the protein concentration in milligrams per milliliter,  $l$  is the light path length in centimeters and  $\theta$  is the measured ellipticity in degrees at a wavelength  $\lambda$ . The instrument was calibrated with (+)-10-camphorsulfonic acid, assuming  $[\theta]_{291} = 7820 \text{ deg cm}^2 \text{dmol}^{-1}$  (Schippers *et al.*, 1981) and with JASCO standard nonhydroscopic ammonium (+)-10-camphorsulfonate, assuming  $[\theta]_{290.5} = 7910 \text{ deg cm}^2 \text{dmol}^{-1}$  (Takakuwa *et al.*, 1985). Noise in the data was smoothed using the JASCO J-715 software, including the fast Fourier-transform noise reduction routine which allows enhancement of most noisy spectra without distorting their peak shapes (Protasevich *et al.*, 1997; Ataie *et al.*, 2004; Khajeh *et al.*, 2001).

#### *Intrinsic Fluorescence Measurements*

The fluorescence emission spectra of the enzyme were performed in a Perkin-Elmer luminescence spectrometer LS50B. The spectra were measured in 100 mM phosphate buffer, pH 7.0 and the final concentration of 10  $\mu\text{M}$  for lysozyme. The fluorescence emission was scanned between 300 and 400 nm with an excitation wavelength of 280 nm.

#### *Aggregation Measurements*

Lysozyme at a concentration of 0.5  $\text{mg mL}^{-1}$  in 100 mM phosphate buffer, pH 7.0, in the presence of different concentrations of GO and DCGO were placed in Perkin-Elmer luminescence spectrometer LS50B cuvette. The excitation and emission monochromators were set at 350 and 355 nm with the band passes of 1.5 nm and the extent of light scattering was monitored. The scattering effect, due to different concentrations of GO and DCGO, was corrected in all relevant cases.

Results presented in this paper are the mean from at least three repeated experiments in a typical run to confirm reproducibility.

## **Results and Discussion**

#### *Catalytic Parameters of Lysozyme in the Presence of $\alpha$ -dioxime Derivatives*

The activity of lysozyme has been estimated in the presence of different concentrations of glyoxime and dichloroglyoxime. The enzyme activity decreases as the concentration of GO and DCGO increase (Fig. 1). Effects of the inhibitors on lysozyme is time-independent and

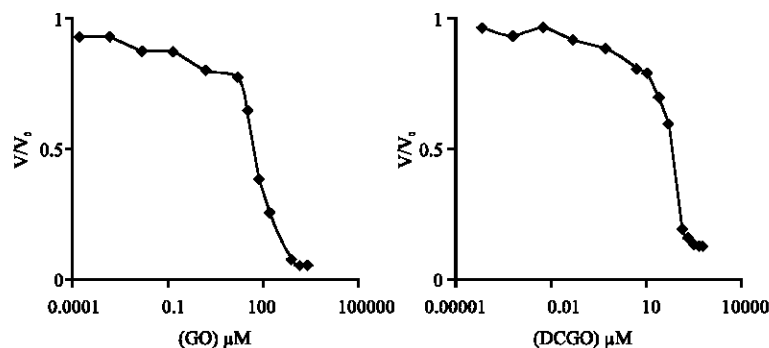


Fig. 1: Dose-response curves of lysozyme activity as a function of different concentrations of glyoxime (a) and dichloroglyoxime (b)

Table 1: Kinetic parameters for lysozyme in the absence and presence of glyoxime and dichloroglyoxime

Ligand	C ( $\mu\text{M}$ )	$K_m$ ( $\text{mg mL}^{-1}$ )	$V_{max}$ (unit)
Control	-	0.69	139
	120.00	0.29	60
	12.00	0.61	124
+Glyoxime	1.20	0.68	138
	0.12	0.69	139
	64.00	0.31	62
	6.40	0.61	124
+Dichloroglyoxime	0.64	0.68	138
	0.07	0.69	139

