

Structure and Properties of Weak Interaction in Protein

related with Frozen Food

Takahide Yamaguchi¹, Attila Taborosi¹, Alexandros Koutsioubas², Henrich Freilinghaus², and Takamitsu Kohzuma¹

¹Institute of Quantum Beam Science, Ibaraki University

²Julich Centre for Neutron Science at Heinz Maier-Leibnitz Zentrum
Forschungszentrum Julich GmbH

The freezing technology is very important for keeping freshness of many variety of foods. Many of fishery companies are utilizing very deep freezing method (less than -40 °C) by the reason of the low temperature damage of fish meat at normal frozen conditions. The low temperature damage of fish might be caused by cold denaturation of protein. The kinetic studies on the protein folding/unfolding have been performed to know the mechanisms [1,2]. The quite limited number of structure the folding/unfolding intermediate has so far been reported.

In this presentation we would like to report the unfolding protein structure of cytochrome *c* from *Alcaligenes xylosoxidans* to add further knowledge of the protein denaturation (unfolding) mechanisms.

The alkaline structure transition mechanism of a typical four- α -helices bundle heme-protein, Cytochrome *c* (Cyt *c*) was provided on the basis of the solution structures determined by small angle neutron scattering (SANS) under the various pH conditions. The four- α -helices bundle Cyt *c* was transited to an intermediate structure of “open-bundle” structure like a joint-clubs consisting of the four- α -helices connected by small loops at pD \simeq 13, and the unique alkaline structure was suggested as the structure of unfolding intermediate. The structure of Cyt *c* is compactly folded ($R_g = 18 \text{ \AA}$ for dimer of Cyt *c*) at neutral-weak alkaline pH, and the compactly folded Cyt *c* is transited to extremely large “open-bundle” Cyt *c* at pD \simeq 13 and unstructured random coil at pD = 1.7 ($R_g = 25 \text{ \AA}$). This is the first report for the determination of the alkaline transit intermediate structure of Cyt *c* at pD \simeq 13. The solution structures involving such intermediate structure determined by SANS allowed us to add a good example for the general explanation of protein folding/unfolding mechanisms.

1. T. Kiefhaber, *Proc. Natl. Acad. Sci.* **1995**, 92, 9029–9033.

2. G. A. Elöve, A. K. Bhuya, H. Roder, *Biochemistry* **1994**, 33, 6925–6935.