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EXCLI Journal 2014;13:611-622 – ISSN 1611-2156
Received: March 07, 2014, accepted: April 14, 2014, published: May 27, 2014

Original article:

CONFORMATIONAL CHANGES OF A CHEMICALLY MODIFIED HRP: FORMATION OF A MOLTEN GLOBULE LIKE STRUCTURE AT pH 5

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ABSTRACT

Horseradish peroxidase is an all alpha-helical enzyme, which widely used in biochemistry applications mainly because of its ability to enhance the weak signals of target molecules. This monomeric heme-containing plant peroxidase is also used as a reagent for the organic synthesis, biotransformation, chemiluminescent assays, immunoassays, bioremediation, and treatment of wastewaters as well. Accordingly, enhancing stability and catalytic activity of this protein for biotechnological uses has been one of the important issues in the field of biological investigations in recent years. In this study, pH-induced structural alterations of native (HRP), and modified (MHRP) forms of Horseradish peroxidase have been investigated. Based on the results, dramatic loss of the tertiary structure and also the enzymatic activity for both forms of enzymes recorded at pH values lower than 6 and higher than 8. Ellipticiy measurements, however, indicated very slight variations in the secondary structure for MHRP at pH 5. Spectroscopic analysis also indicated that melting of the tertiary structure of MHRP at pH 5 starts at around 45° C, which is associated to the pK_a of His 42 that has a serious role in keeping of the heme prostethic group in its native position through natural hydrogen bond network in the enzyme structure.

According to our data, a molten globule like structure of a chemically modified form of Horseradish peroxidase at pH 5 with initial steps of conformational transition in tertiary structure with almost no changes in the secondary structure has been detected. Despite of some conformational changes in the tertiary structure of MHRP at pH 5, this modified form still keeps its catalytic activity to some extent besides enhanced thermal stability. These findings also indicated that a molten globular state does not necessarily preclude efficient catalytic activity.

Keywords: Horseradish peroxidase, conformational transition, molten globule like structure

INTRODUCTION

Peroxidases are a class of heme-containing enzymes that are catalytically active in the ferric form, oxidizing several substrates such as cytochrome c, substituted phenols, and some of the more negative methoxybenzenes (Sakurada et al., 1986; Kersten et al., 1990). According to the origin, peroxidases are generally divided into three classes including prokaryotes (class I), fungi (class II), and plant peroxidases (class III) (Welinder, 1992). Horseradish peroxidase isoenzyme C (HRP, EC 1.11.1.7), one

of the best-characterized peroxidases, belongs to class III, which its X-ray structure has been reported in Protein Data Bank (Gajhede et al., 1997). The structure of this enzyme, like the other peroxidases such as peanut peroxidase (Schuller et al., 1996), and the major peroxidases from barley (Henriksen et al., 1998), shows the similar overall protein fold with two Ca^{2+} ions buried in the proximal and distal portions of the heme pocket (Figure 1). This monomeric heme-containing plant peroxidase is widely used as a reagent for the organic synthesis, biotransformation, chemiluminescent assays, immunoassays, bioremediation, and treatment of wastewaters (Veitch and Smith, 2001; Krieg and Halbhuber, 2003; Veitch, 2004). Several investigations have been performed in order to increase the enzyme's structural stability and functionality as well. Based on some of these studies, the structural Ca^{2+} ions play a very important role in the activity and the thermal stability of the enzyme. NMR experimental studies have also indicated that the Ca^{2+} ions are essential in maintaining the native fold structure of the protein and furthermore, the refolding of the recombinant HRP is dependent on the presence of these ions in the buffer solution (Garguilo et al., 1993; Pappa and Cass, 1993). Several strategies have been employed to thermodynamically and kinetically increasing the stability of this enzyme, using several approaches such as site-directed mutagenesis, directed evolution (Hult and Berglund, 2003; DeSantis and Jones, 1999), and chemical modifications as well (Davis, 2003; Hassani et al., 2006). Chemical modification approaches are useful tools to determine the physico-chemical properties of the individual amino acids, their participation in the native folded state (Torchilin et al., 1979), protein stabilization (Ryan et al., 1994; Miland et al., 1996a, b; Mozhaev et al., 1988, 1992), and also their transition into the molten globule structures (Hosseinkhani et al., 2004; Naseem et al., 2004; Khatunhaq et al., 2002). In the previous investigations, significant stabilization achieved using chemical modifications (Mozhaev et al., 1988; Wong and Wong, 1992), and surface modifications have also shown to stabilize the native fold of the proteins (Hassani et al., 2006; Khajeh et al., 2001a, b). In the present study, using citraconic anhydride, modification of the ε-amino groups of the Lys residues in horseradish peroxidase has been performed. The following induced structural changes have been measured by means of circular dichroism and fluorescence spectroscopy. According to the results, we can suggest that the formation of a molten globule-like structure occurs due to the chemical modification at slightly acidic pH conditions. The results of thermal studies have also shown different transition phases for the protein structure.