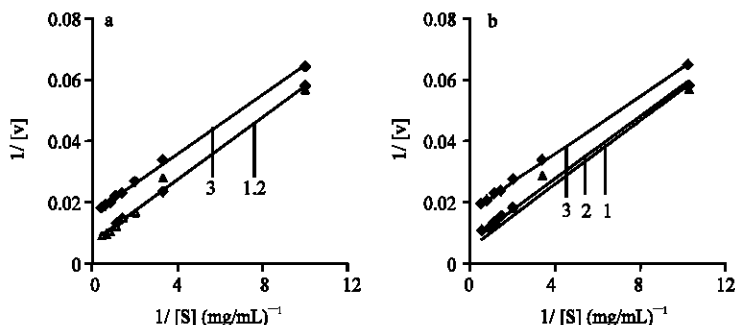


Fig. 2: Lineweaver-Burk plots of lysozyme in the absence and presence of different concentrations of glyoxime (a) (1) 0, (2) 0.12, (3) 120  $\mu\text{M}$  and dichloroglyoxime (b) (1) 0, (2) 6.4 and (3) 64  $\mu\text{M}$

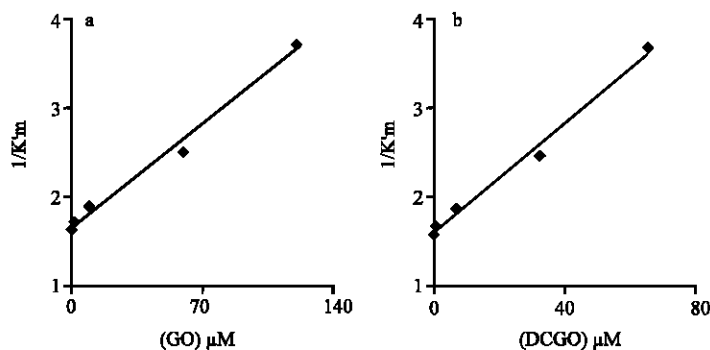


Fig. 3: Plot of  $1/K'_m$  versus different concentration of inhibitors;  $K'_m$  is the apparent Michaelis constant in the presence of inhibitor glyoxime (a) and dichloroglyoxime (b)

after effects of inhibitor on lysozyme is eliminated with dialysis against buffer, activity of the enzyme is recovered (data not shown). These results show that lysozyme inhibition with GO and DCGO is reversible. To compare the inhibition effects of GO and DCGO,  $IC_{50}$  values of these compounds based on Fig. 1 were evaluated. These values are 60 and 95  $\mu\text{M}$  for DCGO and GO, respectively. Our results indicate that inhibition strength of DCGO is higher compared to GO. This could be due to the presence of chloride in DCGO and its high electronegativity. Fig. 2 shows lineweaver-Burk plots of lysozyme in the absence and the presence of different concentrations of GO and DCGO.  $V_{max}$  and  $K_m$  of the enzyme, in the

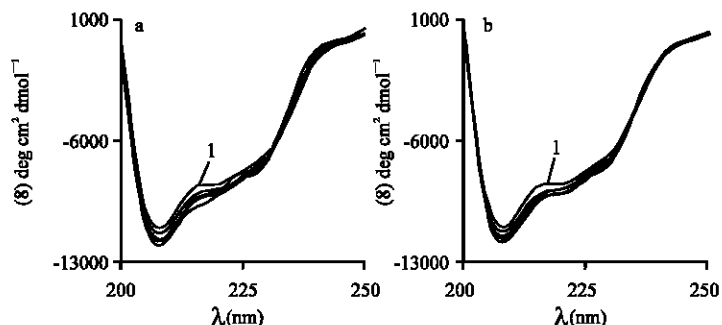


Fig. 4: Far-UV CD spectra of lysozyme in the absence and presence of the different concentrations of glyoxime (a) and dichloroglyoxime (b). (1) in the absence and others in the presence of glyoxime and dichloroglyoxime

presence and absence of inhibitors, were obtained and the type of inhibition was discussed.  $V_{max}$  and  $K_m$  decreased as the concentration of these substances increased (Table 1). These results indicate that inhibition mechanism is uncompetitive (Copeland, 2000). The secondary plot was prepared to calculate  $K_i$  (Fig. 3) (Copeland, 2000; Saboury *et al.*, 2002) and subsequently, the inhibition constants for GO and DCGO were shown to be 99 and 52  $\mu\text{M}$ , respectively. These results confirm the finding that inhibition strength of DCGO is higher than GO.

