Hayuki SUGIMOTO, Ph.D.

Assistant Professor

Program: Life and Food Sciences

Area: Applied Life and Food Sciences

Undergraduate: Dept. of Applied Biological Chemistry

Professional Expertise

Her research focuses on the mechanisms of protein stability and folding. A newly synthesized protein folds into a unique three-dimensional structure to acquire a biologically active conformation. A folding process is controlled only by rules of physical chemistry, and an unfolded protein folds into its final folded conformation which is the thermodynamically most stable state. Native proteins are only marginally stable in physiological conditions. Therefore, removal of a disulfide bond or a noncovalent interaction often makes a large contribution to protein folding and stability. She aims to understand the biophysical basis of the protein folding and stability. Her research is based on an expertise in calorimetry and it remains a strong feature of her work.

Research Fields of Interest

Effects of the disulfide bond on the stability and folding of the starch binding domain of *Aspergillus niger* glucoamylase

She has investigated effects of disulfide bonds on protein folding and stability. The starch-binding domain (SBD) of *Aspergillus niger* glucoamylase is a small globular protein consisting of 110 amino acid residues. The protein molecule contains a single disulfide bond bridging the N- and C-termini of the protein, C3-C98 (Fig. 1a). This disulfide bond played important roles not only in the structural stability but also in the refolding of a thermally unfolded SBD. In the case of the wild-type SBD, no intermediates accumulated during refolding. The thermal unfolding of a disulfide-deficient mutant of SBD, C3G/C98G, was also reversible; however, it was shown that before folding into the native state, a kinetically trapped metastable intermediate is formed by a rapid lowering of temperature from a higher temperature. Her most recent work using NMR spectroscopy showed that in the intermediate, the aromatic cluster at the surface is structurally less organized, whereas the interior of the protein has relatively rigid, native-like side-chain packing (Fig. 1b). More detailed biophysical analysis is now being carried out to reveal why the non-native interactions are formed in the intermediate and how the precise interactions develop around the cluster.

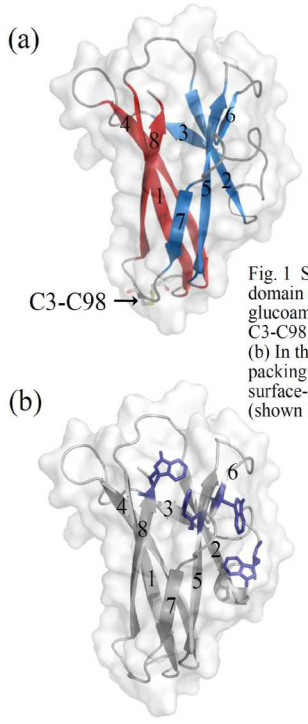

Fig. 1 Structure of the starch-binding domain of *Aspergillus niger* glucoamylase (a) The disulfide bond, C3-C98, is shown as sticks. (b) In the intermediate, native-like packing was lost at the surface-exposed aromatic cluster (shown in navy).

Education

2008: Ph.D., Graduate School of Bioresources, Mie University, Japan
2005: M.S. in Biostudies, Graduate School of Biostudies, Kyoto University, Japan
2003: B.S. in Bioresources, Faculty of Bioresources, Mie University, Japan

Professional Societies and Activities

1. The Japan Society of Calorimetry and Thermal Analysis
2. Protein Science Society of Japan
3. The Biophysical Society of Japan
4. The Japanese Biochemical Society
5. Japan Society of Bioscience, Biotechnology, and Agrochemistry
6. The Protein Society (USA)

Major Publications

Papers

[1] "NMR analysis of a kinetically trapped intermediate of a disulfide-deficient mutant of the starch-binding domain of glucoamylase", *J. Mol. Biol.*, 412, 304-315, 2011.

[2] "Kinetically trapped metastable intermediate of a disulfide-deficient mutant of the starch-binding domain of glucoamylase", *Protein Sci.*, 18, 1715-1723, 2009.

[3] "Phosphocholine-containing glycosyl inositol-phosphoceremides from *Trichoderma viride* induce defense responses in cultured rice cells", *Biosci. Biotechnol. Biochem.*, 73, 74-80, 2009.

[4] "Structural and thermodynamic analyses of solute-binding protein from *Bifidobacterium longum* specific for core 1 disaccharide and lacto-*N*-biose", *J. Biol. Chem.*, 283, 13165-13173, 2008.

[5] "Stabilization mechanism of chloride ion on thermal denaturation of *Arthrobacter* sarcosine oxidase", *Netsu Sokutei*, 35, 76-80, 2008.

[6] "Thermodynamic effects of disulfide bond on thermal unfolding of the starch-binding domain of *Aspergillus niger* glucoamylase", *Biosci. Biotechnol. Biochem.*, 71, 1535-1541, 2007.

[7] "Differential scanning calorimetry of the effects of Ca2+ on the thermal unfolding of *Pseudomonas cepacia* lipase", *Biosci. Biotechnol. Biochem.*, 67, 207-210, 2003.