Figure 1: Schematic representation of the tertiary structure of HRP (PDB accession code: 6ATJ). Three Lys residues 174, 232, and 241 that have been modified by citraconic anhydride are depicted in blue, two structural calcium ions in green, heme prosthetic group in red, and the His 42 in yellow.

MATERIALS AND METHODS

Chemicals

Lyophilized powder of horseradish peroxidase isoenzyme C was purchased from Sigma chemical company (St. Louis, USA) and used without further purifications. The purity of the peroxidase preparations was determined by assessing the ratio of the heme absorbance at 403 nm to the protein absorbance at 280 nm, which is denoted as the R_Z value (Hassani et al., 2006). The R_Z of the protein solution used for the experiments was above 3.0. The concentration of HRP

EXCLI Journal 2014;13:611-622 – ISSN 1611-2156
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was determined spectrophotometrically using the extinction coefficient of 102 $M^{-1}\cdot cm^{-1}$ at 403 nm (Hassani et al., 2006; Goto et al., 1990a, b). All of the reagents were of analytical grade and supplied by Merck (Darmstadt, Germany) or Sigma.

Spectroscopic studies

The pH-induced conformational changes of HRP were measured by fluorescence and CD spectroscopy. Intrinsic fluorescence intensity measurements were carried out using a PerkinElmer (LS-50 B) fluorimeter with a 1 cm light-path cell. Tryptophan fluorescence was induced by the excitation of the sample at 295 nm and the emission was recorded between 320 and 400 nm. Extrinsic fluorescence studies were carried out using 1-anilino-8-naphthalenesulfonic acid as a fluorescent probe (Hosseinkhani et al., 2004). All of the experiments were carried out at 25° C with ANS and protein concentrations of 50 μM and 1 μM in 0.02 M phosphate buffer. An excitation wavelength of 380 nm was used and the emission recording was scanned from 400 to 600 nm. CD measurements were carried out using a Jascospectropolarimeter, model J-715. The ellipticity values were obtained in millidegrees directly from the instrument and converted to the molecular ellipticity, $[\theta]_{MRW}$, expressed in $deg\cdot cm^2\cdot dmol^{-1}$ (Goto et al., 1990a; b; Strickland, 1968), based on a mean amino acid residue weight (MRW), assuming the average weight for HRP to be 110. The molar ellipticity was determined using the equation:

$$[\theta]_{MRW} = \frac{\theta \times 100\ MRW}{c \times l}$$

where c is the protein concentration in mg/ml, l is the light path length in centimeters, and θ is the measured ellipticity in degrees at wavelength λ. The instrument was calibrated with (+)-10-camphorsulfonic acid, assuming $[\theta]_{291} = 7820\ deg\cdot cm^2\cdot dmol^{-1}$ (Hewlett et al., 1991), and with Jascostandard nonhydroscopic ammonium (+)-10-camphorsulfonate assuming $[\theta]_{290.5} = 7910\ deg\cdot cm^2\cdot dmol^{-1}$ (Merrill et al., 1990). Noise in the data was smoothed using the Jasco (J-715) software including the fast Fourier-transform noise reduction routine, which allows refinement of the recorded spectra without distorting the peak shapes (Merrill et al., 1993). The far-UV CD spectra were measured using a rectangular quartz cell of 1 mm path length with a sample concentration of 0.15 mg/ml. Each spectrum was an average of at least three scans between 250 and 200 nm. The resultant ellipticities of the HRP solutions were calculated by subtracting the ellipticity of the buffer solution. The visible CD spectra were measured using a rectangular quartz cell of 1 cm path length and a sample concentration of 2 mg/ml. Each spectrum was an average of at least three scans between 450 and 350 nm. The wavelengths of 222 and 407 nm were used to monitor the thermal denaturation in the far-UV and the visible CD range, respectively. In the thermal studies, the temperature was raised stepwise from 30° C to 90° C with an equilibration time of 1 min for each 2° C. pH values were measured before and after of each run and its variations were not greater than ± 0.1 pH unit.