Comprehensive structural studies have been reported for GlcNAc oligosaccharides, urea and DMSO all of which bind to the active site of the enzyme both in crystal (Blake *et al.*, 1994) and in solution (Cohen and Jardetzky, 1968; Lumb and Dobson, 1992). DMSO, at low concentration, binds to the active cleft and the protein surface and at high concentration, disrupts the tertiary fold of lysozyme (Johannesson *et al.*, 1997). GO and DCGO can form as many hydrogen bonds with the enzyme as N-acetyl glucose amine or urea, the similarity of their structures with acetamido group suggests that they can bind to the active cleft and the enzyme surface. Our results show that GO and DCGO is able bind to enzyme-substrate [ES] complex.

#### *Circular Dichroism and Fluorescence Measurements of GO- and DCGO- Induced Equilibrium Denaturation*

The far-UV-CD spectra of the lysozyme obtained in phosphate buffer, pH 7.0 at different GO and DCGO concentrations are shown in Fig. 4. Percentage of secondary structures in lysozyme, in the absence and presence of glyoxime and dichloroglyoxime, are displayed in Table 2.

Upon the addition of the mentioned inhibitors (0.00064-640  $\mu\text{M}$  of DCGO and 0.0012-1200  $\mu\text{M}$  of GO) CD spectra of lysozyme show a very slight increase in the negative ellipticity at 208 and 222 nm with respect to that of the proteins in the buffer only. In fact, these results show that the enzyme ellipticity at 222 nm, characteristic of the  $\alpha$ -helical conformation, does not change in the presence of GO and DCGO, indicating that a native-like secondary structure persists even at 640  $\mu\text{M}$  of DCGO and 1200  $\mu\text{M}$  of GO. The fluorescence emission spectra of lysozyme in phosphate buffer, pH 7.0 at different concentrations of GO and DCGO are shown in Fig. 5. The observed effect of initial increase of lysozyme fluorescence could be interpreted as the consequence of inhibitor binding in the cleft region, in the proximity of Trp62, Trp63 or Trp108, which decreases the accessibility of indole rings for water molecules. Upon addition of these substances, the tryptophan fluorescence of the lysozyme gradually decreases. The decrease is observed in the fluorescence intensity, suggesting that

Table 2: Secondary structure percentage of lysozyme in the absence and presence of glyoxime and dichloroglyoxime

Ligand	C ( $\mu\text{M}$ )	$\alpha$ -helix (%)	$\alpha$ -structure (%)	Random coil (%)
Control	-	29.3	32.5	38.3
	$1.2 \times 10^{-3}$	30.1	31.6	38.2
	$1.2 \times 10^{-1}$	30	32.4	37.6
	12	30.1	31.6	38.3
+Glyoxime	120	29.4	31.9	38.8
	580	29.7	32.7	37.6
	870	30.2	32.4	37.4
	1200	31.3	31.5	37.2
	$6.4 \times 10^{-4}$	30.7	30.9	38.6
	$6.4 \times 10^{-2}$	30.6	31.4	38.0
	6.4	30.9	30.9	38.2
+Dichloroglyoxime	64	30.1	32.1	37.8
	320	30.7	32.2	37.1
	480	30.3	31.5	38.1
	640	30.8	30.8	38.4

