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Structural analysis of α-helix rich intermediate of bovine β-lactoglobulin on its folding pathway

Zie-jie Qin¹, Yoshitaka Matsumura², Masaji Shinjo² and Hiroshi Kihara^{2*} ¹ Department of Chemistry and Biochemistry, University of California at Santa Cruz, 95064, USA ² Department of Physics, Kansai Medical University, Hirakata 573-1136, Japan

Introduction

We have reported that bovine β -lactoglobulin (BLG) took two intermediates (I₁ and I₂) on its early stage of folding at -28°C in the presence of 45% ethylene glycol¹). Both I₁ and I₂ are rich in α -helix, though I₂ is richer. To investigate structures of the intermediates, we have done cryo-stopped-flow monitored by X-ray solution scattering method. The shape of I₂ was calculated by GASBOR program²).

Experiment

BLG forms dimmer at physiological condition and dissociate to monomer at acidic pH. At pH2, we performed time-resolved refolding experiments by circular dichroism (CD) and X-ray solution scattering methods. Experiments were done with stopped flow apparatus.

<u>Result</u>

Fig.1 shows θ_{222} in kinetic CD measurements^{1,3)}. α -helix rich intermediate (I₁ and I₂) are shown. The burst phase corresponds to I₁ After increase of α -helix, θ_{222} keeps constant (I₂) at this temperature. Fig .2 shows time-resolved radius of gyration (*R*g). The first one point corresponds to the transient point from I₁ to I₂. But the difference of I₁ and I₂ is not clear. From X-ray scattering profile, we calculated molecular structure of I₂ by GASBOR program.²⁾ Fig.3 shows the calculated shape. Two domains structure was obtained.

The native structure of BLG looks to be composed of two divided structures as shown in Fig.4. It seems plausible that the two local structures were formed in the early stage of protein folding and combined into the native structure.

References

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- 2) Svergun et al. (2001) Biophys. J, 80, 2946-2953
- 3) Matsumura *et al.* (2008) Biophys. Chem. 134, 84-92

*kihara@makino.kmu.ac.jp



Fig.1 kinetic CD measurement of θ_{222} at -28°C^{1,3)}



Fig.2 *R*g obtained by kinetic SAXS measurement at -28°C. Broken line shows averaged *R*g from 185ms to 2985ms.



Fig.3 Reconstructed structures of I_2 (1085-1485ms) calculated by GASBOR.²⁾ Large spheres express C α atoms and small spheres express water molecules.





90 degree rotated

Fig.4 BLG crystal structure on PDB. (PDB ID: 1BEB :extract chain A) Red: 1-75 residues, Green: 74-85 residues, Blue: 86-160 residues