Activity assays

All assays of the enzymatic activity were carried out in 96-well flat-bottomed microtiter plates (Ryan et al., 1994). 20 μl of HRP (5×10^{-4} mg/ml) solution in 0.02 M phosphate buffer was dispensed into each well and followed by 180 μl of buffered substrate solution (0.2 M phosphate buffer, containing 0.0017 M hydrogen peroxide and 0.0025 M 4-aminoantipyrine with 0.17 M phenol) (Parker et al., 1994). Reactions took place at 25° C for 4 min. A_{495}values were then read in an Anthos 2020 ELISA reader instrument. All of the kinetic parameters for the enzyme were determined from the average of at least three substrate measurements at each substrate concentration and pH. Values for K_m and k_{cat} were obtained from the Lineweaver–Burk equation. The dependence of the initial velocity upon substrate concentration was hyperbolic at each pH value under investiga-

tion and all of the Lineweaver–Burk plots were linear.

Modification of Lysine residues

The modification process was carried out using citraconic anhydride as a specific blocking agent for the Lysine residues following the standard procedure (Steer and Merrill, 1994). The protein was used at 5 mg/ml in 5 ml of 0.1 M borate buffer at pH 8 and the procedure was carried out at room temperature with stepwise addition of 3 µl aliquots of the modifier up to a total volume of 20 µl. Finally, the sample was dialyzed against 0.02 M phosphate buffer at pH8 for 48 h. To determine the number of the modified Lysine residues, the number of the free amino groups was measured following the standard methods (Steer and Merrill, 1995). Three Lysine residues out of the total of the six Lysines were found to be modified (Hassani et al., 2006; Chattopadhyay and Mazumdar, 2000).

RESULTS AND DISCUSSION

pH-dependent enzymatic activity

Enzymatic activity versus different pH values was recorded with a maximum value for this parameter between pH 6 and pH 8 (Figure 2), which is decreased on either side of this pH range for both Horseradish peroxidase (HRP) and the modified form (MHRP) of this enzyme. As it may be supposed, the general trend is a bell shaped graph, however, the path following by MHRP is under the one recorded by HRP, which implies that modification process induced some irreversible structural changes to the native form of the enzyme affecting the catalytic activity of MHRP. The impact of pHs 4 to 10 on kinetic parameters for both forms are also listed in Table 1. These parameters implied that some changes must be occurred in the protein structure due to the chemical modification. Analysis of the kinetic constants for MHRP at pH 5 showed that the modified form of the enzyme at this pH possesses the maximum value for the K_m, and the minimum value for k_{cat}/K_m. As shown in Table 1, the values of the different kinetic constants for MHRP at pH 5 generally differ from those recorded in other experiments. It could be suggested that the chemical modification significantly affect the catalytic constant (k_{cat}), and the substrate affinity (K_m) of MHRP at this pH. Based on the results the catalytic efficiency (k_{cat}/K_m) of MHRP at pH 5 is significantly lower than that of the native and modified form at the other pH values. It can be related to the pH-induced conformational changes in the secondary/tertiary, or both structures. The probability of the molten globule-like structure formation could not be also excluded, which usually arise at slightly acidic conditions and mildly ionic strengths (Pina et al., 2001; Carvalho et al., 2003).

pH-dependent structural changes

Circular dichroism spectroscopy has been used to provide more information on the structural changes of the protein molecule (Shanon et al., 1966). We have also used these data to detect the occurred changes in the HRP structure using the following protocol:

(1) Far-UV CD (190–250 nm): changes in the secondary structure of the apoprotein.
(2) Near-UV CD (250–320 nm): changes in the tertiary structure of the apoprotein.

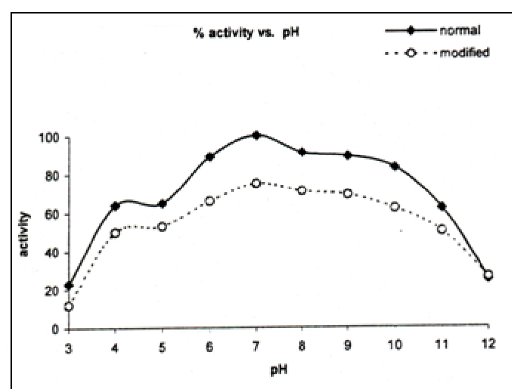

Figure 2: Enzymatic activity of HRP and MHRP versus different pH values. The general trend is a bell shaped graph with the maximum activity in pH values between 6 – 8 for both forms, however, modification induced some structural changes to the MHRP that caused its catalytic activity to be suppressed.