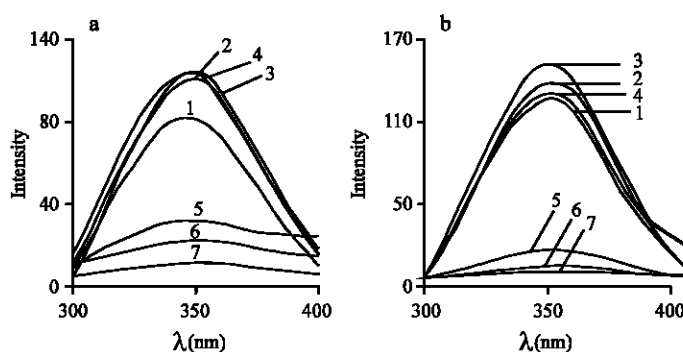


Fig. 5: Fluorescence emission spectra of lysozyme in the absence and presence of different concentrations of glyoxime (a) (1) 0, (2)  $1.2 \times 10^{-3}$ , (3)  $1.2 \times 10^{-1}$ , (4) 12, (5) 580, (6) 870 and (7) 1200  $\mu\text{M}$  and dichloroglyoxime (b) (1) 0, (2)  $6.4 \times 10^{-4}$ , (3)  $6.4 \times 10^{-2}$ , (4) 6.4, (5) 320, (6) 480 and (7) 640  $\mu\text{M}$

at high concentrations of GO (580-1200  $\mu\text{M}$ ) and DCGO (320-640  $\mu\text{M}$ ), there is a change in the tertiary structure of the protein, resulting in the exposure of the buried tryptophans to the polar solvent. In other words, the intrinsic fluorescence reduction along with the red shift shows that the enzyme has denatured at high concentrations of glyoxime and dichloroglyoxime. The tertiary fold reduction of lysozyme at high concentrations of these reagents (especially DCGO) could probably be the consequence of water structure breaking down by the formation of strong hydrogen bonds between these reagents and the water molecules. The expansion of the protein structure, occurs at the 1200  $\mu\text{M}$  and 640  $\mu\text{M}$  of GO and DCGO, respectively. Previously, the neutron diffraction and the computer simulation studies of DMSO-water mixtures revealed similar results (Soper *et al.*, 1992; Luzar *et al.*, 1993; Iwase *et al.*, 1999). Present results indicate that at high concentrations of both reagents, lysozyme adopts the features of the molten globule state, with substantial secondary structure and at the same time, the tertiary structure is less organized than that of the native state (Hosseinkhani *et al.*, 2004; Asghari *et al.*, 2004; Boren *et al.*, 1999).

#### Aggregation Measurements

Light scattering methods provide a sensitive measure of aggregate formation in protein solutions (Rajaraman *et al.*, 1996). Figure 6 shows the light scattering profile of the lysozyme ( $0.2 \text{ mg mL}^{-1}$ ) as

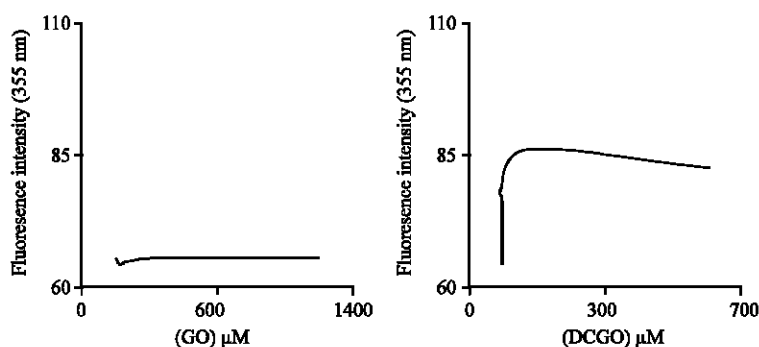


Fig. 6: Light scattering profiles of lysozyme as a function of different concentrations of glyoxime (a) and dichloroglyoxime (b)

a function of different concentrations of GO and DCGO. Results indicate that in the presence of DCGO, significant aggregation takes place since the folding or unfolding intermediates of proteins, including the molten globule intermediates, expose hydrophobic surfaces and create a tendency to aggregate (Fig. 6).

Thus, lysozyme activity, at low concentrations of GO and DCGO is inhibited by a mechanism that is uncompetitive and in the presence of high concentrations of these reagents, the enzyme displays structural characteristics of a molten globule like state. Several proteins in this state have been shown to be sticky and prone to aggregation (Goto, 1991; Sivaraman *et al.*, 1997). However, in the light of the aggregation data obtained, the probability of molten globule state induction for lysozyme is higher in the presence of DCGO

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