## **Guanidine Hydrochloride-Induced Denaturation of Bovine Serum Albumin: A Comparative Study and Analysis using Different Probes**

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**ABSTRACT** The denaturation of bovine serum albumin (BSA) by guanidine hydrochloride (GdnHCl) showed a single-step, two-state transition, when monitored by different probes such as intrinsic fluorescence at 338 and 333 nm after excitation at 280 and 295 nm respectively, UV difference spectral signal at 288 nm, 1-anilinonaphthalene-8-sulphonate (ANS) fluorescence at 470 nm after excitation at 380 nm, bromophenol blue (BPB)-induced difference spectral signal at 619 nm and  $\lambda_{max}$  of positive difference spectral signal of BPB-BSA complex. A comparison of the denaturation curves obtained with the above mentioned probes showed differences in the requirement of GdnHCl concentration for the transition to start and complete. The values for the mid-point of denaturation transition and free energy change associated with GdnHCl denaturation ( $\Delta G_D^{H2O}$ ) also varied from each other, using different probes.

(Bovine serum albumin, bromophenol blue, denaturation, fluorescence measurements, guanidine hydrochloride)

## **INTRODUCTION**

Most of the proteins require specific interactions to fold into their globular conformation from a structure-less denatured state to their biologically-active native state. This makes the study of protein folding an interesting subject to get insight into the basic mechanism and producing large amount of refolded proteins from inclusion bodies [1, 2]. In order to understand the protein folding/denaturation phenomena, many biophysical techniques such as kinetics, fluorescence, ellipticity, ultraviolet (UV)difference spectroscopy and 1-anilinonaphthalene-8-sulphonate (ANS) fluorescence measurements [3, 4, 5, 6] have been used and conclusions have been drawn regarding conformational stability of proteins and pathways of denaturation/folding [7, 8, 9]. It is necessary to choose appropriate probe to monitor conformational changes in search of intermediate(s) formed, if any, during protein denaturation process [10, 11, 12]. Different probes like UV absorption difference at 287 nm [5], fluorescence at 340 nm upon excitation at 282 nm [13], tryptophan fluorescence upon excitation at 295 nm [5], ellipticity at 222 nm [6, 14]. ANS fluorescence [6], differential calorimetry [15] and bromophenol blue (BPB) binding [16] have been successfully used by several groups in studying the denaturation of a single chain multidomain protein, serum albumin. Denaturation of serum albumin has been reported to follow a single-step [6, 13], two-step [6, 11, 12, 13] or multiple-step [17] transition depending upon the reaction conditions and probes used. For example, urea denaturation of serum albumin has been shown to follow a single-step, two-state transition when studied by UV difference spectroscopy at 293 nm [5] but became two-step, three-state transition involving one intermediate when monitored by fluorescence, UV difference spectroscopy at 288 nm and ellipticity measurements [5, 6, 14]. Similarly, denaturation of serum albumin with guanidine hydrochloride (GdnHCl) which has about the same effect as urea on protein conformation [18], has been reported to follow both single-step and two-step transitions [6, 12]. Both ANS and BPB binding probes have shown the urea/GdnHCl denaturation of serum albumin as a single-step transition [6, 16]. Although denaturation of serum *Malaysian Journal of Science* **27** (2): 9 – 17 (2008)

## REFERENCES

- Shakhnovich, E. and Fersht, A. R. (1998). Folding and binding. *Curr. Opin. Struct. Biol.* 8: 65 – 67.
- Fink, A. L. (1998). Protein aggregation: Folding aggregates, inclusion bodies and amyloid. *Fold Des.* 3: 9 – 23.
- Nolting, B., Golbik, R. and Fersht, A. R. (1995). Submilisecond events in protein folding. *Proc. Natl. Acad. Sci. USA* 92: 10668 – 10672.
- Plaxo, K. W. and Dobson, C. M. (1996). Time-resolved biophysical methods in the study of protein folding. *Curr. Opin. Struct. Biol.* 6: 630 – 636.
- Khan, M. Y., Agarwal, S. K. and Hangloo, S. (1987). Urea-induced structural transformations in bovine serum albumin. J. Biochem. 102: 31 3 – 317.
- Muzammil, S., Kumar, Y. and Tayyab, S. (2000). Anion-induced stabilization of human serum albumin prevents the formation of intermediate during urea denaturation. *Proteins: Struct. Funct. Genet.* 40: 29 38.
- Kamatari, Y. O., Konno, T., Kataoka, M. and Akasaka, K. (1998). The methanol-induced transition and the expanded helical conformation in hen lysozyme. *Protein Sci.* 7: 681 – 688.
- Jansens, A., van Duijn, E. and Braakman, I. (2002). Coordinated nonvectorial folding in a newly synthesized multidomain protein. *Science* 298: 2401 – 2402.
- Konno, T. (1998). Conformational diversity of acid-denatured cytochrome c studied by a matrix analysis of far-UV CD spectra. *Protein Sci.* 7: 975 – 982.
- Muzammil, S., Kumar, Y. and Tayyab, S. (2000). Anion-induced refolding of human serum albumin under low pH conditions. *Biochim. Biophys. Acta* 1476: 139 – 148.
- Tayyab, S., Ahmad, B., Kumar, Y. and Khan, M. M. (2002). Salt-induced refolding in different domains of partially folded bovine serum albumin. *Int. J. Biol. Macromol.* **30**: 17 – 22.
- Santra, M. K., Banerjee, A., Krishnakumar, S. S., Rahman, O. and Panda, D. (2004). Multiple-probe analysis of folding and unfolding pathways of human serum albumin. *Eur. J. Biochem.* 271: 1789 – 1797.
- 13. Ahmad, N. and Qasim, M. A. (1995). Fatty acid binding to bovine serum albumin