EXCLI Journal 2014;13:611-622 – ISSN 1611-2156
Received: March 07, 2014, accepted: April 14, 2014, published: May 27, 2014

Table 1: Kinetic parameters for the native and modified horseradish peroxidase in pH values between 4 - 10

pH	HRP			MHRP		
	K_m(mM)	k_{cat}(min^{-1})	k_{cat} /K_m(mM^{-1}min^{-1})	K_m(mM)	k_{cat}(min^{-1})	k_{cat} /K_m (mM^{-1}min^{-1})
4	1.30	1985	1533	0.66	1570	2378
5	2.50	1477	583	4.05	1185	292
6	0.45	2399	5292	0.65	2398	3654
7	0.79	2895	3640	0.89	2688	2990
8	1.15	2770	2400	1.82	2564	1404
9	0.85	2688	3180	1.55	2316	1488
10	2.25	1446	642	0.55	1322	2411

(3) Visible CD (350–450 nm): dissociation of the prosthetic heme group from the apoprotein and structural changes in regions that surrounding the prosthetic heme.

Figure 3 shows the pH-dependent secondary structural changes for both forms of the enzyme. Comparisons indicated that the percentage of the secondary structure of MHRP is similar to that of the HRP at pH 5. Thus the modification was inert to the secondary structure at least in this pH value. However, according to the Near-UV, and Visible CD spectra it could be concluded that the percentage of the tertiary structure for MHRP in comparison to the HRP has been reduced in some extent (Figures 4 and 5). Tertiary structural changes have been also assessed by means of the fluorescence spectroscopy, using Trp residues as fluorophores to measure the introduced changes in the local microenvironment of hydrophobic patches (Welinder, 1979; Schippers and Dekkers, 1981; Takakuwa et al., 1985; Protasevich et al., 1997; Trinder, 1969). It is known that the intrinsic fluorescence of the enzyme is dependent on the fluorescence energy transferring from a Trp residue into the heme prosthetic group (Dixon and Perham, 1968; Fields, 1971). Accordingly, changes in the structure and folding of the heme cavity of the enzyme may affect the orientation or the distance between the heme group and the Trp residue, which can also alter the intensity of the intrinsic fluorescence emission of the en-

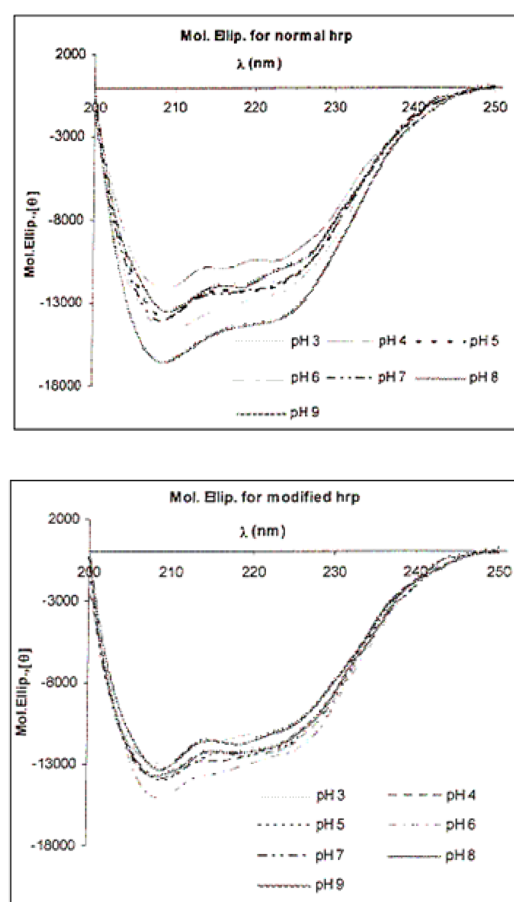

Figure 3: Far-UV CD spectra for the HRP **(a)**, and MHRP **(b)** in different pH values. Comparisons indicate that the secondary structures of HRP and MHRP are almost similar in pH values 5, 7, 9, and 10. In pH 6 the secondary structure of HRP is reduced comparing to that of the MHRP. Although, in pH 8 the secondary structure of the native form is enhanced comparing to the modified enzyme.

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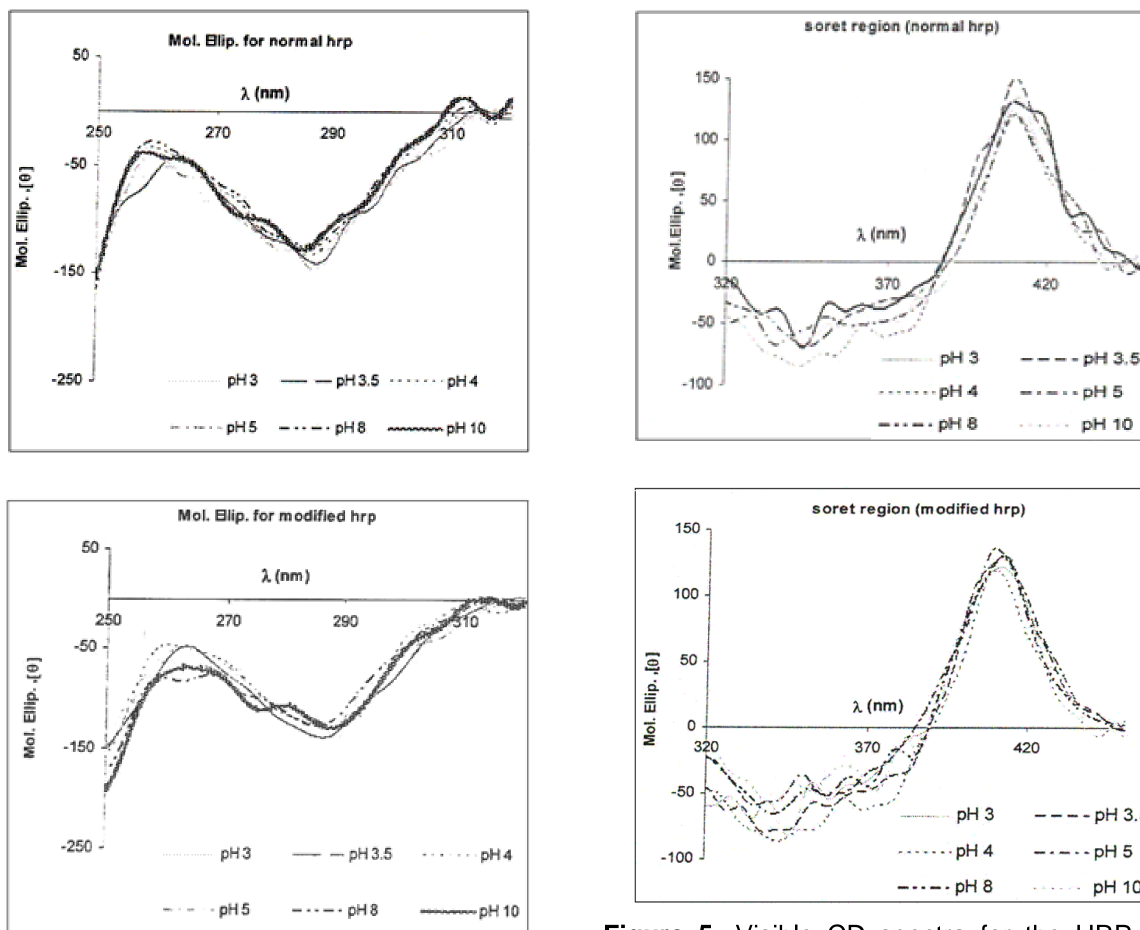

Figure 4: Near-UV CD spectra for the HRP **(a),** and MHRP **(b)** in different pH values. Generally, both forms of the enzymes are similar in the tertiary structure, with an exception in pH 5 that the structure of MHRP is experiencing some decrease in comparison to the native form.

Figure 5: Visible CD spectra for the HRP **(a),** and MHRP **(b)** in different pH values. Comparing figures a and b indicates that a reduction in the enzyme's structure around heme region for the modified form could be detected in comparison to the native form in different pH values.

zyme. It is known that HRP contains one Trp residue (Trp 117) and five tyrosine residues (Strickland, 1968), which all of them have fluorescence emission. We chose Trp residues to probe conformational changes of the enzyme as described in other studies (Dixon and Perham, 1968). Figure 6 illustrates the fluorescence spectra at some selected pH values for the native (Figure 6a) and modified (Figure 6b) forms of the enzyme at room temperature with an excitation wavelength of 295 nm. As Figure 6b shows, the intensity of Trp fluorescence emission sharply decreases for MHRP at pH 5. It may be due to the changes in the relative orientation or distance between the heme and the Trp residue, leading to an increase in the efficiency of the energy transfer from Trp into the heme as a quenching prosthetic group (Dixon and Perham, 1968; Fraczkiewicz and Braun, 1998). Conformational changes in the secondary structure of the enzyme were also followed by assessing the alterations in the CD spectra at 222 nm. Tertiary structural changes also recorded by the fluorescence emission at 340 nm. Figure 7 shows the impact of different pH values on the conformational changes of the secondary and tertiary structure for the native (a) and modified (b) forms of the enzyme. As Figure 7 illustrates, the CD intensity at 222 nm was almost unchanged in the pH range under investigation, which means almost no variations in the secondary structure of the enzyme has been recorded.