prevents formation of intermediate during denaturation. *Eur. J. Biochem.* **227**: 563 – 565.

- Kumar, Y., Muzammil, S. and Tayyab, S. (2005). Influence of fluoro, chloro and alkyl alcohols on the folding of human serum albumin. *J. Biochem.* 138: 335 341.
- Tavirani1, M. R., Moghaddamnia, S. H., Ranjbar, B., Amani, M. and Marashi, S. A. (2006). Conformational study of human serum albumin in pre-denaturation temperatures by differential scanning calorimetry, circular dichroism and UV spectroscopy. J. Biochem. Mol. Biol. 39: 530 – 536.
- Halim, A. A. A., Kadir, H. A. and Tayyab, S. (2008). Bromophenol blue binding as a probe to study urea and guanidine hydrochloride denaturation of boyine serum albumin. *J. Biochem.* 144: 33 38.
- Flora, K., Brennan, J. D., Baker, G. A., Doddy, M. A. and Bright, F. V. (1998). Unfolding of acrylodan-labeled human serum albumin probed by steady state and time-resolved fluorescence method. *Biophys.* J. 75: 1084 – 1096.
- Viallet, P. M., Dinh, T. V., Ribou, A. C., Vigo, J. and Salmon, J. M. (2000). Native fluorescence and mag-indo-1-protein interaction as tools for probing unfolding and refolding sequences of the bovine serum albumin subdomain in the presence of guanidine hydrochloride. *J. Protein Chem.* 19: 431 – 439.
- Pace, C. N., Vajdos, F., Fee, L., Grimsley, G. and Gray, T. (1995). How to measure and predict the molar absorption coefficient of a protein. *Protein Sci.* 4: 2411 – 2423.
- Mulqueen, P. M. and Kronman, M. J. (1982). Binding of naphthalene dyes to the N and A conformers of bovine α-lactalbumin. *Arch. Biochem. Biophys.* 215: 28 – 39.
- Lakowics, J. (1983). Principle of Fluorescence spectroscopy. Plenum Press, New York, pp. 341 – 365.
- Sulkowska, A., Rownicka, J., Pozycka, J., Bojko, B. and Sulkowski, W. W. (2005). The effect of concentration of guanidine hydrochloride on the sulfasalazine-serum albumin complex. *J. Mol. Struct.* 744 – 747: 775 – 779.
- 23. Sogami, M. and Ogura, S. (1973). Structural transitions of bovine plasma albumin. Location of tyrosyl and tryptophyl residues

Malaysian Journal of Science 27 (2): 9-17 (2008)

by solvent perturbation difference spectra. *J. Biochem.* **73**: 324 – 334.

- Stryer, L. (1965). The interaction of naphthalene dye with apomyglobin and apohemoglobin. A fluorescence probe of non-polar binding sites. *J. Mol. Biol.* 13: 482 – 495.
- 25. Farruggia, B. and Pico, G. A. (1999). Thermodynamic features of the chemical and thermal denaturations of human serum albumin. *Int. J. Biol. Macromol.* **26**: 317 – 323.
- 26. Hayakawa, I., Kajihara, J., Morikawa, K., Oda, M. and Fujio, Y. (1992). Denaturation of bovine serum albumin (BSA) and ovalbumin by high pressure, heat and chemicals. J. Food. Sci. 57: 288 – 292.
- Kosa, T., Maruyama, T. and Otagiri, M. (1998). Species differences of serum albumin: II. Chemical and thermal stability. *Pharm. Res.* 15: 449 454.
- Efink, M. R. (1991). Fluorescence techniques for studying protein structure. *Methods Biochem. Anal.* 35: 127 – 205.
- 29. Eftink, M. R. and Ghiron, C. A. (1977). Exposure of tryptophanyl residues and protein dynamics. *Biochemistry* **16**: 5546 – 5551.
- Peterman, B. F. and Laidler, K. J. (1980). Study of reactivity of tryptophan residue in serum albumin and lysozyme by Nbromosuccinamide fluorescence quenching. *Arch. Biochem. Biophys.* 199: 158 – 164.
- 31. Peters, T. Jr. (1996). All About Albumin. Biochemistry, Genetics and Medical Applications. Academic Press Inc., New York.