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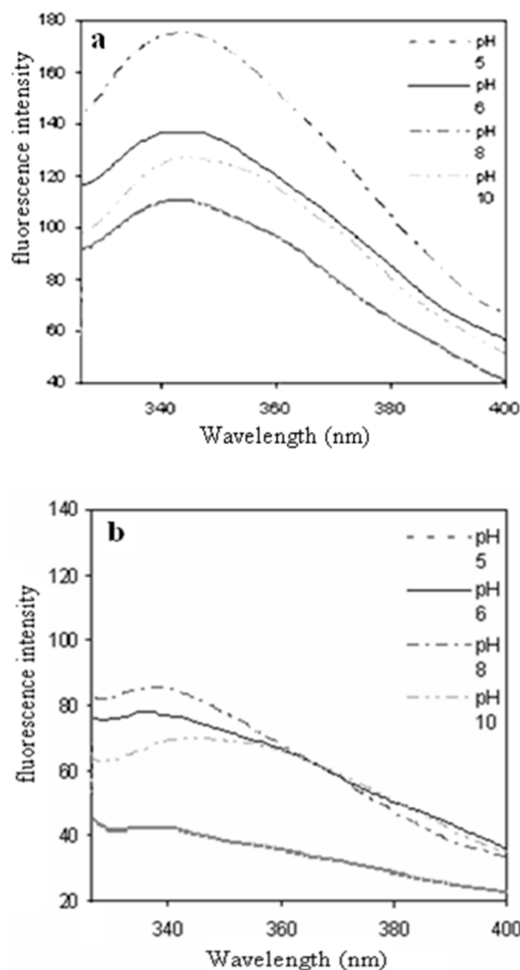

Figure 6: Tryptophan fluorescence emission spectra upon excitation at 295 nm for **(a)** native, and **(b)** modified HRP in some selected pH values. Measurements were carried out at 25° C with protein concentrations of 150 µM in 0.02 M phosphate buffer.

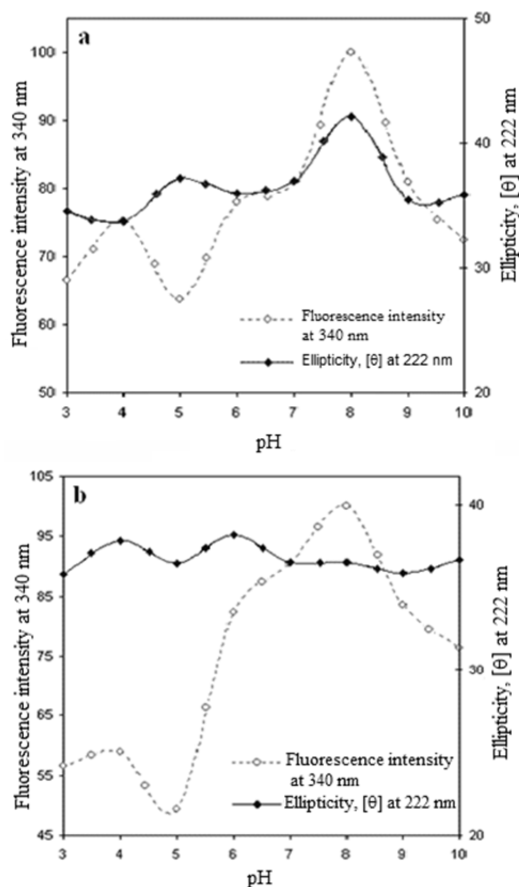

Figure 7: Correlation between the tertiary and the secondary structure of the **(a)** native and **(b)** modified forms of HRP followed by recording Trp emission at 340 nm. Trp fluorescence was induced by excitation of the sample at 295 nm and the CD signals at 222 nm of the enzymes were obtained in some selected pH values. Fluorescence and CD experiments were carried out at 25° C with protein concentrations of 150 µM and 0.15 mg/ml respectively, in 0.02 M phosphate buffer

However, an interesting trend arises at pH 5 for the modified enzyme in which the secondary structure is the same as its content at pH 7, while its tertiary structure shows the minimum value in the pH range under investigation. The pH-dependent structural changes and kinetic constants of horseradish peroxidase indicate that the molten globule-like form of MHRP occurs at pH 5, revealing that these structural changes are mediated by the protonation of the ionizable groups. It may be proposed that upon slightly acidic conditions, intramolecular charge repulsion is the main driving force for partial unfolding of the chemically modified protein, followed by the exposure of the hydrophobic patches out of the hydrophobic core of the protein and getting accessible to the polar water molecules of the surrounding solvent. To confirm the exposure of the hydrophobic patches of horseradish peroxidase in the modified form at pH 5, ANS was further used as a widely used hydrophobic reporter compound. This probe has been known to be a useful detector

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for trapping the molten globular states, which can bind to the hydrophobic patches of the molten globule structures more strongly than the native structures, with an increasing in its fluorescence intensity (Hosseinkhani et al., 2004). The results of the ANS experiments (Figure 8) imply an enhancement of the ANS fluorescence emission for the modified form of horseradish peroxidase at pH 5 (Figure 8b), which confirms that a molten globule-like structure has been detected.

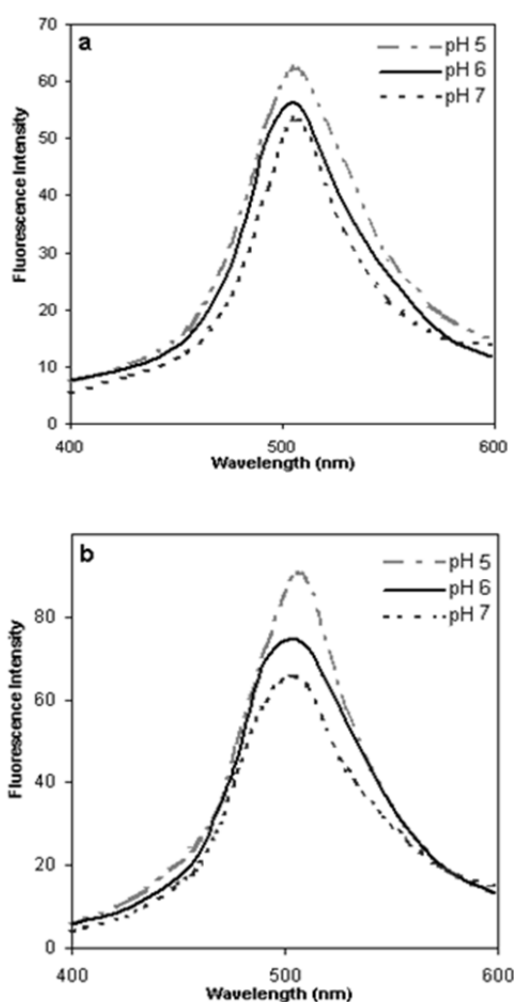

Figure 8: ANS fluorescence emission spectra upon excitation at 380 nm for the **(a)** native and **(b)** modified HRP in some selected pH values. The final concentration of the ANS in the enzyme solutions was 50 µM and the molar ratio of protein to ANS was 1:50. Measurements were performed at 25° C in 0.02 M phosphate buffer. For more details please see materials and methods section.

Thermal unfolding of MHRP

Circular dichroism measurement of the heme prosthetic group is an informative strategy to study the introduced structural changes of the heme containing proteins. Accordingly, thermally induced structural phase transitions of MHRP at pH 5 were monitored by means of circular dichroism. Figure 9 shows the observed alterations in the ellipticity of MHRP at 222 nm in the slightly acidic conditions, which indicates a two-state transition pattern for the secondary structure of MHRP (curve b). CD spectra in the visible region were further monitored to determine the effects of the temperature-induced conformational changes on the tertiary structure, particularly around the heme cavity (curve a). Based on the data, two separated phases of the structural transitions for the secondary structure can be recognized. The first phase starts at around 30° C and continues to around 65° C, following by another phase of unfolding that starts at 65° C and reaches to the fully unfolded structure at around 90° C. However, according to Figure 9 curve a, three separated trends for the conformational transitions in the tertiary structure of the enzyme could be recognized. The first phase from 30 to around 45° C, the second one from 45 to at around 70° C and finally from 70 to 90° C. Comparing curves a, and b implying that a structural intermediate state of MHRP exists between temperatures 45° C and 70° C. Considering different phases of the thermally induced unfolding of MHRP demonstrates two distinct patterns in the structural transition. From Figure 9, a specific structural region between 45 to around 70° C is detectable that is associated with a significant change in the tertiary structure of the enzyme, at least around the active site, accompanied by almost little variations in the secondary structure. The second phase of the transition in the secondary structure also is related to the complete removal of the heme prosthetic group out of the enzyme's active site as detected by the complete absence of the CD signals at 407 nm. We propose that modification of the ε-

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amino groups of the Lysine residues (pK_a around 10) alters the global electrostatic charge of the enzyme from positive into the negative charge, which consequently leads to the presence of an intermediate molten globule-like structure at pH 5. This idea is also supported by an obvious change in the intrinsic fluorescence spectra and the disappearance of the emission intensity at 340 nm because of the exposure of Trp 117 to the polar solvent (Figure 6). These data are also in good agreement with the previous studies (Hassani et al., 2006; Hosseinkhani et al., 2004). Based on the results, the transition to a molten globule is accompanied by the loss of the tertiary interactions, while almost all of the secondary structure preserved. The results of the thermal CD also revealed that unlike the melting of the secondary structure, temperature-induced unfolding of the tertiary structure leads to the existence of an intermediate state, which promotes formation of a molten globule-like structure of Horseradish peroxidase at pH 5. Irreversible thermal inactivation experiments (Figure 10) revealed that the modified enzyme keeps its catalytic activity during the time, which means that the modification process is also capable of increasing the half-life of the enzyme.

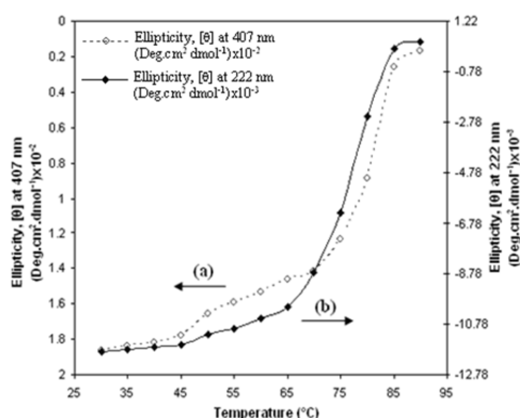

Figure 9: Thermal unfolding of MHRP at pH 5 followed by CD signals at 407 nm and 222 nm for probing structural phase transitions around heme cavity and secondary structure, respectively. **(a)**: CD signals for the tertiary structure around heme prosthetic group and **(b)**: CD signals for the secondary structure. CD spectra were measured using a sample concentration of 2 mg/ml in 0.02 M phosphate buffer at each pH and temperature.

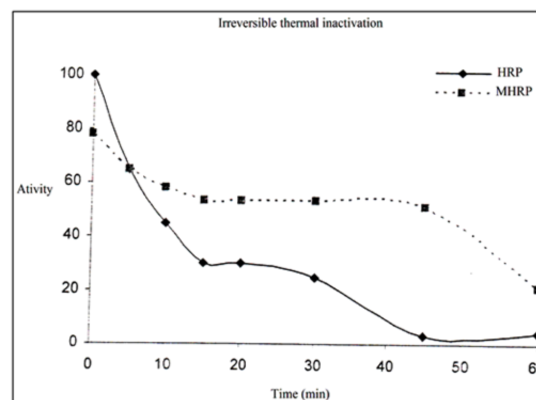

Figure 10: Irreversible thermal inactivation of HRP and MHRP which is recorded for 60 minutes at pH 5. The incubation environment set at 70 °C. The modified enzyme keeps its catalytic activity during the time, which means that the modification process is capable of increasing the half-life of the enzyme.

CONCLUSIONS

In the present study, a comprehensive investigation on kinetics and structural properties of Horseradish peroxidase has been performed. This study is important at least from two points of view. Technologically, Horseradish peroxidases have been used in industry and a wide range of biotechnological applications as well. Therefore, stabilizing experiments, like the specific chemical modification process that performed and analyzed in the present work, may clarify the impact of denaturants such as acidic/basic pH situations, and high temperatures on the functionality/efficiency of the enzyme molecule. According to the irreversible thermal inactivation, the catalytic activity of MHRP remains during the time period of the experiment, which is not detected for the native enzyme. Thus, it seems that the modification protocol is capable of increasing the half-life of the enzyme. On the other hand, there was limited data on the conformational changes and structural characteristics of this modified Horseradish peroxidase in comparison to the native form of this enzyme. According to our study, a modified structure (MHRP) of the enzyme at pH 5 with almost intact secondary structure, while reduced tertiary structure was detected that is the general feature of a

molten globule-like structure. Despite of some conformational changes in the tertiary structure of MHRP at pH 5, this modified form still keeps its catalytic activity to some extent besides enhanced thermal stability during the time period of the experiment. These findings are also in agreement to that of by Vamvaca and colleagues (2004) claiming that a molten globular state does not necessarily preclude efficient catalytic activity.

ACKNOWLEDGEMENTS

We thank the reviewers for valuable comments. Special thanks also go to Dr. Reza Hassan-Sajedi for the comments. This work was supported by the Research Council of Tarbiat Modares University.

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Received: March 07, 2014, accepted: April 14, 2014, published: May 27, 2014

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